



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 12, 2024 – 03:17 PM EDT

PDB ID : 1KGY  
Title : Crystal Structure of the EphB2-ephrinB2 complex  
Authors : Himanen, J.P.; Rajashankar, K.R.; Lackmann, M.; Cowan, C.A.; Henkemeyer, M.; Nikolov, D.B.  
Deposited on : 2001-11-28  
Resolution : 2.70 Å (reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Xtrriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

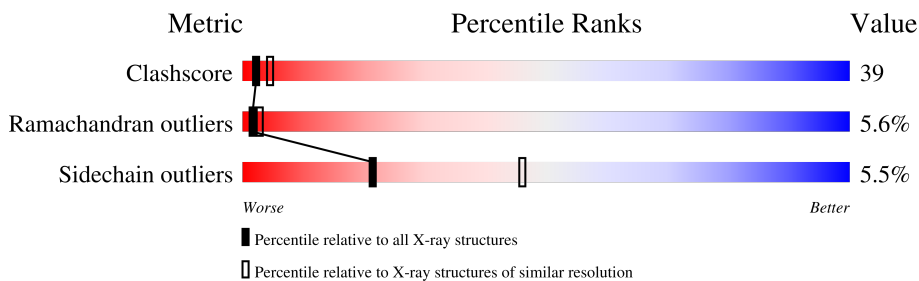
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	181	
1	B	181	
1	C	181	
1	D	181	
2	E	138	
2	F	138	
2	G	138	
2	H	138	

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 10260 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called EPHRIN TYPE-B RECEPTOR 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	181	1463	925	252	274	12	0	0	0
1	B	181	1463	925	252	274	12	0	0	0
1	C	181	1463	925	252	274	12	0	0	0
1	D	181	1463	925	252	274	12	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	27	ALA	VAL	CONFLICT	UNP P54763
B	227	ALA	VAL	CONFLICT	UNP P54763
C	427	ALA	VAL	CONFLICT	UNP P54763
D	627	ALA	VAL	CONFLICT	UNP P54763

- Molecule 2 is a protein called EPHRIN-B2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	E	138	1102	706	179	210	7	0	0	0
2	F	138	1102	706	179	210	7	0	0	0
2	G	138	1102	706	179	210	7	0	0	0
2	H	138	1102	706	179	210	7	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	1049	GLY	GLN	CONFLICT	UNP P52800
F	1249	GLY	GLN	CONFLICT	UNP P52800
G	1449	GLY	GLN	CONFLICT	UNP P52800
H	1649	GLY	GLN	CONFLICT	UNP P52800

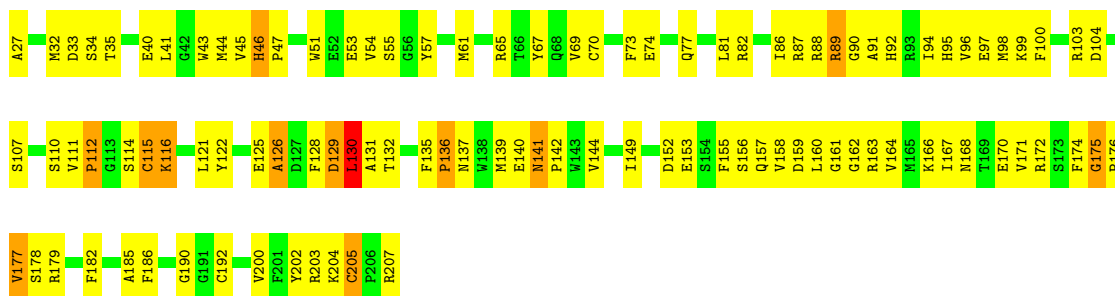
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

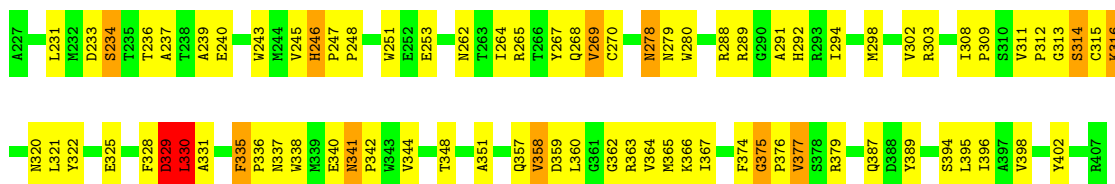
- Molecule 1: EPHRIN TYPE-B RECEPTOR 2

Chain A:  43% 50% 7%



- Molecule 1: EPHRIN TYPE-B RECEPTOR 2

Chain B:  56% 37% 6%

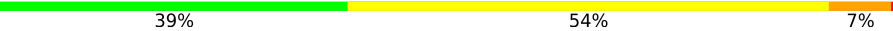


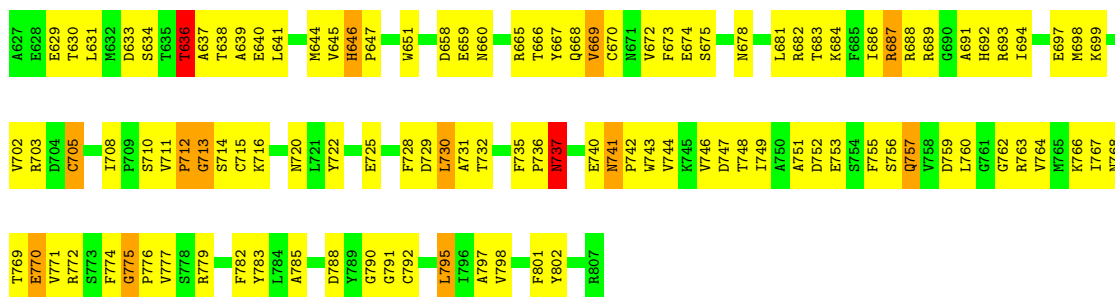
- Molecule 1: EPHRIN TYPE-B RECEPTOR 2

Chain C:  52% 39% 7%



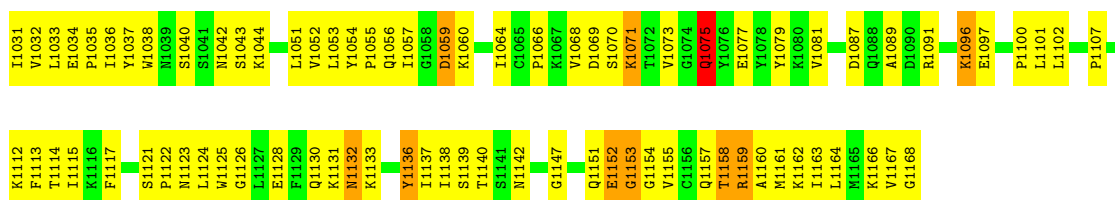
- Molecule 1: EPHRIN TYPE-B RECEPTOR 2

Chain D:  39% 54% 7%



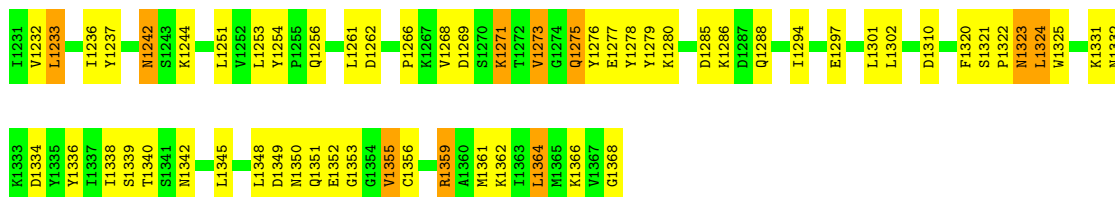
• Molecule 2: EPHRIN-B2

Chain E:  42% 51% 7%



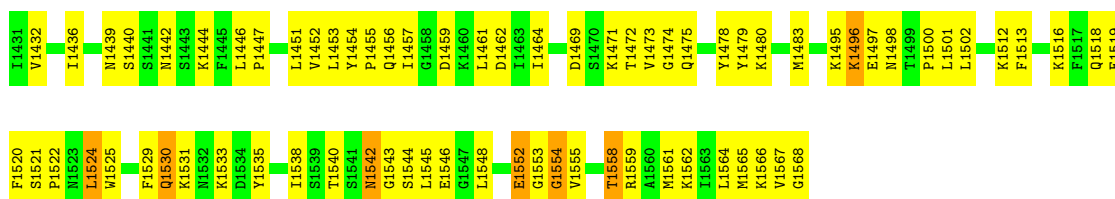
• Molecule 2: EPHRIN-B2

Chain F:  57% 36% 7%



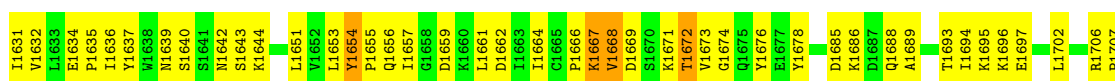
• Molecule 2: EPHRIN-B2

Chain G:  48% 47% 5%



• Molecule 2: EPHRIN-B2

Chain H:  43% 51% 6%



D1708	Q1709	D1710	V1711	K1712	F1713	T1714	I1715	K1716	F1717	Q1718	E1719	F1720	S1721	P1722	M1723	L1724	W1725	E1728	F1729	Q1730	K1731	N1732	Y1736	I1737	I1738	N1742	G1743	S1744	L1745	E1746	G1747	L1748	Q1751	E1752	V1755	T1758	R1759	A1760	M1761	K1762	I1763	K1766	V1767	G1768
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## 4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	78.00Å 78.00Å 78.00Å 69.00° 75.00° 69.00°	Depositor
Resolution (Å)	25.00 – 2.70	Depositor
% Data completeness (in resolution range)	(Not available) (25.00-2.70)	Depositor
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	CNS	Depositor
R, $R_{free}$	0.243 , 0.296	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	10260	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	wwPDB-VP



## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.43	0/1502	0.74	0/2035
1	B	0.46	0/1502	0.72	0/2035
1	C	0.44	0/1502	0.74	0/2035
1	D	0.41	0/1502	0.69	0/2035
2	E	0.42	0/1125	0.75	0/1519
2	F	0.42	0/1125	0.74	0/1519
2	G	0.47	0/1125	0.79	0/1519
2	H	0.43	0/1125	0.75	0/1519
All	All	0.43	0/10508	0.74	0/14216

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1463	0	1389	206	0
1	B	1463	0	1389	93	0
1	C	1463	0	1389	87	0
1	D	1463	0	1389	112	0
2	E	1102	0	1096	137	0
2	F	1102	0	1096	67	0
2	G	1102	0	1096	78	0
2	H	1102	0	1096	154	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	10260	0	9940	790	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 39.

All (790) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128:PHE:CZ	2:H:1639:ASN:HB3	1.84	1.12
1:A:128:PHE:HB3	2:H:1637:TYR:CD2	1.86	1.10
1:A:89:ARG:HA	2:H:1671:LYS:CG	1.83	1.09
1:A:89:ARG:N	2:H:1671:LYS:NZ	2.02	1.08
1:A:135:PHE:CE2	2:H:1634:GLU:OE2	2.08	1.06
2:E:1031:ILE:HG23	2:E:1059:ASP:HB3	1.37	1.05
1:A:166:LYS:HB3	2:E:1124:LEU:HD22	1.33	1.05
1:D:646:HIS:HB3	1:D:647:PRO:HD3	1.36	1.02
2:G:1555:VAL:H	2:G:1558:THR:HB	1.24	1.01
1:A:46:HIS:HB3	1:A:47:PRO:HD3	1.42	1.01
1:A:166:LYS:CB	2:E:1124:LEU:HD22	1.90	0.99
2:F:1268:VAL:HG22	2:F:1276:TYR:HB2	1.44	0.99
1:A:89:ARG:HA	2:H:1671:LYS:HG3	1.00	0.97
1:A:89:ARG:N	2:H:1671:LYS:HZ2	1.59	0.97
1:B:341:ASN:HB3	1:B:342:PRO:HD3	1.47	0.96
2:H:1759:ARG:HH11	2:H:1759:ARG:HB3	1.29	0.96
1:B:246:HIS:HB3	1:B:247:PRO:HD3	1.44	0.96
1:A:89:ARG:CA	2:H:1671:LYS:HG3	1.96	0.94
1:A:130:LEU:HB3	2:H:1637:TYR:CE1	2.04	0.93
1:A:158:VAL:CG1	2:E:1121:SER:HB3	1.99	0.92
1:A:166:LYS:HB2	2:E:1124:LEU:CD2	1.99	0.92
1:C:446:HIS:HB3	1:C:447:PRO:HD3	1.48	0.92
1:A:96:VAL:HG21	1:A:121:LEU:HD21	1.53	0.90
1:B:357:GLN:HB3	1:B:363:ARG:HH11	1.33	0.90
2:F:1285:ASP:HB3	2:F:1288:GLN:HG3	1.53	0.90
2:H:1672:THR:HG22	2:H:1673:VAL:H	1.35	0.90
1:A:129:ASP:HB3	2:H:1637:TYR:OH	1.72	0.90
1:A:166:LYS:CB	2:E:1124:LEU:CD2	2.51	0.87
2:E:1155:VAL:H	2:E:1158:THR:HB	1.38	0.87
1:A:103:ARG:HB2	2:E:1122:PRO:HA	1.54	0.86
2:E:1036:ILE:HD11	2:E:1053:LEU:HD11	1.55	0.86
1:A:130:LEU:CA	2:H:1637:TYR:HE1	1.87	0.86
2:F:1355:VAL:HG13	2:F:1361:MET:HB2	1.58	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:LEU:HB3	2:H:1637:TYR:CD1	2.10	0.85
1:D:770:GLU:HG3	1:D:772:ARG:HH21	1.40	0.85
1:A:88:ARG:NH1	1:A:178:SER:HA	1.91	0.85
1:A:89:ARG:H	2:H:1671:LYS:HZ3	1.19	0.85
2:E:1096:LYS:HG2	2:E:1097:GLU:HG3	1.58	0.85
1:C:606:PRO:O	1:C:607:ARG:HB2	1.76	0.85
2:G:1542:ASN:ND2	2:G:1544:SER:H	1.75	0.84
1:A:65:ARG:NH2	2:E:1112:LYS:HD2	1.92	0.84
1:A:89:ARG:H	2:H:1671:LYS:NZ	1.67	0.84
1:A:128:PHE:CB	2:H:1637:TYR:CD2	2.62	0.83
1:A:135:PHE:CE1	2:H:1634:GLU:OE1	2.31	0.83
1:A:167:ILE:HG21	2:E:1125:TRP:CZ3	2.13	0.82
1:D:691:ALA:HB2	1:D:802:TYR:CD2	2.15	0.82
2:E:1068:VAL:HA	2:E:1073:VAL:HG11	1.58	0.82
1:B:289:ARG:HD3	2:G:1471:LYS:HD2	1.59	0.82
1:A:55:SER:OG	2:E:1114:THR:N	2.12	0.82
2:E:1040:SER:HA	2:E:1161:MET:HE1	1.62	0.82
2:E:1130:GLN:HB2	2:E:1133:LYS:HG3	1.61	0.82
1:D:760:LEU:HD23	2:H:1725:TRP:HA	1.63	0.81
1:A:158:VAL:HG11	2:E:1121:SER:HB3	1.63	0.81
1:A:107:SER:HB3	1:A:156:SER:OG	1.79	0.81
1:A:128:PHE:HB3	2:H:1637:TYR:CE2	2.15	0.81
2:H:1719:GLU:OE2	2:H:1731:LYS:HE3	1.81	0.81
1:A:128:PHE:CE2	2:H:1639:ASN:HB3	2.15	0.80
2:H:1716:LYS:O	2:H:1718:GLN:HG2	1.80	0.80
2:H:1730:GLN:NE2	2:H:1731:LYS:HG2	1.96	0.80
1:D:722:TYR:HE2	1:D:740:GLU:HG3	1.47	0.80
2:H:1730:GLN:HE21	2:H:1731:LYS:HG2	1.48	0.79
1:A:135:PHE:CD2	2:H:1634:GLU:OE2	2.35	0.79
1:D:752:ASP:H	1:D:768:ASN:ND2	1.81	0.79
2:G:1456:GLN:HE22	2:G:1568:GLY:HA2	1.48	0.78
1:A:130:LEU:N	2:H:1637:TYR:CE1	2.51	0.78
1:A:55:SER:CB	2:E:1114:THR:H	1.97	0.78
1:A:55:SER:H	2:E:1114:THR:HB	1.47	0.78
1:A:65:ARG:NH2	2:E:1112:LYS:CD	2.47	0.78
1:A:128:PHE:CE2	2:H:1639:ASN:CB	2.67	0.77
1:B:288:ARG:HD3	1:B:377:VAL:HG12	1.66	0.77
1:C:451:TRP:HA	1:C:469:VAL:HG13	1.66	0.77
1:B:231:LEU:HD23	1:B:289:ARG:HH21	1.48	0.77
1:B:289:ARG:HH11	2:G:1471:LYS:HE2	1.49	0.77
1:C:539:MET:HG3	1:C:541:ASN:HB3	1.66	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:1738:ILE:HG22	2:H:1762:LYS:HG2	1.67	0.76
1:C:516:LYS:HD3	1:C:590:GLY:HA3	1.67	0.76
1:D:753:GLU:H	1:D:768:ASN:HD21	1.34	0.76
1:A:141:ASN:HB3	1:A:142:PRO:CD	2.16	0.75
2:E:1056:GLN:HE22	2:E:1168:GLY:C	1.90	0.75
1:C:483:THR:HG22	1:C:484:LYS:O	1.87	0.75
2:E:1031:ILE:CG2	2:E:1059:ASP:HB3	2.16	0.75
1:A:130:LEU:HA	2:H:1635:PRO:HG3	1.67	0.75
1:A:44:MET:HG2	1:A:82:ARG:HH21	1.53	0.74
1:A:135:PHE:HB3	1:A:136:PRO:HD3	1.70	0.74
1:D:683:THR:HG22	1:D:684:LYS:N	2.03	0.74
2:E:1140:THR:HG21	2:E:1151:GLN:C	2.08	0.74
2:F:1237:TYR:HD2	2:F:1266:PRO:HG3	1.52	0.73
2:E:1040:SER:HA	2:E:1161:MET:CE	2.18	0.73
1:A:91:ALA:HB2	1:A:202:TYR:CD2	2.23	0.73
2:F:1359:ARG:HB2	2:F:1361:MET:HG3	1.71	0.73
1:A:141:ASN:HB3	1:A:142:PRO:HD2	1.71	0.73
1:A:88:ARG:HH11	1:A:178:SER:HA	1.53	0.73
1:A:130:LEU:CA	2:H:1637:TYR:CE1	2.71	0.73
1:A:166:LYS:HB2	2:E:1124:LEU:HD21	1.70	0.72
1:D:646:HIS:HB3	1:D:647:PRO:CD	2.16	0.72
2:H:1631:ILE:HB	2:H:1659:ASP:OD1	1.90	0.72
2:E:1087:ASP:OD1	2:E:1091:ARG:HD2	1.89	0.72
1:C:446:HIS:HB3	1:C:447:PRO:CD	2.20	0.71
2:G:1516:LYS:O	2:G:1518:GLN:HG2	1.91	0.71
2:H:1755:VAL:HA	2:H:1758:THR:HB	1.71	0.71
2:G:1559:ARG:HD3	2:G:1561:MET:HE2	1.70	0.71
2:H:1702:LEU:HD22	2:H:1711:VAL:HG12	1.73	0.71
1:A:125:GLU:HB3	1:A:179:ARG:HG3	1.72	0.71
2:E:1064:ILE:HG12	2:E:1112:LYS:HE3	1.71	0.71
2:E:1069:ASP:H	2:E:1073:VAL:CG2	2.05	0.70
2:H:1742:ASN:C	2:H:1742:ASN:HD22	1.94	0.70
1:D:735:PHE:O	1:D:737:ASN:N	2.25	0.70
1:A:130:LEU:HA	2:H:1637:TYR:HE1	1.56	0.70
1:A:114:SER:HB3	1:A:116:LYS:HE3	1.72	0.70
1:A:128:PHE:CB	2:H:1637:TYR:CG	2.73	0.70
2:H:1636:ILE:HG13	2:H:1661:LEU:HD11	1.73	0.70
1:D:672:VAL:HB	1:D:712:PRO:HG3	1.73	0.70
2:E:1140:THR:HG21	2:E:1152:GLU:N	2.07	0.70
1:B:357:GLN:HB3	1:B:363:ARG:NH1	2.07	0.70
1:D:683:THR:HG22	1:D:684:LYS:O	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:1533:LYS:HB2	2:G:1533:LYS:NZ	2.07	0.69
2:E:1123:ASN:ND2	2:E:1124:LEU:O	2.25	0.69
1:A:57:TYR:OH	2:E:1101:LEU:HD23	1.93	0.69
1:B:337:ASN:HB2	1:B:342:PRO:HG2	1.72	0.69
1:A:130:LEU:CB	2:H:1637:TYR:CE1	2.76	0.69
1:D:752:ASP:H	1:D:768:ASN:HD22	1.40	0.69
2:E:1155:VAL:HG22	2:E:1159:ARG:HH21	1.56	0.69
1:A:128:PHE:CZ	2:H:1639:ASN:CB	2.69	0.69
2:E:1054:TYR:CE2	2:E:1166:LYS:HD2	2.28	0.69
2:F:1338:ILE:HG22	2:F:1362:LYS:HB2	1.74	0.69
1:A:128:PHE:CD2	2:H:1666:PRO:HG2	2.28	0.68
2:G:1529:PHE:O	2:G:1530:GLN:HB2	1.93	0.68
1:B:357:GLN:O	1:B:358:VAL:HB	1.94	0.68
2:G:1542:ASN:HD22	2:G:1543:GLY:N	1.91	0.68
1:D:714:SER:HB2	1:D:716:LYS:NZ	2.09	0.68
1:D:770:GLU:CG	1:D:772:ARG:HH21	2.06	0.68
1:B:302:VAL:HG21	1:B:351:ALA:HB2	1.75	0.68
2:H:1678:TYR:HB3	2:H:1748:LEU:HD13	1.76	0.68
1:C:564:VAL:O	1:C:567:ILE:HG22	1.93	0.68
2:E:1140:THR:O	2:E:1140:THR:HG22	1.92	0.67
2:H:1640:SER:HA	2:H:1761:MET:CE	2.24	0.67
1:A:46:HIS:HB3	1:A:47:PRO:CD	2.22	0.67
1:A:135:PHE:CZ	2:H:1634:GLU:OE1	2.47	0.67
1:C:563:ARG:HD3	1:C:566:LYS:HG3	1.76	0.67
2:F:1271:LYS:N	2:F:1271:LYS:HD2	2.09	0.67
1:A:65:ARG:HH21	2:E:1112:LYS:CD	2.06	0.67
1:C:525:GLU:HB3	1:C:579:ARG:HB2	1.77	0.67
2:E:1069:ASP:H	2:E:1073:VAL:HG21	1.59	0.67
1:D:756:SER:H	1:D:763:ARG:HH12	1.43	0.67
1:A:162:GLY:O	2:E:1125:TRP:NE1	2.28	0.66
1:A:130:LEU:HD13	2:H:1634:GLU:OE2	1.95	0.66
1:B:308:ILE:H	1:B:308:ILE:HD12	1.59	0.66
2:H:1640:SER:HA	2:H:1761:MET:HE1	1.75	0.66
1:A:54:VAL:HG22	2:E:1060:LYS:NZ	2.10	0.66
2:E:1158:THR:HG22	2:E:1159:ARG:N	2.11	0.66
1:A:82:ARG:NH1	1:A:131:ALA:HB1	2.11	0.66
2:F:1237:TYR:CD2	2:F:1266:PRO:HG3	2.31	0.66
1:A:132:THR:CG2	2:H:1635:PRO:HD3	2.25	0.65
1:A:65:ARG:HH21	2:E:1112:LYS:HD2	1.60	0.65
2:E:1042:ASN:O	2:E:1044:LYS:N	2.28	0.65
1:A:157:GLN:HB3	1:A:163:ARG:HH12	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:692:HIS:O	1:D:776:PRO:HA	1.95	0.65
1:D:699:LYS:HB2	1:D:797:ALA:HB3	1.79	0.65
1:C:488:ARG:HD2	1:C:577:VAL:HG23	1.79	0.65
2:F:1278:TYR:HB3	2:F:1348:LEU:HD13	1.78	0.65
1:A:130:LEU:HA	2:H:1635:PRO:CG	2.27	0.64
1:A:167:ILE:HD12	1:A:167:ILE:C	2.18	0.64
2:G:1442:ASN:OD1	2:G:1444:LYS:HD3	1.97	0.64
2:F:1236:ILE:HD11	2:F:1253:LEU:HD11	1.78	0.64
1:B:292:HIS:O	1:B:376:PRO:O	2.15	0.64
1:A:89:ARG:N	2:H:1671:LYS:HZ3	1.80	0.64
2:H:1718:GLN:HE21	2:H:1721:SER:HB2	1.63	0.64
1:A:122:TYR:HE2	1:A:140:GLU:CG	2.10	0.64
2:G:1440:SER:HA	2:G:1561:MET:HE2	1.79	0.64
2:F:1285:ASP:HB2	2:F:1288:GLN:HE21	1.61	0.64
2:G:1542:ASN:HD22	2:G:1542:ASN:C	1.98	0.64
2:H:1724:LEU:HD23	2:H:1725:TRP:N	2.13	0.64
1:A:135:PHE:O	1:A:137:ASN:N	2.31	0.64
1:A:130:LEU:O	2:H:1635:PRO:CG	2.46	0.64
1:B:289:ARG:CD	2:G:1471:LYS:HD2	2.27	0.64
1:A:159:ASP:O	2:E:1125:TRP:CD1	2.51	0.63
1:C:516:LYS:HD2	1:C:516:LYS:N	2.13	0.63
2:E:1131:LYS:O	2:E:1132:ASN:HB2	1.98	0.63
2:F:1331:LYS:O	2:F:1332:ASN:HB2	1.98	0.63
2:H:1685:ASP:HB2	2:H:1688:GLN:HE21	1.62	0.63
1:B:357:GLN:NE2	1:B:363:ARG:HD2	2.13	0.63
2:H:1759:ARG:HB3	2:H:1759:ARG:NH1	2.08	0.63
2:H:1668:VAL:O	2:H:1668:VAL:HG13	1.99	0.62
1:B:322:TYR:HE2	1:B:340:GLU:HG3	1.64	0.62
2:H:1637:TYR:HD2	2:H:1666:PRO:HG3	1.63	0.62
2:H:1742:ASN:HD22	2:H:1743:GLY:N	1.96	0.62
2:G:1501:LEU:C	2:G:1502:LEU:HD12	2.20	0.62
1:D:722:TYR:CE2	1:D:740:GLU:HG3	2.34	0.62
1:D:683:THR:CG2	1:D:684:LYS:N	2.62	0.62
1:D:763:ARG:HD3	1:D:766:LYS:HG3	1.80	0.62
2:E:1154:GLY:H	2:E:1157:GLN:HB3	1.64	0.62
1:A:33:ASP:O	1:A:35:THR:N	2.30	0.62
1:D:703:ARG:HG2	2:H:1722:PRO:HA	1.82	0.62
2:H:1685:ASP:HB3	2:H:1688:GLN:HG3	1.81	0.62
2:E:1057:ILE:N	2:E:1057:ILE:HD12	2.15	0.62
1:A:27:ALA:HB1	1:A:203:ARG:HH12	1.65	0.62
1:A:167:ILE:HG21	2:E:1125:TRP:CE3	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:725:GLU:HB3	1:D:779:ARG:HG3	1.82	0.62
2:G:1554:GLY:O	2:G:1555:VAL:HB	1.99	0.62
1:B:341:ASN:HB3	1:B:342:PRO:CD	2.24	0.61
1:C:502:VAL:HG21	1:C:551:ALA:HB2	1.81	0.61
1:B:246:HIS:HB3	1:B:247:PRO:CD	2.27	0.61
2:F:1237:TYR:HD2	2:F:1266:PRO:CG	2.12	0.61
1:A:159:ASP:O	2:E:1125:TRP:HD1	1.83	0.61
2:G:1559:ARG:HH11	2:G:1559:ARG:HG2	1.65	0.61
2:H:1672:THR:HG22	2:H:1673:VAL:N	2.11	0.61
1:A:130:LEU:HB2	2:H:1635:PRO:HG2	1.81	0.61
2:G:1483:MET:HE2	2:G:1535:TYR:HB3	1.81	0.61
1:B:364:VAL:O	1:B:367:ILE:HG12	1.99	0.61
2:F:1338:ILE:HG22	2:F:1362:LYS:CB	2.30	0.61
1:C:431:LEU:HD22	1:C:489:ARG:HH11	1.66	0.61
2:E:1031:ILE:HG23	2:E:1059:ASP:CB	2.23	0.61
1:B:240:GLU:OE1	1:B:265:ARG:NH2	2.34	0.60
1:D:651:TRP:HA	1:D:668:GLN:O	2.01	0.60
1:D:728:PHE:O	1:D:730:LEU:HG	2.01	0.60
1:B:246:HIS:CB	1:B:247:PRO:HD3	2.27	0.60
2:H:1654:TYR:CE2	2:H:1766:LYS:HD3	2.36	0.60
2:G:1559:ARG:HG2	2:G:1559:ARG:NH1	2.16	0.60
2:G:1469:ASP:OD2	2:G:1471:LYS:HB2	2.00	0.60
1:A:116:LYS:HD2	1:A:116:LYS:N	2.16	0.60
1:C:517:GLU:HB3	1:C:551:ALA:HB3	1.84	0.60
2:G:1524:LEU:HD13	2:G:1525:TRP:CD1	2.36	0.60
1:A:87:ARG:HB2	1:A:89:ARG:NH1	2.17	0.60
1:B:325:GLU:HB3	1:B:379:ARG:HG3	1.84	0.60
1:B:251:TRP:HA	1:B:269:VAL:HG13	1.84	0.60
1:C:489:ARG:HE	2:F:1271:LYS:HZ1	1.48	0.60
1:D:646:HIS:CB	1:D:647:PRO:HD3	2.23	0.59
2:G:1440:SER:HA	2:G:1561:MET:CE	2.32	0.59
1:A:57:TYR:CZ	2:E:1113:PHE:HE1	2.20	0.59
2:E:1054:TYR:N	2:E:1055:PRO:HD3	2.17	0.59
1:D:720:ASN:HD22	1:D:748:THR:HA	1.68	0.59
2:E:1037:TYR:HD2	2:E:1066:PRO:HG3	1.67	0.59
2:F:1280:LYS:HE2	2:F:1349:ASP:OD1	2.02	0.59
1:C:483:THR:CG2	1:C:484:LYS:N	2.64	0.59
2:E:1054:TYR:HA	2:E:1166:LYS:O	2.02	0.59
2:G:1483:MET:CE	2:G:1535:TYR:HB3	2.32	0.59
1:B:233:ASP:O	1:B:398:VAL:O	2.21	0.59
2:F:1261:LEU:HD23	2:F:1262:ASP:N	2.18	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:1657:ILE:HD12	2:H:1731:LYS:HE2	1.85	0.59
2:H:1664:ILE:HG12	2:H:1712:LYS:HG2	1.83	0.59
1:B:294:ILE:HD12	1:B:294:ILE:N	2.18	0.59
1:C:451:TRP:CA	1:C:469:VAL:HG13	2.32	0.59
1:B:335:PHE:HB3	1:B:336:PRO:HD3	1.85	0.58
1:A:103:ARG:NH1	2:E:1121:SER:O	2.36	0.58
1:D:749:ILE:HD12	1:D:749:ILE:N	2.19	0.58
2:G:1542:ASN:HD22	2:G:1544:SER:H	1.50	0.58
1:A:97:GLU:HG3	1:A:171:VAL:HG22	1.85	0.58
2:F:1340:THR:OG1	2:F:1351:GLN:HA	2.04	0.58
2:H:1667:LYS:HG3	2:H:1709:GLN:HA	1.86	0.58
1:A:174:PHE:O	1:A:175:GLY:O	2.22	0.58
2:F:1242:ASN:C	2:F:1242:ASN:HD22	2.07	0.58
1:A:57:TYR:CZ	2:E:1113:PHE:CE1	2.91	0.58
2:G:1552:GLU:H	2:G:1552:GLU:CD	2.07	0.58
1:A:158:VAL:HG22	2:E:1128:GLU:OE2	2.03	0.58
2:F:1273:VAL:O	2:F:1273:VAL:HG22	2.04	0.58
1:D:752:ASP:N	1:D:768:ASN:ND2	2.51	0.57
1:A:54:VAL:HG22	2:E:1060:LYS:HZ2	1.69	0.57
1:D:694:ILE:HD13	1:D:777:VAL:HG21	1.85	0.57
1:D:694:ILE:HG12	1:D:782:PHE:CE2	2.39	0.57
1:B:231:LEU:HD21	1:B:402:TYR:CE2	2.39	0.57
1:D:712:PRO:HG2	1:D:713:GLY:H	1.68	0.57
1:A:164:VAL:HA	2:E:1125:TRP:CZ2	2.39	0.57
1:D:659:GLU:CD	1:D:659:GLU:H	2.07	0.57
2:H:1759:ARG:HH11	2:H:1759:ARG:CB	2.12	0.57
1:A:46:HIS:CB	1:A:47:PRO:HD3	2.27	0.57
1:C:541:ASN:HB3	1:C:542:PRO:CD	2.33	0.57
2:H:1653:LEU:O	2:H:1654:TYR:HB2	2.04	0.57
2:H:1745:LEU:C	2:H:1747:GLY:N	2.55	0.57
1:B:253:GLU:CD	1:B:265:ARG:HH21	2.07	0.57
1:B:302:VAL:HG21	1:B:351:ALA:CB	2.34	0.57
1:B:316:LYS:HD2	1:B:316:LYS:N	2.19	0.57
2:G:1456:GLN:OE1	2:G:1531:LYS:HE2	2.04	0.57
1:D:741:ASN:HB3	1:D:742:PRO:CD	2.35	0.57
2:H:1642:ASN:O	2:H:1644:LYS:N	2.38	0.56
1:A:92:HIS:O	1:A:176:PRO:O	2.23	0.56
1:B:291:ALA:HB2	1:B:402:TYR:CD2	2.40	0.56
1:C:552:ASP:H	1:C:568:ASN:ND2	2.02	0.56
2:F:1285:ASP:CB	2:F:1288:GLN:HE21	2.17	0.56
2:H:1662:ASP:OD2	2:H:1714:THR:HA	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:374:PHE:O	1:B:375:GLY:O	2.23	0.56
1:A:135:PHE:CE2	2:H:1634:GLU:CD	2.78	0.56
1:B:278:ASN:HD21	1:B:280:TRP:HE1	1.52	0.56
1:C:516:LYS:HD2	1:C:516:LYS:H	1.69	0.56
1:D:673:PHE:CE2	1:D:710:SER:HB3	2.41	0.56
2:G:1454:TYR:CE2	2:G:1566:LYS:HD3	2.41	0.56
1:A:98:MET:SD	1:A:121:LEU:HD22	2.46	0.56
1:D:630:THR:HA	1:D:801:PHE:HB3	1.88	0.56
1:D:729:ASP:O	1:D:731:ALA:N	2.39	0.56
1:C:535:PHE:HB3	1:C:536:PRO:HD3	1.88	0.56
1:D:633:ASP:HB3	1:D:636:THR:CG2	2.35	0.56
1:D:774:PHE:O	1:D:775:GLY:O	2.24	0.56
2:F:1355:VAL:CG1	2:F:1361:MET:HB2	2.34	0.56
2:H:1745:LEU:C	2:H:1747:GLY:H	2.08	0.56
1:C:529:ASP:O	1:C:530:LEU:HG	2.07	0.55
1:D:633:ASP:O	1:D:798:VAL:O	2.23	0.55
2:F:1323:ASN:ND2	2:F:1325:TRP:H	2.04	0.55
2:F:1345:LEU:C	2:F:1345:LEU:HD13	2.25	0.55
1:C:433:ASP:O	1:C:598:VAL:O	2.24	0.55
1:C:489:ARG:HE	2:F:1271:LYS:NZ	2.04	0.55
1:B:231:LEU:HD21	1:B:402:TYR:HE2	1.71	0.55
1:D:645:VAL:HG11	1:D:651:TRP:O	2.06	0.55
1:A:122:TYR:HE2	1:A:140:GLU:HG3	1.70	0.55
1:A:114:SER:O	1:A:115:CYS:HB3	2.06	0.55
1:B:357:GLN:H	1:B:363:ARG:HH12	1.54	0.55
2:H:1755:VAL:HG21	2:H:1761:MET:SD	2.46	0.55
1:B:308:ILE:HD12	1:B:308:ILE:N	2.20	0.55
1:D:760:LEU:HD23	2:H:1725:TRP:CA	2.33	0.55
2:G:1555:VAL:N	2:G:1558:THR:HB	2.08	0.55
1:A:128:PHE:HB2	2:H:1637:TYR:CG	2.41	0.54
1:A:130:LEU:CB	2:H:1637:TYR:HE1	2.18	0.54
1:A:163:ARG:O	2:E:1124:LEU:HD21	2.06	0.54
1:D:639:ALA:O	1:D:665:ARG:NE	2.40	0.54
2:G:1436:ILE:HD11	2:G:1453:LEU:HD11	1.89	0.54
1:A:116:LYS:CD	1:A:116:LYS:H	2.20	0.54
2:E:1069:ASP:HB3	2:E:1073:VAL:HG23	1.88	0.54
1:A:137:ASN:HB2	1:A:142:PRO:HG3	1.89	0.54
1:C:488:ARG:HH11	1:C:491:ALA:H	1.55	0.54
1:D:698:MET:O	1:D:769:THR:HA	2.06	0.54
1:D:763:ARG:HB3	1:D:766:LYS:CG	2.37	0.54
1:C:487:ARG:HD2	2:F:1271:LYS:HD3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:567:ILE:HD13	1:C:568:ASN:N	2.22	0.54
1:D:740:GLU:O	1:D:740:GLU:HG2	2.06	0.54
2:G:1502:LEU:HD11	2:G:1513:PHE:HB2	1.89	0.54
1:C:483:THR:HG22	1:C:484:LYS:N	2.21	0.54
1:A:135:PHE:CZ	2:H:1634:GLU:CD	2.81	0.54
2:G:1464:ILE:HG12	2:G:1512:LYS:HG2	1.90	0.54
2:G:1479:TYR:HE2	2:G:1555:VAL:HG21	1.73	0.54
1:A:70:CYS:HA	1:A:192:CYS:HA	1.90	0.54
2:H:1653:LEU:N	2:H:1653:LEU:HD22	2.23	0.54
1:A:163:ARG:O	1:A:166:LYS:HB2	2.08	0.54
1:B:288:ARG:CD	1:B:377:VAL:HG12	2.38	0.54
2:H:1724:LEU:HD23	2:H:1725:TRP:H	1.71	0.54
1:B:325:GLU:OE2	1:B:377:VAL:HA	2.07	0.53
1:A:45:VAL:HG11	1:A:51:TRP:O	2.08	0.53
1:A:77:GLN:HG3	1:A:190:GLY:HA2	1.90	0.53
2:H:1742:ASN:C	2:H:1742:ASN:ND2	2.61	0.53
1:B:357:GLN:H	1:B:363:ARG:NH1	2.06	0.53
1:D:714:SER:HB2	1:D:716:LYS:HZ1	1.70	0.53
2:E:1124:LEU:O	2:E:1125:TRP:HB2	2.09	0.53
2:G:1495:LYS:O	2:G:1496:LYS:HB2	2.07	0.53
1:A:89:ARG:CA	2:H:1671:LYS:NZ	2.71	0.53
1:C:446:HIS:CB	1:C:447:PRO:HD3	2.30	0.53
2:E:1137:ILE:N	2:E:1137:ILE:HD12	2.23	0.53
2:F:1355:VAL:HG22	2:F:1359:ARG:CG	2.39	0.53
2:G:1453:LEU:O	2:G:1454:TYR:HB2	2.09	0.53
2:G:1457:ILE:HD13	2:G:1519:GLU:CG	2.39	0.53
1:C:472:VAL:HG13	1:C:515:CYS:HB2	1.91	0.53
2:G:1555:VAL:HG12	2:G:1561:MET:HB2	1.90	0.53
2:H:1667:LYS:HB2	2:H:1667:LYS:NZ	2.23	0.53
1:A:103:ARG:HD3	2:E:1121:SER:O	2.09	0.53
1:D:674:GLU:HG2	1:D:675:SER:H	1.74	0.53
2:E:1051:LEU:HD23	2:E:1052:VAL:N	2.23	0.53
2:G:1455:PRO:O	2:G:1567:VAL:HA	2.09	0.53
1:A:65:ARG:HH21	2:E:1112:LYS:CG	2.22	0.53
1:B:357:GLN:O	1:B:358:VAL:CB	2.57	0.53
1:C:445:VAL:HG11	1:C:451:TRP:O	2.09	0.53
2:E:1036:ILE:CD1	2:E:1053:LEU:HD11	2.36	0.53
2:E:1140:THR:HG23	2:E:1153:GLY:O	2.09	0.53
1:B:246:HIS:HB2	1:B:338:TRP:CD2	2.43	0.53
1:B:330:LEU:HD12	1:B:331:ALA:N	2.24	0.53
1:C:497:GLU:HG3	1:C:571:VAL:HG22	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:1559:ARG:HD3	2:G:1561:MET:CE	2.38	0.53
2:H:1736:TYR:CD1	2:H:1736:TYR:N	2.77	0.53
2:E:1069:ASP:HB3	2:E:1071:LYS:O	2.09	0.52
2:F:1286:LYS:HE2	2:F:1336:TYR:OH	2.09	0.52
2:H:1654:TYR:H	2:H:1655:PRO:HD3	1.75	0.52
1:A:116:LYS:HD2	1:A:116:LYS:H	1.73	0.52
1:C:541:ASN:ND2	1:C:542:PRO:HD3	2.24	0.52
1:D:670:CYS:HA	1:D:791:GLY:O	2.09	0.52
1:D:766:LYS:HB2	2:H:1724:LEU:HD11	1.91	0.52
2:E:1057:ILE:HD12	2:E:1057:ILE:H	1.75	0.52
1:D:674:GLU:HG2	1:D:675:SER:N	2.23	0.52
2:F:1323:ASN:HD22	2:F:1324:LEU:N	2.08	0.52
2:G:1529:PHE:O	2:G:1530:GLN:CB	2.52	0.52
1:A:128:PHE:CE2	2:H:1666:PRO:HG2	2.44	0.52
1:C:535:PHE:O	1:C:537:ASN:N	2.42	0.52
2:H:1667:LYS:O	2:H:1668:VAL:HB	2.09	0.52
1:D:673:PHE:HE2	1:D:710:SER:HB3	1.75	0.52
1:D:747:ASP:OD1	1:D:748:THR:N	2.43	0.52
2:G:1566:LYS:HB3	2:G:1566:LYS:NZ	2.24	0.52
1:B:322:TYR:CE2	1:B:340:GLU:HG3	2.44	0.52
1:C:541:ASN:CB	1:C:542:PRO:CD	2.88	0.52
2:E:1138:ILE:CG2	2:E:1139:SER:N	2.72	0.52
2:G:1555:VAL:HG13	2:G:1561:MET:SD	2.49	0.52
1:A:160:LEU:HA	2:E:1125:TRP:CD1	2.45	0.52
1:D:716:LYS:HD2	1:D:716:LYS:N	2.25	0.52
2:E:1032:VAL:O	2:E:1033:LEU:HB2	2.10	0.52
2:F:1236:ILE:CD1	2:F:1253:LEU:HD11	2.40	0.52
2:G:1533:LYS:HB2	2:G:1533:LYS:HZ2	1.72	0.52
2:H:1724:LEU:O	2:H:1725:TRP:HB2	2.09	0.52
1:B:328:PHE:HZ	2:G:1439:ASN:HD22	1.58	0.52
1:D:634:SER:C	1:D:636:THR:H	2.12	0.52
2:H:1654:TYR:HA	2:H:1766:LYS:O	2.09	0.52
1:B:262:ASN:O	1:B:264:ILE:HG23	2.10	0.51
1:B:298:MET:CE	1:B:321:LEU:HD22	2.41	0.51
1:D:716:LYS:HD3	1:D:790:GLY:O	2.10	0.51
2:H:1686:LYS:HB2	2:H:1736:TYR:CZ	2.45	0.51
1:B:329:ASP:O	1:B:330:LEU:HG	2.10	0.51
1:C:520:ASN:ND2	1:C:589:TYR:HE2	2.07	0.51
2:E:1057:ILE:HA	2:E:1117:PHE:O	2.10	0.51
2:E:1077:GLU:HB3	2:E:1079:TYR:CE1	2.45	0.51
1:A:33:ASP:C	1:A:35:THR:H	2.13	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:ARG:CD	1:A:177:VAL:HG12	2.40	0.51
2:E:1158:THR:O	2:E:1160:ALA:N	2.42	0.51
1:C:485:PHE:CZ	1:C:581:GLY:HA3	2.45	0.51
1:C:514:SER:O	1:C:515:CYS:HB3	2.10	0.51
1:C:574:PHE:O	1:C:575:GLY:O	2.28	0.51
2:F:1242:ASN:ND2	2:F:1244:LYS:H	2.07	0.51
2:H:1676:TYR:CD1	2:H:1707:PRO:HA	2.45	0.51
1:A:87:ARG:HG3	1:A:87:ARG:HH11	1.75	0.51
1:A:141:ASN:CB	1:A:142:PRO:CD	2.88	0.51
1:C:503:ARG:HD2	1:C:507:SER:HB2	1.92	0.51
1:A:53:GLU:OE2	1:A:65:ARG:HD2	2.10	0.51
1:B:328:PHE:HE1	2:G:1442:ASN:HA	1.74	0.51
1:D:735:PHE:HB3	1:D:736:PRO:HD3	1.93	0.51
2:E:1040:SER:CA	2:E:1161:MET:HE1	2.37	0.51
1:A:130:LEU:CA	2:H:1635:PRO:CG	2.89	0.51
1:D:630:THR:HA	1:D:801:PHE:CB	2.40	0.51
2:H:1686:LYS:HB2	2:H:1736:TYR:CE1	2.45	0.51
1:A:130:LEU:O	2:H:1635:PRO:HD2	2.10	0.51
1:A:155:PHE:HZ	2:E:1122:PRO:C	2.15	0.51
1:C:460:ASN:O	1:C:461:MET:HB2	2.11	0.51
1:D:755:PHE:HB2	1:D:763:ARG:NH1	2.25	0.50
1:A:51:TRP:HA	1:A:69:VAL:HG22	1.92	0.50
1:B:314:SER:O	1:B:315:CYS:HB3	2.10	0.50
2:E:1056:GLN:HE22	2:E:1168:GLY:CA	2.24	0.50
2:E:1130:GLN:HB2	2:E:1133:LYS:CG	2.38	0.50
2:E:1136:TYR:N	2:E:1136:TYR:CD1	2.79	0.50
1:A:204:LYS:O	1:A:205:CYS:SG	2.70	0.50
1:C:570:GLU:HG3	1:C:572:ARG:HH12	1.75	0.50
1:B:376:PRO:O	1:B:377:VAL:HB	2.11	0.50
1:D:764:VAL:O	1:D:767:ILE:HG22	2.11	0.50
1:C:488:ARG:HH12	1:C:490:GLY:HA2	1.76	0.50
2:E:1154:GLY:O	2:E:1155:VAL:HB	2.12	0.50
2:H:1702:LEU:HD21	2:H:1712:LYS:C	2.31	0.50
1:B:335:PHE:O	1:B:337:ASN:N	2.45	0.50
1:C:606:PRO:O	1:C:607:ARG:CB	2.53	0.50
2:H:1654:TYR:N	2:H:1655:PRO:HD3	2.27	0.50
1:A:132:THR:CG2	2:H:1635:PRO:CD	2.90	0.50
1:D:681:LEU:O	1:D:785:ALA:HA	2.12	0.50
2:E:1155:VAL:N	2:E:1158:THR:HB	2.16	0.50
2:H:1718:GLN:NE2	2:H:1721:SER:HB2	2.25	0.50
1:C:539:MET:HG3	1:C:541:ASN:CB	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:694:ILE:HD13	1:D:777:VAL:CG2	2.42	0.49
2:G:1502:LEU:CD1	2:G:1513:PHE:HB2	2.42	0.49
2:H:1745:LEU:O	2:H:1747:GLY:N	2.44	0.49
1:A:139:MET:HG3	1:A:141:ASN:H	1.76	0.49
1:A:130:LEU:O	2:H:1635:PRO:CD	2.60	0.49
2:E:1155:VAL:HG13	2:E:1161:MET:SD	2.52	0.49
1:B:278:ASN:HD21	1:B:387:GLN:HE21	1.61	0.49
2:G:1542:ASN:ND2	2:G:1542:ASN:C	2.66	0.49
1:B:243:TRP:HH2	1:B:398:VAL:HG21	1.76	0.49
1:C:541:ASN:HB3	1:C:542:PRO:HD2	1.94	0.49
2:F:1323:ASN:HD22	2:F:1323:ASN:C	2.16	0.49
2:H:1671:LYS:HD2	2:H:1672:THR:OG1	2.12	0.49
1:A:65:ARG:HH21	2:E:1112:LYS:HG3	1.78	0.49
1:A:90:GLY:N	2:H:1671:LYS:HD3	2.28	0.49
1:C:488:ARG:NH1	1:C:490:GLY:HA2	2.27	0.49
2:E:1136:TYR:CE2	2:E:1164:LEU:HD23	2.48	0.49
2:E:1057:ILE:H	2:E:1057:ILE:CD1	2.26	0.49
2:H:1632:VAL:HG13	2:H:1632:VAL:O	2.12	0.49
2:H:1755:VAL:CG2	2:H:1759:ARG:HB2	2.42	0.49
1:A:130:LEU:HD12	1:A:131:ALA:N	2.27	0.49
1:B:278:ASN:ND2	1:B:387:GLN:HE21	2.11	0.49
1:B:365:MET:C	1:B:366:LYS:HD2	2.33	0.49
1:C:489:ARG:NE	2:F:1271:LYS:NZ	2.61	0.49
1:A:155:PHE:HA	1:A:166:LYS:NZ	2.28	0.49
1:C:563:ARG:HG2	1:C:563:ARG:HH11	1.78	0.49
1:D:757:GLN:NE2	1:D:763:ARG:HH22	2.09	0.49
1:B:289:ARG:HD3	2:G:1471:LYS:CD	2.39	0.49
1:B:308:ILE:H	1:B:308:ILE:CD1	2.25	0.49
1:C:552:ASP:HB3	1:C:568:ASN:HD22	1.78	0.49
1:D:714:SER:HB2	1:D:716:LYS:HZ2	1.77	0.49
2:E:1068:VAL:HA	2:E:1073:VAL:CG1	2.37	0.49
1:A:89:ARG:CA	2:H:1671:LYS:HZ2	2.26	0.48
1:D:688:ARG:HB3	1:D:688:ARG:NH1	2.29	0.48
1:D:759:ASP:OD1	1:D:762:GLY:HA3	2.12	0.48
2:F:1353:GLY:O	2:F:1356:CYS:HB3	2.14	0.48
2:F:1266:PRO:HA	2:F:1310:ASP:OD1	2.13	0.48
1:A:130:LEU:CA	2:H:1635:PRO:HG3	2.39	0.48
1:A:160:LEU:HA	2:E:1125:TRP:HD1	1.77	0.48
1:B:233:ASP:O	1:B:234:SER:CB	2.61	0.48
1:C:515:CYS:HA	1:C:590:GLY:O	2.11	0.48
1:A:51:TRP:CD2	1:A:69:VAL:HG23	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:TYR:CE2	1:A:140:GLU:CG	2.94	0.48
1:A:149:ILE:N	1:A:149:ILE:HD12	2.28	0.48
1:D:731:ALA:HB1	1:D:736:PRO:HG2	1.95	0.48
1:D:753:GLU:H	1:D:768:ASN:ND2	2.07	0.48
2:E:1137:ILE:O	2:E:1138:ILE:HD13	2.13	0.48
1:A:40:GLU:H	1:A:40:GLU:CD	2.17	0.48
1:B:237:ALA:C	1:B:239:ALA:H	2.16	0.48
1:D:760:LEU:HA	2:H:1725:TRP:HD1	1.78	0.48
1:D:770:GLU:CG	1:D:772:ARG:NH2	2.75	0.48
2:E:1055:PRO:O	2:E:1167:VAL:HA	2.12	0.48
2:G:1538:ILE:HG22	2:G:1562:LYS:CB	2.43	0.48
1:D:631:LEU:HD21	1:D:802:TYR:CE2	2.49	0.48
2:G:1454:TYR:N	2:G:1455:PRO:CD	2.77	0.48
1:A:57:TYR:CE2	2:E:1113:PHE:HE1	2.31	0.48
1:A:94:ILE:HD12	1:A:94:ILE:N	2.29	0.48
2:E:1032:VAL:O	2:E:1060:LYS:O	2.32	0.48
2:F:1301:LEU:C	2:F:1302:LEU:HD12	2.33	0.48
1:A:166:LYS:HB3	2:E:1124:LEU:CD2	2.17	0.48
1:C:446:HIS:CE1	1:C:538:TRP:CD1	3.02	0.48
1:C:472:VAL:HG21	1:C:592:CYS:HB2	1.96	0.48
1:D:637:ALA:O	1:D:638:THR:HG22	2.12	0.48
1:A:86:ILE:HD13	1:A:200:VAL:HG21	1.96	0.48
1:C:579:ARG:HG3	1:C:579:ARG:HH11	1.79	0.48
1:D:682:ARG:NH2	1:D:732:THR:O	2.41	0.48
2:F:1321:SER:C	2:F:1323:ASN:H	2.17	0.48
1:A:77:GLN:HB2	1:A:190:GLY:N	2.29	0.47
1:D:688:ARG:NH1	1:D:779:ARG:O	2.47	0.47
1:D:703:ARG:HB2	1:D:792:CYS:SG	2.53	0.47
2:E:1158:THR:HG22	2:E:1159:ARG:H	1.79	0.47
1:A:129:ASP:O	1:A:131:ALA:N	2.47	0.47
1:A:135:PHE:CD2	2:H:1634:GLU:CD	2.86	0.47
1:D:651:TRP:HA	1:D:669:VAL:HG13	1.96	0.47
1:D:755:PHE:HB2	1:D:763:ARG:HH11	1.76	0.47
1:D:766:LYS:HB2	2:H:1724:LEU:CD1	2.43	0.47
1:A:96:VAL:CG2	1:A:121:LEU:HD21	2.35	0.47
1:B:325:GLU:HB3	1:B:379:ARG:CG	2.44	0.47
2:E:1155:VAL:H	2:E:1158:THR:CB	2.19	0.47
1:A:110:SER:C	1:A:112:PRO:HD3	2.34	0.47
1:C:502:VAL:HG21	1:C:551:ALA:CB	2.44	0.47
2:H:1651:LEU:HD21	2:H:1653:LEU:HD11	1.95	0.47
1:A:130:LEU:CB	2:H:1635:PRO:HG2	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:192:CYS:SG	2:E:1122:PRO:HB3	2.54	0.47
2:F:1268:VAL:CG2	2:F:1276:TYR:HB2	2.29	0.47
2:H:1706:ARG:HA	2:H:1706:ARG:HD3	1.62	0.47
1:D:687:ARG:HH12	2:E:1069:ASP:CG	2.18	0.47
2:G:1542:ASN:HD21	2:G:1544:SER:H	1.59	0.47
1:A:61:MET:HE2	2:E:1100:PRO:HD2	1.97	0.47
1:A:116:LYS:N	1:A:116:LYS:CD	2.77	0.47
1:B:289:ARG:HH11	2:G:1471:LYS:CE	2.22	0.47
2:E:1038:TRP:HZ2	2:E:1139:SER:HB3	1.80	0.47
2:E:1087:ASP:O	2:E:1091:ARG:HG3	2.15	0.47
2:E:1142:ASN:OD1	2:E:1147:GLY:HA3	2.15	0.47
2:G:1432:VAL:HG23	2:G:1432:VAL:O	2.13	0.47
2:G:1451:LEU:HD12	2:G:1452:VAL:N	2.30	0.47
2:G:1520:PHE:HD1	2:G:1520:PHE:O	1.98	0.47
2:G:1538:ILE:HG22	2:G:1562:LYS:HB2	1.96	0.47
2:E:1102:LEU:HD21	2:E:1112:LYS:HA	1.96	0.47
1:C:530:LEU:HD12	1:C:531:ALA:N	2.30	0.47
1:D:641:LEU:HD12	1:D:667:TYR:HE1	1.79	0.47
1:D:720:ASN:ND2	1:D:748:THR:HA	2.30	0.47
2:E:1081:VAL:HB	2:E:1102:LEU:HB2	1.97	0.47
2:G:1456:GLN:NE2	2:G:1568:GLY:HA2	2.24	0.47
2:H:1669:ASP:OD2	2:H:1671:LYS:HB3	2.15	0.47
1:B:247:PRO:HG2	1:B:279:ASN:HA	1.97	0.46
2:E:1155:VAL:HG22	2:E:1159:ARG:NH2	2.27	0.46
2:H:1694:ILE:HD11	2:H:1751:GLN:HG2	1.97	0.46
1:C:511:VAL:HG23	1:C:511:VAL:O	2.14	0.46
2:E:1140:THR:O	2:E:1140:THR:CG2	2.62	0.46
1:A:158:VAL:HG11	2:E:1121:SER:CB	2.41	0.46
1:A:164:VAL:C	1:A:166:LYS:H	2.19	0.46
1:B:357:GLN:CB	1:B:363:ARG:NH1	2.76	0.46
1:C:451:TRP:CE3	1:C:469:VAL:HG22	2.49	0.46
1:C:524:TYR:HB2	1:C:543:TRP:CE3	2.51	0.46
1:D:693:ARG:HG3	1:D:693:ARG:HH11	1.81	0.46
2:H:1689:ALA:HA	2:H:1738:ILE:HD13	1.98	0.46
1:B:251:TRP:CA	1:B:269:VAL:HG13	2.46	0.46
2:G:1471:LYS:O	2:G:1472:THR:C	2.54	0.46
1:A:88:ARG:HD3	1:A:177:VAL:HG12	1.97	0.46
1:C:493:ARG:NH2	1:D:746:VAL:O	2.48	0.46
1:C:494:ILE:O	1:C:573:SER:HA	2.14	0.46
1:D:712:PRO:HG2	1:D:713:GLY:N	2.30	0.46
2:H:1746:GLU:OE2	2:H:1746:GLU:HA	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:1138:ILE:HG22	2:E:1139:SER:N	2.29	0.46
2:F:1269:ASP:OD2	2:F:1271:LYS:HB2	2.15	0.46
2:F:1334:ASP:OD1	2:F:1366:LYS:HG2	2.16	0.46
2:H:1671:LYS:O	2:H:1672:THR:HB	2.16	0.46
2:H:1718:GLN:NE2	2:H:1721:SER:CB	2.79	0.46
2:H:1731:LYS:O	2:H:1732:ASN:HB2	2.16	0.46
1:A:94:ILE:HG12	1:A:182:PHE:CE2	2.50	0.46
1:A:135:PHE:CZ	2:H:1634:GLU:OE2	2.63	0.46
1:D:666:THR:HB	1:D:795:LEU:O	2.16	0.46
1:D:702:VAL:HG21	1:D:751:ALA:HB2	1.97	0.46
1:D:703:ARG:CG	2:H:1722:PRO:HA	2.44	0.46
2:E:1057:ILE:N	2:E:1057:ILE:CD1	2.78	0.46
1:A:176:PRO:O	1:A:177:VAL:O	2.34	0.46
1:C:439:ALA:HB1	2:G:1512:LYS:HE2	1.98	0.46
2:E:1068:VAL:HG12	2:E:1107:PRO:O	2.16	0.46
2:H:1657:ILE:HD13	2:H:1719:GLU:HG3	1.98	0.46
1:C:500:PHE:N	1:C:500:PHE:CD2	2.85	0.45
2:E:1077:GLU:HB3	2:E:1079:TYR:HE1	1.81	0.45
2:F:1275:GLN:HE21	2:F:1275:GLN:HB3	1.60	0.45
2:H:1656:GLN:N	2:H:1659:ASP:OD2	2.42	0.45
2:H:1667:LYS:HB2	2:H:1667:LYS:HZ2	1.81	0.45
1:A:57:TYR:OH	2:E:1113:PHE:CE1	2.66	0.45
1:C:530:LEU:HD12	1:C:530:LEU:C	2.37	0.45
2:H:1685:ASP:CB	2:H:1688:GLN:HG3	2.44	0.45
1:A:87:ARG:HG3	1:A:87:ARG:NH1	2.30	0.45
1:D:703:ARG:NH2	2:H:1728:GLU:OE1	2.49	0.45
2:G:1436:ILE:CD1	2:G:1453:LEU:HD11	2.46	0.45
2:H:1737:ILE:HB	2:H:1763:ILE:HB	1.97	0.45
1:A:128:PHE:HE1	2:H:1642:ASN:HA	1.81	0.45
1:D:636:THR:HG23	1:D:636:THR:O	2.16	0.45
2:H:1723:ASN:OD1	2:H:1724:LEU:O	2.35	0.45
1:A:53:GLU:HB2	1:A:67:TYR:CE2	2.52	0.45
1:A:139:MET:C	1:A:141:ASN:H	2.20	0.45
1:D:737:ASN:HB3	1:D:742:PRO:HG3	1.98	0.45
2:E:1037:TYR:CD2	2:E:1066:PRO:HG3	2.50	0.45
2:H:1742:ASN:ND2	2:H:1744:SER:H	2.14	0.45
1:C:604:LYS:O	1:C:605:CYS:CB	2.64	0.45
1:D:708:ILE:O	1:D:711:VAL:HG13	2.16	0.45
1:A:55:SER:N	2:E:1114:THR:HB	2.24	0.45
1:A:125:GLU:O	1:A:126:ALA:HB2	2.16	0.45
1:B:340:GLU:O	1:B:340:GLU:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:360:LEU:N	1:B:360:LEU:HD12	2.32	0.45
1:C:521:LEU:HD13	1:C:586:PHE:CE2	2.52	0.45
1:D:687:ARG:O	1:D:689:ARG:NH1	2.50	0.45
2:E:1068:VAL:O	2:E:1068:VAL:HG13	2.16	0.45
2:E:1131:LYS:O	2:E:1132:ASN:CB	2.65	0.45
2:H:1637:TYR:CD2	2:H:1666:PRO:HG3	2.48	0.45
1:A:55:SER:CB	2:E:1114:THR:N	2.71	0.45
1:B:389:TYR:HD1	1:B:389:TYR:O	2.00	0.44
1:D:740:GLU:O	1:D:743:TRP:O	2.35	0.44
1:A:89:ARG:HA	2:H:1671:LYS:CD	2.44	0.44
1:A:100:PHE:N	1:A:100:PHE:CD2	2.85	0.44
1:A:170:GLU:OE2	1:A:172:ARG:NH2	2.48	0.44
1:B:246:HIS:HB2	1:B:338:TRP:CE2	2.52	0.44
2:F:1278:TYR:CE1	2:F:1345:LEU:HB2	2.52	0.44
1:A:111:VAL:N	1:A:112:PRO:HD3	2.31	0.44
1:A:160:LEU:H	1:A:160:LEU:CD1	2.30	0.44
1:C:488:ARG:HG2	1:C:491:ALA:H	1.83	0.44
1:C:489:ARG:HG2	2:F:1271:LYS:HG2	1.99	0.44
1:D:633:ASP:HB3	1:D:636:THR:HG22	1.99	0.44
2:E:1071:LYS:C	2:E:1071:LYS:HD2	2.37	0.44
1:A:57:TYR:OH	2:E:1101:LEU:CD2	2.61	0.44
1:A:99:LYS:HA	1:A:168:ASN:O	2.17	0.44
1:A:203:ARG:NH1	1:A:203:ARG:HG3	2.33	0.44
1:B:251:TRP:CE3	1:B:269:VAL:HG22	2.52	0.44
2:F:1336:TYR:N	2:F:1336:TYR:CD1	2.85	0.44
1:B:294:ILE:HD11	1:B:377:VAL:HG11	1.99	0.44
1:B:330:LEU:HD12	1:B:330:LEU:C	2.38	0.44
1:B:394:SER:O	1:B:396:ILE:HG13	2.18	0.44
1:D:760:LEU:HA	2:H:1725:TRP:CD1	2.52	0.44
2:E:1052:VAL:HG13	2:E:1164:LEU:HD12	2.00	0.44
2:G:1559:ARG:HG2	2:G:1559:ARG:O	2.16	0.44
2:H:1695:LYS:O	2:H:1696:LYS:HB2	2.17	0.44
1:A:51:TRP:CD2	1:A:69:VAL:CG2	3.01	0.44
1:C:546:VAL:O	1:C:547:ASP:HB2	2.18	0.44
2:E:1075:GLN:OE1	2:E:1075:GLN:N	2.51	0.44
2:H:1653:LEU:O	2:H:1654:TYR:CB	2.66	0.44
1:A:95:HIS:HE1	1:A:207:ARG:HH21	1.64	0.44
1:A:128:PHE:CE2	2:H:1639:ASN:CG	2.91	0.44
1:A:128:PHE:O	1:A:130:LEU:HG	2.18	0.44
1:D:688:ARG:HH11	1:D:688:ARG:CB	2.31	0.44
1:A:135:PHE:CE1	2:H:1634:GLU:CD	2.91	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:294:ILE:HD13	1:B:377:VAL:HG21	2.00	0.44
1:D:694:ILE:HG12	1:D:782:PHE:CZ	2.52	0.44
1:D:697:GLU:HG3	1:D:771:VAL:HG22	2.00	0.44
2:G:1531:LYS:NZ	2:G:1568:GLY:HA3	2.33	0.44
2:G:1518:GLN:NE2	2:G:1521:SER:HB2	2.33	0.44
1:A:73:PHE:CD1	1:A:74:GLU:HG3	2.52	0.43
1:A:88:ARG:HG2	1:A:91:ALA:H	1.83	0.43
1:A:96:VAL:HG23	1:A:96:VAL:O	2.18	0.43
1:A:203:ARG:HG3	1:A:203:ARG:HH11	1.83	0.43
1:D:683:THR:HG21	1:D:686:ILE:HD11	2.00	0.43
1:D:763:ARG:HB3	1:D:766:LYS:HG2	2.00	0.43
2:E:1115:ILE:HG21	2:E:1117:PHE:CZ	2.52	0.43
2:H:1651:LEU:HD21	2:H:1653:LEU:CD1	2.48	0.43
1:A:43:TRP:HB2	1:A:67:TYR:CZ	2.53	0.43
1:A:103:ARG:HD3	2:E:1122:PRO:HA	2.00	0.43
2:F:1232:VAL:HG13	2:F:1233:LEU:N	2.33	0.43
2:F:1342:ASN:ND2	2:F:1350:ASN:ND2	2.67	0.43
1:B:270:CYS:SG	2:F:1320:PHE:HE2	2.41	0.43
1:D:693:ARG:HG3	1:D:693:ARG:NH1	2.33	0.43
2:E:1155:VAL:CG2	2:E:1159:ARG:HH21	2.28	0.43
2:E:1158:THR:C	2:E:1160:ALA:H	2.22	0.43
2:G:1521:SER:HA	2:G:1522:PRO:HD3	1.76	0.43
2:H:1667:LYS:NZ	2:H:1667:LYS:CB	2.81	0.43
1:A:130:LEU:O	2:H:1635:PRO:HG3	2.19	0.43
1:C:604:LYS:O	1:C:605:CYS:HB2	2.18	0.43
1:D:683:THR:CG2	1:D:684:LYS:H	2.29	0.43
2:E:1069:ASP:O	2:E:1070:SER:C	2.57	0.43
1:A:53:GLU:HG2	1:A:65:ARG:HH11	1.83	0.43
1:A:135:PHE:CB	1:A:136:PRO:HD3	2.45	0.43
1:B:245:VAL:HG11	1:B:251:TRP:O	2.19	0.43
1:B:366:LYS:HD2	1:B:366:LYS:N	2.34	0.43
1:C:563:ARG:HG2	1:C:563:ARG:NH1	2.33	0.43
1:C:605:CYS:C	1:C:607:ARG:H	2.22	0.43
1:D:762:GLY:O	1:D:763:ARG:C	2.57	0.43
1:A:41:LEU:HB3	1:A:43:TRP:CD1	2.54	0.43
1:B:234:SER:C	1:B:236:THR:H	2.22	0.43
1:B:243:TRP:HH2	1:B:398:VAL:CG2	2.32	0.43
1:C:439:ALA:O	1:C:440:GLU:C	2.57	0.43
1:C:503:ARG:NH1	1:C:556:SER:O	2.51	0.43
2:E:1089:ALA:O	2:E:1162:LYS:NZ	2.52	0.43
2:F:1301:LEU:HB3	2:F:1302:LEU:HD12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:1669:ASP:C	2:H:1671:LYS:H	2.22	0.43
1:B:359:ASP:H	2:F:1324:LEU:CD2	2.32	0.43
2:F:1285:ASP:H	2:F:1288:GLN:HE21	1.67	0.43
2:G:1498:ASN:ND2	2:G:1500:PRO:HG3	2.34	0.43
2:G:1520:PHE:O	2:G:1520:PHE:CD1	2.72	0.43
1:A:130:LEU:CA	2:H:1635:PRO:HG2	2.49	0.42
1:C:529:ASP:O	1:C:530:LEU:CG	2.67	0.42
2:E:1136:TYR:HA	2:E:1163:ILE:O	2.19	0.42
1:A:161:GLY:N	2:E:1125:TRP:CD1	2.88	0.42
1:B:395:LEU:HD11	1:B:398:VAL:HG12	2.02	0.42
2:F:1286:LYS:HG3	2:F:1336:TYR:CZ	2.53	0.42
1:A:160:LEU:H	1:A:160:LEU:HD12	1.84	0.42
2:G:1540:THR:HA	2:G:1553:GLY:O	2.19	0.42
1:A:160:LEU:HD12	1:A:160:LEU:N	2.34	0.42
1:C:508:ILE:HB	1:C:511:VAL:CG1	2.49	0.42
2:F:1242:ASN:HD22	2:F:1244:LYS:H	1.66	0.42
2:F:1271:LYS:C	2:F:1273:VAL:H	2.22	0.42
1:A:54:VAL:HG22	2:E:1060:LYS:HZ1	1.81	0.42
1:B:311:VAL:HA	1:B:312:PRO:HD2	1.89	0.42
1:D:634:SER:C	1:D:636:THR:N	2.73	0.42
1:D:749:ILE:N	1:D:749:ILE:CD1	2.83	0.42
2:E:1040:SER:HA	2:E:1161:MET:HE2	1.99	0.42
2:E:1056:GLN:O	2:E:1059:ASP:OD1	2.38	0.42
2:F:1254:TYR:HA	2:F:1366:LYS:O	2.20	0.42
2:H:1720:PHE:CD1	2:H:1720:PHE:N	2.87	0.42
1:A:81:LEU:O	1:A:185:ALA:HA	2.18	0.42
1:A:88:ARG:C	2:H:1671:LYS:HZ2	2.17	0.42
1:B:328:PHE:CZ	2:G:1439:ASN:HB3	2.54	0.42
1:D:731:ALA:CB	1:D:736:PRO:HG2	2.50	0.42
1:C:539:MET:CG	1:C:541:ASN:HB3	2.42	0.42
2:H:1657:ILE:CD1	2:H:1731:LYS:HB3	2.49	0.42
1:A:43:TRP:HB2	1:A:67:TYR:OH	2.20	0.42
1:A:164:VAL:HA	2:E:1125:TRP:CH2	2.54	0.42
1:B:246:HIS:HB2	1:B:338:TRP:CE3	2.55	0.42
1:A:122:TYR:CE2	1:A:140:GLU:HG2	2.55	0.41
1:A:132:THR:HG22	2:H:1635:PRO:HD3	2.00	0.41
1:C:446:HIS:CB	1:C:447:PRO:CD	2.93	0.41
1:D:760:LEU:C	1:D:762:GLY:H	2.23	0.41
2:H:1664:ILE:HG23	2:H:1712:LYS:HG2	2.02	0.41
1:A:155:PHE:HA	1:A:166:LYS:HZ3	1.84	0.41
2:F:1253:LEU:CD1	2:F:1261:LEU:HD11	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:LEU:N	2:H:1637:TYR:CZ	2.78	0.41
1:C:588:ASP:OD2	1:C:589:TYR:N	2.53	0.41
2:F:1285:ASP:H	2:F:1288:GLN:NE2	2.18	0.41
1:B:251:TRP:HA	1:B:268:GLN:O	2.19	0.41
1:C:468:GLN:NE2	2:G:1522:PRO:HD2	2.35	0.41
1:D:771:VAL:O	1:D:772:ARG:HD3	2.20	0.41
2:F:1294:ILE:HB	2:F:1351:GLN:HB2	2.02	0.41
2:G:1454:TYR:HA	2:G:1566:LYS:O	2.20	0.41
2:G:1552:GLU:CD	2:G:1552:GLU:N	2.73	0.41
1:B:303:ARG:HG2	2:F:1322:PRO:HA	2.03	0.41
1:D:644:MET:HB3	1:D:682:ARG:HB3	2.02	0.41
2:F:1242:ASN:C	2:F:1242:ASN:ND2	2.73	0.41
2:G:1442:ASN:OD1	2:G:1444:LYS:HB2	2.21	0.41
2:H:1693:THR:O	2:H:1693:THR:HG23	2.20	0.41
1:A:115:CYS:HA	1:A:190:GLY:O	2.20	0.41
1:A:160:LEU:HA	2:E:1125:TRP:HA	2.02	0.41
1:B:267:TYR:O	1:B:395:LEU:N	2.54	0.41
1:B:294:ILE:N	1:B:294:ILE:CD1	2.83	0.41
1:B:320:ASN:ND2	1:B:348:THR:OG1	2.49	0.41
2:F:1286:LYS:HE3	2:F:1286:LYS:HB2	1.82	0.41
2:F:1339:SER:O	2:F:1356:CYS:HB2	2.21	0.41
2:H:1657:ILE:HD11	2:H:1731:LYS:HB3	2.02	0.41
1:A:130:LEU:HD12	1:A:130:LEU:C	2.41	0.41
1:B:289:ARG:NH1	2:G:1471:LYS:HE2	2.27	0.41
1:C:508:ILE:HA	1:C:509:PRO:HD3	1.92	0.41
1:D:729:ASP:O	1:D:783:TYR:OH	2.32	0.41
2:E:1069:ASP:H	2:E:1073:VAL:CB	2.33	0.41
2:G:1555:VAL:HG13	2:G:1561:MET:CG	2.50	0.41
1:A:128:PHE:CG	2:H:1637:TYR:CD2	3.08	0.41
1:A:155:PHE:HZ	2:E:1123:ASN:N	2.18	0.41
1:A:186:PHE:CD1	1:A:186:PHE:N	2.89	0.41
1:B:251:TRP:CG	1:B:269:VAL:HG13	2.56	0.41
1:D:658:ASP:O	1:D:659:GLU:C	2.59	0.41
1:A:132:THR:HG23	2:H:1635:PRO:HD2	2.03	0.41
1:B:245:VAL:O	1:B:246:HIS:C	2.59	0.41
2:F:1320:PHE:O	2:F:1320:PHE:CG	2.74	0.41
2:F:1355:VAL:HG22	2:F:1359:ARG:HG3	2.01	0.41
2:F:1364:LEU:HD22	2:F:1366:LYS:HG3	2.02	0.41
2:G:1440:SER:O	2:G:1559:ARG:NE	2.54	0.41
2:G:1446:LEU:HA	2:G:1447:PRO:HD3	1.94	0.41
2:G:1456:GLN:O	2:G:1459:ASP:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:1461:LEU:HD23	2:G:1565:MET:HE2	2.01	0.41
2:H:1755:VAL:HG22	2:H:1759:ARG:HB2	2.02	0.41
1:C:522:TYR:CD2	1:C:545:LYS:HA	2.57	0.40
2:E:1071:LYS:C	2:E:1073:VAL:H	2.24	0.40
2:F:1236:ILE:HD13	2:F:1251:LEU:HD21	2.02	0.40
2:F:1256:GLN:HE22	2:F:1368:GLY:HA2	1.86	0.40
2:G:1478:TYR:HB3	2:G:1548:LEU:HD13	2.02	0.40
1:B:278:ASN:ND2	1:B:280:TRP:HE1	2.18	0.40
1:D:757:GLN:H	1:D:763:ARG:HH12	1.68	0.40
2:E:1034:GLU:HA	2:E:1035:PRO:HD3	1.85	0.40
1:B:246:HIS:O	1:B:248:PRO:HD3	2.21	0.40
1:C:503:ARG:HG2	1:C:508:ILE:HD11	2.02	0.40
1:C:553:GLU:H	1:C:568:ASN:HD21	1.68	0.40
1:C:606:PRO:C	1:C:607:ARG:HD2	2.41	0.40
2:F:1277:GLU:HB3	2:F:1279:TYR:CE1	2.56	0.40
1:A:160:LEU:HD11	2:E:1126:GLY:O	2.21	0.40
1:C:492:HIS:O	1:C:576:PRO:HA	2.21	0.40
1:A:128:PHE:CD2	2:H:1666:PRO:CG	3.02	0.40
1:A:152:ASP:OD1	1:A:153:GLU:HG2	2.21	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	179/181 (99%)	144 (80%)	22 (12%)	13 (7%)	<b>1</b>   <b>1</b>
1	B	179/181 (99%)	135 (75%)	32 (18%)	12 (7%)	<b>1</b>   <b>1</b>
1	C	179/181 (99%)	144 (80%)	24 (13%)	11 (6%)	<b>1</b>   <b>2</b>
1	D	179/181 (99%)	138 (77%)	31 (17%)	10 (6%)	<b>2</b>   <b>3</b>
2	E	136/138 (99%)	112 (82%)	18 (13%)	6 (4%)	<b>2</b>   <b>5</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	F	136/138 (99%)	110 (81%)	23 (17%)	3 (2%)	6	17
2	G	136/138 (99%)	112 (82%)	17 (12%)	7 (5%)	2	3
2	H	136/138 (99%)	110 (81%)	18 (13%)	8 (6%)	1	2
All	All	1260/1276 (99%)	1005 (80%)	185 (15%)	70 (6%)	2	3

All (70) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	34	SER
1	A	130	LEU
1	A	175	GLY
1	B	309	PRO
1	B	375	GLY
1	C	446	HIS
1	C	514	SER
1	C	575	GLY
1	D	705	CYS
1	D	730	LEU
1	D	775	GLY
2	E	1043	SER
2	E	1075	GLN
2	E	1158	THR
2	E	1159	ARG
2	H	1643	SER
2	H	1668	VAL
2	H	1697	GLU
1	A	177	VAL
1	B	314	SER
1	B	329	ASP
1	B	358	VAL
1	C	529	ASP
1	D	646	HIS
1	D	712	PRO
2	E	1153	GLY
2	F	1297	GLU
2	G	1554	GLY
2	H	1674	GLY
1	A	46	HIS
1	A	129	ASP
1	B	246	HIS
1	B	313	GLY

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Mol	Chain	Res	Type
1	B	362	GLY
1	C	440	GLU
1	C	512	PRO
1	D	715	CYS
1	D	737	ASN
2	G	1496	LYS
2	H	1667	LYS
2	H	1672	THR
1	A	126	ALA
1	A	141	ASN
1	C	605	CYS
1	D	636	THR
2	E	1096	LYS
2	F	1233	LEU
2	G	1474	GLY
2	G	1475	GLN
1	A	89	ARG
1	A	115	CYS
1	B	234	SER
1	B	330	LEU
1	B	377	VAL
1	C	515	CYS
1	C	530	LEU
1	C	541	ASN
1	D	678	ASN
2	G	1473	VAL
2	G	1546	GLU
1	C	535	PHE
2	G	1530	GLN
2	H	1654	TYR
1	A	205	CYS
1	A	112	PRO
2	F	1273	VAL
1	D	713	GLY
1	B	335	PHE
2	H	1747	GLY
1	A	136	PRO

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar

resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	160/160 (100%)	155 (97%)	5 (3%)	40	69
1	B	160/160 (100%)	153 (96%)	7 (4%)	28	56
1	C	160/160 (100%)	152 (95%)	8 (5%)	24	51
1	D	160/160 (100%)	146 (91%)	14 (9%)	10	23
2	E	124/124 (100%)	118 (95%)	6 (5%)	25	53
2	F	124/124 (100%)	115 (93%)	9 (7%)	14	33
2	G	124/124 (100%)	115 (93%)	9 (7%)	14	33
2	H	124/124 (100%)	120 (97%)	4 (3%)	39	68
All	All	1136/1136 (100%)	1074 (94%)	62 (6%)	21	46

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	MET
1	A	104	ASP
1	A	116	LYS
1	A	130	LEU
1	A	144	VAL
1	B	269	VAL
1	B	278	ASN
1	B	316	LYS
1	B	329	ASP
1	B	330	LEU
1	B	341	ASN
1	B	344	VAL
1	C	469	VAL
1	C	516	LYS
1	C	528	PHE
1	C	529	ASP
1	C	530	LEU
1	C	567	ILE
1	C	570	GLU
1	C	607	ARG
1	D	629	GLU
1	D	636	THR
1	D	640	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	D	660	ASN
1	D	669	VAL
1	D	687	ARG
1	D	705	CYS
1	D	737	ASN
1	D	741	ASN
1	D	744	VAL
1	D	757	GLN
1	D	770	GLU
1	D	788	ASP
1	D	795	LEU
2	E	1059	ASP
2	E	1071	LYS
2	E	1075	GLN
2	E	1132	ASN
2	E	1136	TYR
2	E	1152	GLU
2	F	1242	ASN
2	F	1271	LYS
2	F	1275	GLN
2	F	1323	ASN
2	F	1324	LEU
2	F	1352	GLU
2	F	1355	VAL
2	F	1359	ARG
2	F	1364	LEU
2	G	1462	ASP
2	G	1480	LYS
2	G	1497	GLU
2	G	1524	LEU
2	G	1542	ASN
2	G	1545	LEU
2	G	1552	GLU
2	G	1558	THR
2	G	1564	LEU
2	H	1720	PHE
2	H	1742	ASN
2	H	1752	GLU
2	H	1759	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (49) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	68	GLN
1	A	71	ASN
1	A	77	GLN
1	A	95	HIS
1	A	157	GLN
1	A	180	ASN
1	B	268	GLN
1	B	278	ASN
1	B	320	ASN
1	B	341	ASN
1	B	357	GLN
1	B	380	ASN
1	C	446	HIS
1	C	468	GLN
1	C	471	ASN
1	C	541	ASN
1	C	568	ASN
1	D	660	ASN
1	D	668	GLN
1	D	671	ASN
1	D	720	ASN
1	D	737	ASN
1	D	741	ASN
1	D	757	GLN
1	D	768	ASN
1	D	780	ASN
2	E	1056	GLN
2	E	1109	GLN
2	E	1118	GLN
2	E	1123	ASN
2	E	1157	GLN
2	F	1242	ASN
2	F	1256	GLN
2	F	1275	GLN
2	F	1288	GLN
2	F	1309	GLN
2	F	1323	ASN
2	F	1342	ASN
2	G	1439	ASN
2	G	1498	ASN
2	G	1509	GLN
2	G	1532	ASN
2	G	1542	ASN

*Continued on next page...*

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Mol	Chain	Res	Type
2	H	1656	GLN
2	H	1688	GLN
2	H	1703	ASN
2	H	1730	GLN
2	H	1742	ASN
2	H	1751	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

### 6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.