



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 6, 2023 – 03:06 am GMT

PDB ID : 1H1L
Title : NITROGENASE MO-FE PROTEIN FROM KLEBSIELLA PNEUMONIAE,
NIFV MUTANT
Authors : Mayer, S.M.; Gormal, C.A.; Smith, B.E.; Lawson, D.M.
Deposited on : 2002-07-18
Resolution : 1.90 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

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>.

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

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

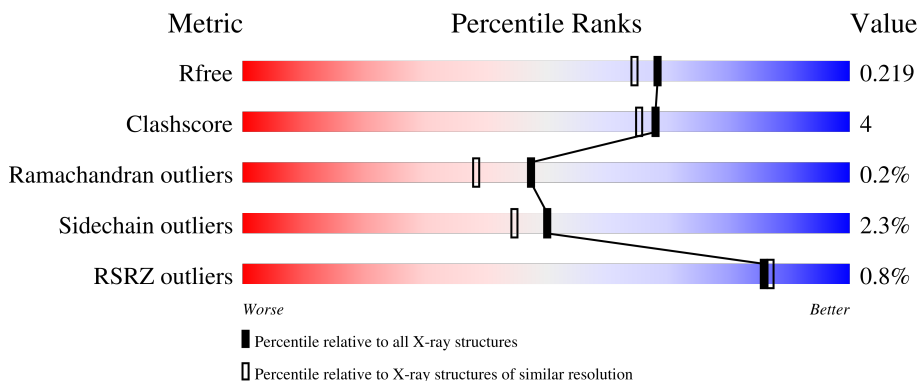
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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))
R_{free}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 ≥ 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	481	 80% 18% ..
1	C	481	 75% 22% ..
2	B	519	 83% 16% .
2	D	519	 82% 16% .

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 17025 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 NITROGENASE MOLYBDENUM IRON PROTEIN ALPHA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	478	3664	2331	627	682	24	0	0	0
1	C	478	3674	2335	629	686	24	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	85	VAL	ALA	conflict	UNP P00466
A	94	GLY	GLU	conflict	UNP P00466
C	85	VAL	ALA	conflict	UNP P00466
C	94	GLY	GLU	conflict	UNP P00466

- Molecule 2 is a protein called NITROGENASE MOLYBDENUM IRON PROTEIN BETA CHAIN.

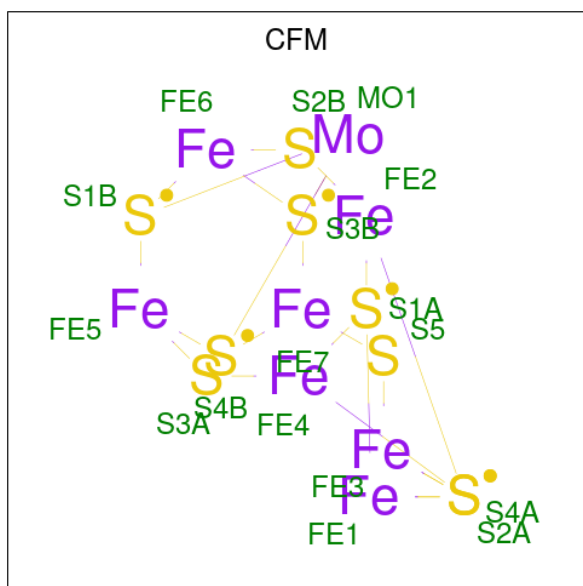
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	519	4026	2567	679	752	28	0	0	0
2	D	519	4028	2568	678	754	28	0	0	0

- Molecule 3 is CITRIC ACID (three-letter code: CIT) (formula: C₆H₈O₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	6	7		
3	C	1	Total	C	O	0	0
			13	6	7		

- Molecule 4 is FE-MO-S CLUSTER (three-letter code: CFM) (formula: Fe₇MoS₉).

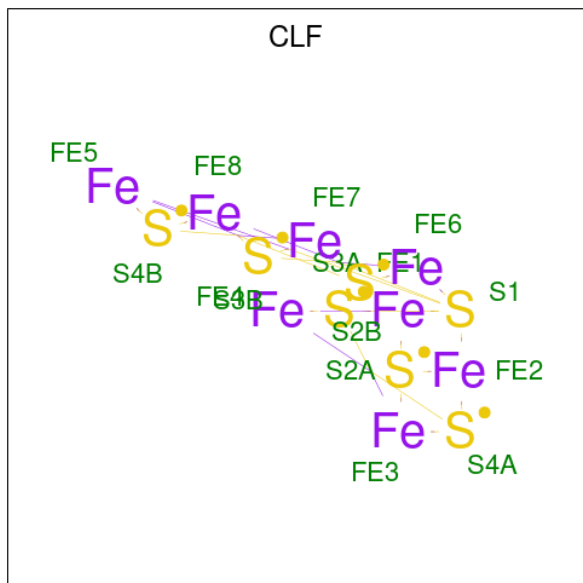


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	Fe	Mo	S	0	0
			17	7	1	9		
4	C	1	Total	Fe	Mo	S	0	0
			17	7	1	9		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	2	Total Mg 2 2	0	0
5	B	2	Total Mg 2 2	0	0

- Molecule 6 is FE(8)-S(7) CLUSTER (three-letter code: CLF) (formula: Fe₈S₇).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total Fe S 15 8 7	0	0
6	D	1	Total Fe S 15 8 7	0	0

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	1	Total Cl 1 1	0	0
7	D	1	Total Cl 1 1	0	0

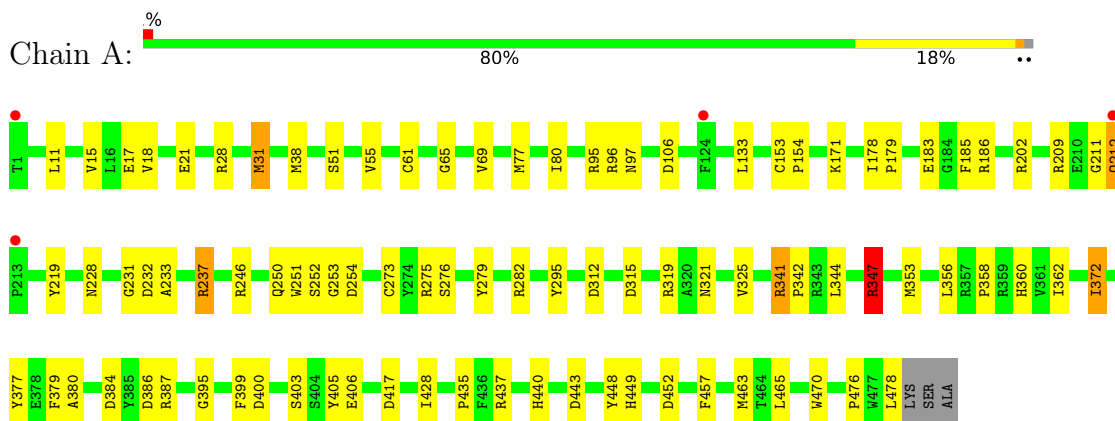
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	309	Total 309	O 309	0	0
8	B	474	Total 474	O 474	0	0
8	C	283	Total 283	O 283	0	0
8	D	471	Total 471	O 471	0	0

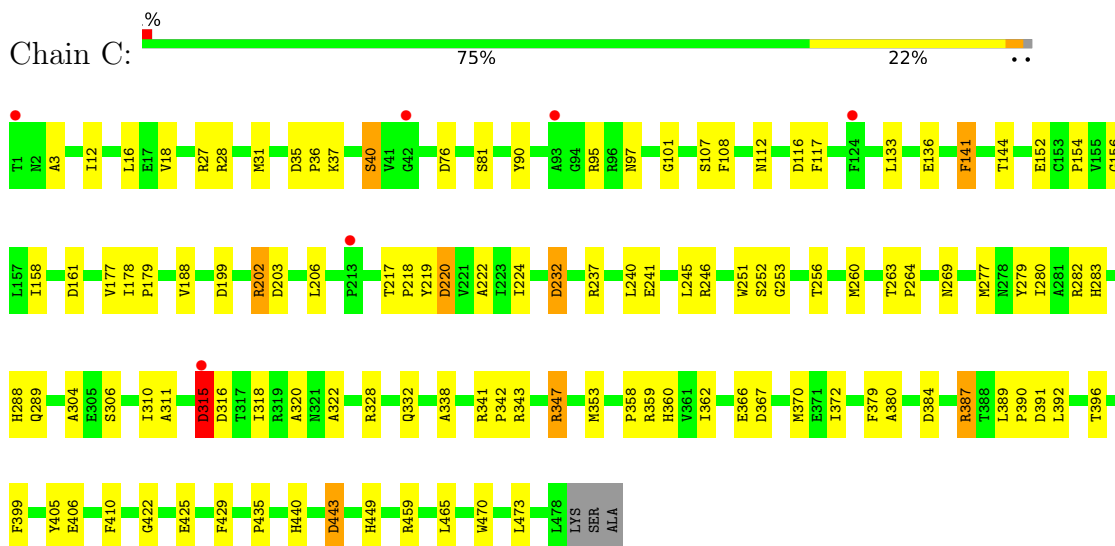
3 Residue-property plots i

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

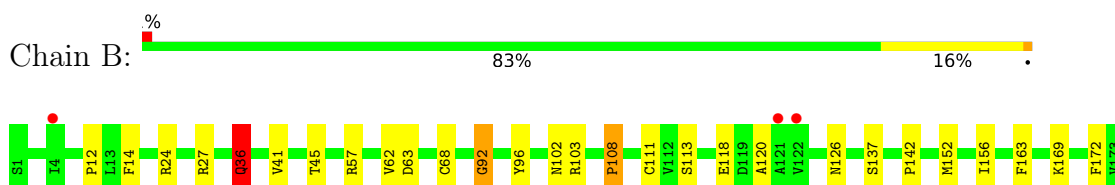
• Molecule 1: NITROGENASE MOLYBDENUM IRON PROTEIN ALPHA CHAIN

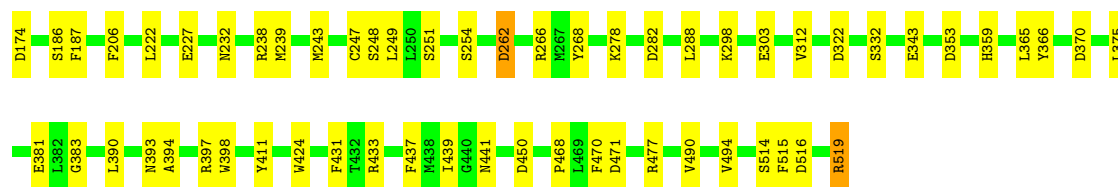


• Molecule 1: NITROGENASE MOLYBDENUM IRON PROTEIN ALPHA CHAIN

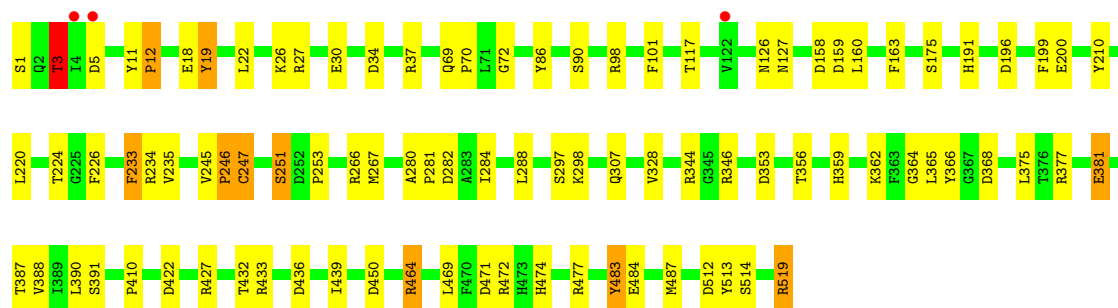
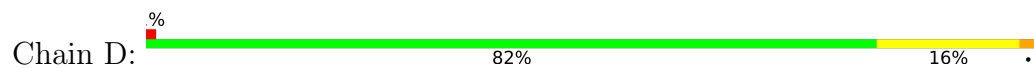


• Molecule 2: NITROGENASE MOLYBDENUM IRON PROTEIN BETA CHAIN





• Molecule 2: NITROGENASE MOLYBDENUM IRON PROTEIN BETA CHAIN



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	204.06Å 75.06Å 164.26Å 90.00° 123.95° 90.00°	Depositor
Resolution (Å)	40.00 – 1.90 39.36 – 1.90	Depositor EDS
% Data completeness (in resolution range)	94.2 (40.00-1.90) 94.3 (39.36-1.90)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.50 (at 1.89Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.176 , 0.236 0.164 , 0.219	Depositor DCC
R_{free} test set	7646 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	20.3	Xtrriage
Anisotropy	0.255	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 57.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	17025	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.23% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: CIT, CFM, MG, CLF, CL

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	0.68	0/3751	1.53	48/5090 (0.9%)
1	C	0.65	0/3761	1.53	45/5102 (0.9%)
2	B	0.70	0/4124	1.48	53/5604 (0.9%)
2	D	0.74	2/4126 (0.0%)	1.49	56/5606 (1.0%)
All	All	0.69	2/15762 (0.0%)	1.51	202/21402 (0.9%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	12
1	C	0	22
2	B	0	13
2	D	0	14
All	All	0	61

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	307	GLN	CD-NE2	6.91	1.50	1.32
2	D	307	GLN	CG-CD	-5.23	1.39	1.51

All (202) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	328	ARG	NE-CZ-NH1	15.59	128.10	120.30
2	D	433	ARG	NE-CZ-NH1	14.45	127.53	120.30
1	A	96	ARG	NE-CZ-NH1	-14.41	113.09	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	282	ASP	CB-CG-OD1	13.86	130.78	118.30
2	D	344	ARG	NE-CZ-NH2	-12.54	114.03	120.30
1	A	315	ASP	CB-CG-OD1	12.32	129.39	118.30
1	C	95	ARG	NE-CZ-NH2	-11.78	114.41	120.30
1	A	96	ARG	NE-CZ-NH2	11.73	126.17	120.30
1	C	347	ARG	NE-CZ-NH1	11.06	125.83	120.30
1	A	341	ARG	NE-CZ-NH2	11.01	125.81	120.30
2	B	103	ARG	NE-CZ-NH1	10.42	125.51	120.30
1	C	95	ARG	NE-CZ-NH1	10.33	125.46	120.30
2	B	519	ARG	NE-CZ-NH1	-10.31	115.15	120.30
2	D	234	ARG	NE-CZ-NH1	10.28	125.44	120.30
1	A	209	ARG	CD-NE-CZ	9.98	137.57	123.60
2	D	427	ARG	NE-CZ-NH1	9.95	125.28	120.30
2	B	238	ARG	NE-CZ-NH2	-9.80	115.40	120.30
1	A	202	ARG	NE-CZ-NH2	-9.79	115.41	120.30
2	B	24	ARG	NE-CZ-NH2	-9.67	115.47	120.30
1	C	141	PHE	CB-CG-CD1	-9.67	114.03	120.80
1	C	347	ARG	NE-CZ-NH2	-9.57	115.51	120.30
1	A	246	ARG	NE-CZ-NH2	-9.22	115.69	120.30
1	C	328	ARG	NE-CZ-NH2	-9.15	115.72	120.30
2	B	27	ARG	NE-CZ-NH2	9.12	124.86	120.30
2	B	431	PHE	CB-CG-CD2	-9.11	114.42	120.80
1	C	343	ARG	NE-CZ-NH2	-9.06	115.77	120.30
2	B	103	ARG	NE-CZ-NH2	-9.04	115.78	120.30
2	B	282	ASP	CB-CG-OD2	-9.03	110.18	118.30
2	D	353	ASP	CB-CG-OD1	8.95	126.36	118.30
1	A	106	ASP	CB-CG-OD1	8.73	126.16	118.30
1	C	28	ARG	CD-NE-CZ	8.63	135.69	123.60
2	D	234	ARG	NE-CZ-NH2	-8.60	116.00	120.30
2	D	37	ARG	CD-NE-CZ	8.56	135.59	123.60
2	D	450	ASP	CB-CG-OD2	8.46	125.91	118.30
2	B	431	PHE	CB-CG-CD1	8.40	126.68	120.80
2	D	472	ARG	NE-CZ-NH2	-8.36	116.12	120.30
2	B	433	ARG	NE-CZ-NH1	8.28	124.44	120.30
1	C	141	PHE	CB-CG-CD2	8.23	126.56	120.80
1	A	319	ARG	NE-CZ-NH2	-8.22	116.19	120.30
2	B	516	ASP	CB-CG-OD1	8.10	125.59	118.30
1	C	399	PHE	CB-CG-CD1	8.04	126.43	120.80
2	D	199	PHE	CB-CG-CD1	-7.86	115.30	120.80
2	B	433	ARG	NE-CZ-NH2	-7.82	116.39	120.30
1	A	295	TYR	CB-CG-CD1	7.73	125.64	121.00
1	C	443	ASP	CB-CG-OD2	7.72	125.25	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	307	GLN	CG-CD-NE2	-7.68	98.26	116.70
2	D	377	ARG	NE-CZ-NH1	7.68	124.14	120.30
1	A	341	ARG	NE-CZ-NH1	-7.68	116.46	120.30
2	D	27	ARG	NE-CZ-NH1	7.64	124.12	120.30
1	C	203	ASP	CB-CG-OD2	7.59	125.13	118.30
2	B	519	ARG	NE-CZ-NH2	7.59	124.09	120.30
2	B	433	ARG	CD-NE-CZ	7.58	134.22	123.60
1	A	254	ASP	CB-CG-OD1	7.58	125.12	118.30
2	B	36	GLN	N-CA-CB	-7.57	96.97	110.60
1	A	319	ARG	CD-NE-CZ	7.54	134.16	123.60
1	C	459	ARG	NE-CZ-NH1	7.52	124.06	120.30
1	A	95	ARG	NE-CZ-NH1	-7.48	116.56	120.30
1	A	282	ARG	NE-CZ-NH2	7.44	124.02	120.30
2	D	159	ASP	CB-CG-OD2	-7.35	111.69	118.30
2	B	450	ASP	CB-CG-OD1	7.32	124.89	118.30
1	A	219	TYR	CB-CG-CD1	-7.25	116.65	121.00
2	B	24	ARG	NE-CZ-NH1	7.24	123.92	120.30
1	C	117	PHE	CB-CG-CD1	7.20	125.84	120.80
2	B	477	ARG	NE-CZ-NH1	-7.13	116.74	120.30
2	D	422	ASP	CB-CG-OD1	7.10	124.69	118.30
1	C	425	GLU	OE1-CD-OE2	-7.09	114.79	123.30
1	A	387	ARG	NE-CZ-NH2	-7.09	116.75	120.30
2	B	353	ASP	CB-CG-OD1	6.97	124.57	118.30
2	D	282	ASP	CB-CG-OD2	-6.90	112.09	118.30
1	C	108	PHE	CB-CG-CD2	-6.78	116.06	120.80
2	D	163	PHE	CB-CG-CD1	6.78	125.54	120.80
1	A	183	GLU	CA-C-O	6.76	134.30	120.10
1	C	410	PHE	CB-CG-CD1	6.76	125.53	120.80
1	A	28	ARG	NE-CZ-NH2	-6.76	116.92	120.30
2	D	433	ARG	NE-CZ-NH2	-6.73	116.93	120.30
2	B	515	PHE	CB-CG-CD2	-6.72	116.10	120.80
1	A	379	PHE	CB-CG-CD1	6.71	125.50	120.80
2	B	381	GLU	CB-CG-CD	6.69	132.26	114.20
1	C	410	PHE	CB-CG-CD2	-6.69	116.12	120.80
2	D	98	ARG	NE-CZ-NH2	-6.67	116.97	120.30
1	A	437	ARG	NE-CZ-NH1	6.66	123.63	120.30
2	D	90	SER	N-CA-CB	-6.63	100.56	110.50
1	C	232	ASP	CB-CG-OD1	6.58	124.23	118.30
1	C	199	ASP	CB-CG-OD2	-6.58	112.38	118.30
1	A	186	ARG	NE-CZ-NH2	6.56	123.58	120.30
2	D	464	ARG	NE-CZ-NH1	6.56	123.58	120.30
2	B	187	PHE	CB-CG-CD1	-6.55	116.22	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	202	ARG	NE-CZ-NH2	-6.54	117.03	120.30
1	C	232	ASP	CB-CG-OD2	-6.51	112.44	118.30
2	D	27	ARG	NE-CZ-NH2	-6.50	117.05	120.30
2	D	34	ASP	CB-CG-OD2	-6.46	112.48	118.30
2	D	346	ARG	NE-CZ-NH2	-6.44	117.08	120.30
1	C	379	PHE	CB-CG-CD2	-6.42	116.31	120.80
1	C	399	PHE	CB-CG-CD2	-6.41	116.31	120.80
1	A	219	TYR	CB-CG-CD2	6.39	124.84	121.00
1	A	406	GLU	OE1-CD-OE2	-6.38	115.64	123.30
1	C	117	PHE	CB-CG-CD2	-6.31	116.38	120.80
2	D	368	ASP	CB-CG-OD2	6.30	123.97	118.30
2	B	137	SER	CB-CA-C	-6.29	98.14	110.10
2	D	433	ARG	CD-NE-CZ	6.28	132.40	123.60
1	A	448	TYR	CB-CG-CD2	-6.27	117.24	121.00
2	D	226	PHE	CB-CG-CD1	-6.25	116.43	120.80
2	D	381	GLU	CB-CG-CD	6.24	131.05	114.20
1	A	417	ASP	CB-CG-OD2	6.23	123.91	118.30
1	C	161	ASP	CB-CG-OD1	6.17	123.85	118.30
2	D	159	ASP	CB-CG-OD1	6.17	123.85	118.30
1	A	279	TYR	CB-CG-CD2	-6.12	117.33	121.00
2	B	163	PHE	CB-CG-CD2	-6.11	116.53	120.80
2	D	101	PHE	CB-CG-CD2	-6.11	116.53	120.80
1	A	295	TYR	CB-CG-CD2	-6.10	117.34	121.00
1	A	347	ARG	NE-CZ-NH2	-6.07	117.27	120.30
2	D	436	ASP	CB-CG-OD2	6.07	123.76	118.30
1	C	328	ARG	CD-NE-CZ	6.05	132.07	123.60
2	D	196	ASP	CB-CG-OD1	6.05	123.74	118.30
1	A	379	PHE	CB-CG-CD2	-6.01	116.59	120.80
2	B	27	ARG	NE-CZ-NH1	-6.00	117.30	120.30
2	B	57	ARG	NE-CZ-NH1	5.98	123.29	120.30
1	A	399	PHE	CB-CG-CD2	-5.94	116.64	120.80
1	C	27	ARG	NE-CZ-NH2	-5.92	117.34	120.30
2	B	343	GLU	OE1-CD-OE2	-5.92	116.20	123.30
2	B	113	SER	CB-CA-C	-5.91	98.86	110.10
1	C	387	ARG	NE-CZ-NH1	5.91	123.26	120.30
1	A	452	ASP	CB-CG-OD2	-5.91	112.98	118.30
2	B	163	PHE	CB-CG-CD1	5.90	124.93	120.80
2	D	519	ARG	CD-NE-CZ	-5.88	115.36	123.60
1	C	136	GLU	OE1-CD-OE2	-5.82	116.31	123.30
2	D	328	VAL	CA-CB-CG2	-5.82	102.17	110.90
2	B	14	PHE	CB-CG-CD2	-5.75	116.77	120.80
1	A	399	PHE	CB-CG-CD1	5.74	124.82	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	427	ARG	NE-CZ-NH2	-5.73	117.44	120.30
2	B	370	ASP	CB-CG-OD2	5.72	123.45	118.30
2	B	471	ASP	CB-CG-OD1	5.72	123.45	118.30
2	B	24	ARG	CD-NE-CZ	5.71	131.60	123.60
1	A	437	ARG	NE-CZ-NH2	-5.71	117.45	120.30
1	C	315	ASP	CA-CB-CG	5.70	125.94	113.40
1	C	116	ASP	CB-CG-OD2	5.69	123.42	118.30
1	A	347	ARG	NE-CZ-NH1	5.68	123.14	120.30
1	C	387	ARG	NE-CZ-NH2	-5.67	117.47	120.30
1	A	478	LEU	CA-C-O	-5.67	108.20	120.10
1	A	457	PHE	CB-CG-CD1	-5.66	116.84	120.80
1	C	347	ARG	CD-NE-CZ	5.63	131.48	123.60
2	B	515	PHE	CB-CG-CD1	5.62	124.73	120.80
1	A	185	PHE	CB-CG-CD1	-5.61	116.87	120.80
1	C	379	PHE	CB-CG-CD1	5.60	124.72	120.80
2	D	391	SER	N-CA-CB	5.60	118.91	110.50
2	D	483	TYR	CB-CG-CD1	5.59	124.36	121.00
1	C	279	TYR	CB-CG-CD2	-5.56	117.67	121.00
1	A	386	ASP	CB-CG-OD1	5.54	123.29	118.30
2	D	484	GLU	OE1-CD-OE2	-5.54	116.66	123.30
2	D	163	PHE	CB-CG-CD2	-5.53	116.93	120.80
1	C	406	GLU	OE1-CD-OE2	-5.52	116.67	123.30
2	D	477	ARG	NE-CZ-NH2	-5.52	117.54	120.30
1	C	282	ARG	NE-CZ-NH2	5.51	123.06	120.30
2	D	101	PHE	CB-CG-CD1	5.51	124.66	120.80
1	A	312	ASP	CB-CG-OD2	5.50	123.25	118.30
2	D	199	PHE	CB-CG-CD2	5.50	124.65	120.80
2	D	266	ARG	NE-CZ-NH1	5.50	123.05	120.30
2	D	513	TYR	CB-CG-CD1	-5.43	117.74	121.00
1	A	28	ARG	NE-CZ-NH1	5.40	123.00	120.30
2	B	322	ASP	CB-CG-OD1	5.40	123.16	118.30
2	D	127	ASN	N-CA-CB	5.38	120.29	110.60
2	B	322	ASP	CB-CG-OD2	5.37	123.13	118.30
2	B	63	ASP	CB-CG-OD1	5.36	123.12	118.30
2	B	397	ARG	NE-CZ-NH2	5.35	122.97	120.30
2	D	19	TYR	CB-CG-CD1	-5.32	117.81	121.00
2	D	200	GLU	CG-CD-OE1	5.31	128.93	118.30
2	D	483	TYR	CB-CG-CD2	-5.31	117.81	121.00
1	A	237	ARG	NE-CZ-NH1	-5.31	117.65	120.30
1	C	367	ASP	CB-CG-OD2	5.30	123.07	118.30
2	B	96	TYR	CB-CG-CD1	5.30	124.18	121.00
2	B	470	PHE	CB-CG-CD1	5.28	124.50	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	172	PHE	CB-CG-CD1	-5.28	117.11	120.80
2	B	262	ASP	CB-CG-OD1	5.26	123.04	118.30
1	A	183	GLU	O-C-N	-5.26	114.26	123.20
2	B	187	PHE	CB-CG-CD2	5.25	124.48	120.80
2	B	239	MET	CG-SD-CE	5.24	108.58	100.20
2	D	200	GLU	OE1-CD-OE2	-5.22	117.03	123.30
1	C	188	VAL	CA-CB-CG2	5.19	118.69	110.90
1	C	429	PHE	CB-CG-CD2	5.19	124.43	120.80
2	B	437	PHE	CB-CG-CD2	-5.18	117.17	120.80
1	A	186	ARG	NE-CZ-NH1	-5.17	117.71	120.30
2	D	158	ASP	CB-CG-OD2	-5.17	113.65	118.30
1	A	400	ASP	CB-CG-OD1	-5.16	113.66	118.30
2	D	34	ASP	N-CA-CB	5.16	119.88	110.60
1	A	202	ARG	NH1-CZ-NH2	5.15	125.06	119.40
2	D	471	ASP	CB-CG-OD2	-5.14	113.67	118.30
2	D	513	TYR	CB-CG-CD2	5.14	124.08	121.00
2	D	233	PHE	CB-CG-CD1	5.14	124.39	120.80
2	B	248	SER	N-CA-CB	5.12	118.18	110.50
2	B	174	ASP	CB-CG-OD1	5.11	122.90	118.30
2	D	251	SER	N-CA-CB	5.11	118.17	110.50
1	C	370	MET	CG-SD-CE	-5.11	92.02	100.20
2	B	57	ARG	NE-CZ-NH2	-5.11	117.75	120.30
2	D	160	LEU	N-CA-CB	-5.11	100.18	110.40
2	B	322	ASP	OD1-CG-OD2	-5.10	113.62	123.30
2	B	102	ASN	N-CA-CB	5.08	119.74	110.60
1	A	315	ASP	CB-CG-OD2	-5.05	113.75	118.30
2	B	172	PHE	CB-CG-CD2	5.05	124.33	120.80
2	B	268	TYR	CB-CG-CD2	-5.04	117.98	121.00
1	A	275	ARG	CD-NE-CZ	5.03	130.65	123.60
1	C	443	ASP	O-C-N	-5.01	114.69	122.70
1	C	28	ARG	NE-CZ-NH1	5.00	122.80	120.30

There are no chirality outliers.

All (61) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	17	GLU	Mainchain
1	A	171	LYS	Mainchain
1	A	179	PRO	Mainchain
1	A	211	GLY	Mainchain
1	A	212	GLN	Mainchain
1	A	231	GLY	Mainchain

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Mol	Chain	Res	Type	Group
1	A	253	GLY	Mainchain
1	A	276	SER	Mainchain
1	A	31	MET	Mainchain
1	A	377	TYR	Mainchain
1	A	395	GLY	Mainchain
1	A	476	PRO	Mainchain
2	B	111	CYS	Mainchain
2	B	118	GLU	Mainchain
2	B	120	ALA	Mainchain
2	B	142	PRO	Mainchain
2	B	169	LYS	Mainchain
2	B	243	MET	Mainchain
2	B	254	SER	Mainchain
2	B	303	GLU	Mainchain
2	B	312	VAL	Mainchain
2	B	332	SER	Mainchain
2	B	383	GLY	Mainchain
2	B	393	ASN	Mainchain
2	B	92	GLY	Mainchain
1	C	141	PHE	Mainchain
1	C	144	THR	Mainchain
1	C	156	GLY	Mainchain
1	C	177	VAL	Mainchain
1	C	179	PRO	Mainchain
1	C	220	ASP	Mainchain
1	C	240	LEU	Mainchain
1	C	246	ARG	Mainchain
1	C	253	GLY	Mainchain
1	C	277	MET	Mainchain
1	C	3	ALA	Mainchain
1	C	304	ALA	Mainchain
1	C	311	ALA	Mainchain
1	C	318	ILE	Mainchain
1	C	320	ALA	Mainchain
1	C	322	ALA	Mainchain
1	C	338	ALA	Mainchain
1	C	37	LYS	Mainchain
1	C	387	ARG	Mainchain
1	C	40	SER	Mainchain
1	C	422	GLY	Mainchain
1	C	90	TYR	Mainchain
2	D	175	SER	Mainchain

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Mol	Chain	Res	Type	Group
2	D	210	TYR	Mainchain
2	D	224	THR	Mainchain
2	D	245	VAL	Mainchain
2	D	246	PRO	Mainchain
2	D	267	MET	Mainchain
2	D	284	ILE	Mainchain
2	D	297	SER	Mainchain
2	D	3	THR	Mainchain
2	D	356	THR	Mainchain
2	D	410	PRO	Mainchain
2	D	432	THR	Mainchain
2	D	474	HIS	Mainchain
2	D	512	ASP	Mainchain

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	3664	0	3503	30	0
1	C	3674	0	3518	45	0
2	B	4026	0	3872	19	0
2	D	4028	0	3882	23	0
3	A	13	0	4	3	0
3	C	13	0	4	2	0
4	A	17	0	0	0	0
4	C	17	0	0	0	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
6	B	15	0	0	0	0
6	D	15	0	0	0	0
7	B	1	0	0	0	0
7	D	1	0	0	0	0
8	A	309	0	0	4	0
8	B	474	0	0	2	0
8	C	283	0	0	3	0
8	D	471	0	0	3	0
All	All	17025	0	14783	114	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 4.

All (114) 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)
3:A:1479:CIT:O4	8:A:2309:HOH:O	1.71	1.07
1:C:237:ARG:HD3	2:D:22:LEU:HD21	1.50	0.93
1:C:217:THR:HG22	1:C:219:TYR:H	1.29	0.92
1:A:428:ILE:HG13	2:B:108:PRO:HB3	1.69	0.74
2:D:3:THR:HG22	2:D:5:ASP:H	1.52	0.73
1:C:18:VAL:HG11	1:C:405:TYR:CE1	2.24	0.72
1:A:347:ARG:HG2	1:A:465:LEU:HD21	1.71	0.72
3:C:1479:CIT:O2	8:C:2277:HOH:O	2.07	0.72
3:A:1479:CIT:O2	8:A:2307:HOH:O	2.16	0.63
1:A:362:ILE:HG12	1:A:372:ILE:HG12	1.81	0.62
8:C:2135:HOH:O	2:D:117:THR:HG22	1.99	0.62
2:D:519:ARG:HD3	8:D:2468:HOH:O	1.99	0.61
2:B:36:GLN:HB2	8:B:2054:HOH:O	2.00	0.61
1:C:315:ASP:OD1	1:C:316:ASP:N	2.34	0.61
1:A:273:CYS:HA	1:A:356:LEU:HD22	1.84	0.59
1:A:61:CYS:HB3	2:B:92:GLY:HA3	1.84	0.59
1:C:347:ARG:HG3	1:C:465:LEU:HD21	1.84	0.59
1:C:217:THR:HB	1:C:220:ASP:OD1	2.02	0.59
2:D:280:ALA:HB3	2:D:281:PRO:HD3	1.84	0.58
1:C:435:PRO:HA	1:C:470:TRP:CZ2	2.39	0.58
2:B:519:ARG:HD3	8:B:2474:HOH:O	2.05	0.57
1:A:77:MET:HE1	1:A:178:ILE:HD12	1.86	0.56
1:A:463:MET:HG3	2:D:359:HIS:CG	2.41	0.56
1:A:18:VAL:HG11	1:A:405:TYR:CE2	2.42	0.55
1:C:332:GLN:HG3	8:D:2003:HOH:O	2.05	0.55
1:C:12:ILE:HD13	1:C:31:MET:HG3	1.89	0.55
1:C:380:ALA:HB1	1:C:384:ASP:HB2	1.90	0.54
1:A:380:ALA:HB1	1:A:384:ASP:HB2	1.90	0.53
2:D:375:LEU:HD21	2:D:439:ILE:HG21	1.91	0.53
1:C:217:THR:CG2	1:C:219:TYR:H	2.13	0.53
1:C:76:ASP:OD2	1:C:256:THR:HB	2.08	0.53
2:D:26:LYS:NZ	2:D:30:GLU:OE2	2.41	0.53
1:C:217:THR:HG22	1:C:219:TYR:N	2.11	0.52
1:C:206:LEU:HD22	1:C:280:ILE:HD11	1.92	0.52
2:D:366:TYR:HA	2:D:390:LEU:O	2.10	0.51
1:A:153:CYS:HB2	1:A:154:PRO:HD3	1.92	0.51
1:A:237:ARG:HD2	1:A:250:GLN:OE1	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:344:LEU:HD23	1:A:465:LEU:HD23	1.92	0.50
1:A:212:GLN:OE1	8:A:2151:HOH:O	2.19	0.50
2:D:69:GLN:HB2	2:D:70:PRO:HD3	1.92	0.50
2:D:3:THR:HG22	2:D:5:ASP:N	2.23	0.50
1:A:51:SER:HB3	8:A:2259:HOH:O	2.12	0.49
1:C:237:ARG:HD3	2:D:22:LEU:CD2	2.34	0.49
2:D:381:GLU:HG3	8:D:2355:HOH:O	2.11	0.49
1:C:217:THR:HG23	1:C:218:PRO:HD2	1.95	0.49
1:C:224:ILE:HA	1:C:251:TRP:HB2	1.95	0.49
1:C:12:ILE:O	1:C:16:LEU:HG	2.13	0.48
1:C:219:TYR:HB3	1:C:245:LEU:HD23	1.94	0.48
2:B:375:LEU:HD21	2:B:439:ILE:HG21	1.96	0.47
1:A:65:GLY:O	1:A:69:VAL:HB	2.14	0.47
1:C:359:ARG:HA	1:C:362:ILE:HD12	1.96	0.46
1:A:11:LEU:O	1:A:15:VAL:HG23	2.15	0.46
1:C:133:LEU:C	1:C:133:LEU:HD23	2.35	0.46
1:A:80:ILE:HD13	1:A:133:LEU:HD22	1.96	0.46
1:C:154:PRO:O	1:C:158:ILE:HG12	2.15	0.46
1:C:18:VAL:HG11	1:C:405:TYR:CZ	2.51	0.46
1:C:222:ALA:HB3	1:C:269:ASN:OD1	2.16	0.46
2:D:11:TYR:HA	2:D:12:PRO:HA	1.76	0.45
2:D:72:GLY:HA3	2:D:191:HIS:O	2.17	0.45
1:A:228:ASN:HA	1:A:233:ALA:H	1.82	0.44
2:B:366:TYR:HA	2:B:390:LEU:O	2.18	0.44
1:C:101:GLY:HA3	1:C:107:SER:OG	2.17	0.44
1:A:353:MET:HB2	1:A:358:PRO:HD3	1.99	0.44
1:A:440:HIS:HB3	3:A:1479:CIT:O5	2.17	0.44
1:C:232:ASP:HB3	1:C:449:HIS:ND1	2.33	0.44
1:A:232:ASP:HB3	1:A:449:HIS:ND1	2.33	0.44
1:C:362:ILE:O	1:C:366:GLU:HG3	2.17	0.44
1:A:77:MET:CE	1:A:178:ILE:HD12	2.48	0.44
1:A:435:PRO:HA	1:A:470:TRP:CZ2	2.52	0.44
1:C:288:HIS:O	1:C:289:GLN:HB2	2.17	0.44
2:D:364:GLY:HA2	2:D:388:VAL:O	2.17	0.44
1:A:133:LEU:HD23	1:A:133:LEU:C	2.38	0.43
2:B:441:ASN:HB2	2:B:468:PRO:O	2.18	0.43
1:C:440:HIS:HB3	3:C:1479:CIT:O5	2.18	0.43
1:C:353:MET:HB2	1:C:358:PRO:HD3	2.00	0.43
2:B:490:VAL:O	2:B:494:VAL:HG12	2.19	0.43
2:D:362:LYS:HD3	2:D:387:THR:HG21	2.00	0.43
2:D:233:PHE:CE1	2:D:253:PRO:HD2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:55:VAL:O	1:A:403:SER:HB2	2.19	0.43
2:B:359:HIS:HE1	2:B:411:TYR:OH	2.01	0.43
1:C:341:ARG:HB3	1:C:342:PRO:HD3	2.01	0.43
1:C:380:ALA:HB1	1:C:384:ASP:CB	2.47	0.43
2:D:220:LEU:O	2:D:247:CYS:HA	2.18	0.43
2:B:222:LEU:HB2	2:B:249:LEU:HD23	2.01	0.43
1:C:306:SER:O	1:C:310:ILE:HG13	2.18	0.42
2:D:18:GLU:HG2	2:D:19:TYR:N	2.34	0.42
2:B:206:PHE:HD1	2:B:278:LYS:HE3	1.85	0.42
1:C:256:THR:O	1:C:260:MET:HG3	2.20	0.42
2:D:483:TYR:O	2:D:487:MET:HG3	2.20	0.42
1:C:341:ARG:N	1:C:342:PRO:CD	2.82	0.42
1:A:321:ASN:O	1:A:325:VAL:HG23	2.19	0.41
2:B:262:ASP:OD2	2:B:266:ARG:NH2	2.36	0.41
1:C:362:ILE:HG12	1:C:372:ILE:HG13	2.02	0.41
2:B:68:CYS:HB2	2:B:186:SER:HB2	2.02	0.41
1:C:263:THR:N	1:C:264:PRO:CD	2.84	0.41
1:A:341:ARG:HB3	1:A:342:PRO:HD3	2.03	0.41
1:A:341:ARG:N	1:A:342:PRO:CD	2.84	0.41
2:B:41:VAL:O	2:B:45:THR:HG23	2.20	0.41
1:C:251:TRP:HA	1:C:252:SER:HA	1.86	0.41
1:A:61:CYS:HB3	2:B:92:GLY:CA	2.51	0.41
2:B:288:LEU:HD11	2:B:298:LYS:HA	2.03	0.41
1:C:389:LEU:HB2	1:C:390:PRO:HD3	2.01	0.41
1:C:392:LEU:HD22	1:C:396:THR:HG21	2.03	0.41
2:B:227:GLU:OE2	2:B:232:ASN:ND2	2.52	0.41
1:C:18:VAL:H	1:C:18:VAL:HG12	1.56	0.41
2:D:288:LEU:HD11	2:D:298:LYS:HA	2.03	0.41
1:C:202:ARG:HG3	1:C:283:HIS:CE1	2.56	0.40
2:B:394:ALA:HB1	2:B:398:TRP:CE3	2.56	0.40
2:D:464:ARG:HB3	2:D:469:LEU:HD22	2.03	0.40
1:A:251:TRP:HA	1:A:252:SER:HA	1.70	0.40
2:B:62:VAL:HB	2:B:424:TRP:HB2	2.02	0.40
1:C:35:ASP:HA	1:C:36:PRO:HD2	1.88	0.40
1:C:81:SER:HB3	1:C:152:GLU:OE2	2.22	0.40
1:C:315:ASP:HB3	8:C:2150:HOH:O	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	476/481 (99%)	455 (96%)	21 (4%)	0	100	100
1	C	476/481 (99%)	457 (96%)	19 (4%)	0	100	100
2	B	517/519 (100%)	503 (97%)	13 (2%)	1 (0%)	47	38
2	D	517/519 (100%)	503 (97%)	12 (2%)	2 (0%)	34	24
All	All	1986/2000 (99%)	1918 (97%)	65 (3%)	3 (0%)	47	38

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	251	SER
2	B	251	SER
2	D	246	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	372/399 (93%)	364 (98%)	8 (2%)	52	47
1	C	375/399 (94%)	365 (97%)	10 (3%)	44	38
2	B	422/442 (96%)	413 (98%)	9 (2%)	53	48
2	D	425/442 (96%)	416 (98%)	9 (2%)	53	48
All	All	1594/1682 (95%)	1558 (98%)	36 (2%)	50	45

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	GLU
1	A	31	MET
1	A	38	MET
1	A	97	ASN
1	A	347	ARG
1	A	360	HIS
1	A	372	ILE
1	A	443	ASP
2	B	12	PRO
2	B	36	GLN
2	B	108	PRO
2	B	126	ASN
2	B	152	MET
2	B	156	ILE
2	B	247	CYS
2	B	365	LEU
2	B	514	SER
1	C	40	SER
1	C	97	ASN
1	C	112	ASN
1	C	178	ILE
1	C	241	GLU
1	C	315	ASP
1	C	360	HIS
1	C	391	ASP
1	C	443	ASP
1	C	473	LEU
2	D	1	SER
2	D	3	THR
2	D	12	PRO
2	D	86	TYR
2	D	126	ASN
2	D	235	VAL
2	D	247	CYS
2	D	365	LEU
2	D	514	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	118	GLN
2	B	91	GLN
2	B	359	HIS

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Mol	Chain	Res	Type
1	C	112	ASN
1	C	118	GLN
1	C	430	GLN
1	C	471	ASN
2	D	91	GLN
2	D	359	HIS
2	D	434	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](#)

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	CLF	B	1520	1,2	0,24,24	-	-	-		
4	CFM	A	1480	1	0,24,24	-	-	-		
4	CFM	C	1480	1	0,24,24	-	-	-		
3	CIT	A	1479	-	12,12,12	1.49	1 (8%)	17,17,17	1.95	3 (17%)
3	CIT	C	1479	-	12,12,12	1.49	1 (8%)	17,17,17	2.33	7 (41%)
6	CLF	D	1521	1,2	0,24,24	-	-	-		

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	CIT	A	1479	-	-	2/16/16/16	-
3	CIT	C	1479	-	-	5/16/16/16	-
6	CLF	D	1521	1,2	-	-	0/12/10/10
6	CLF	B	1520	1,2	-	-	0/12/10/10

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1479	CIT	C3-C6	-3.77	1.49	1.53
3	C	1479	CIT	C3-C6	-3.01	1.50	1.53

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1479	CIT	O5-C6-C3	-4.54	115.82	122.25
3	C	1479	CIT	C3-C4-C5	4.48	124.66	113.81
3	A	1479	CIT	O5-C6-C3	-4.19	116.32	122.25
3	A	1479	CIT	O4-C5-O3	-4.07	113.15	123.30
3	A	1479	CIT	O6-C6-C3	3.32	118.81	113.05
3	C	1479	CIT	C4-C3-C6	-3.25	103.12	110.11
3	C	1479	CIT	O6-C6-C3	2.97	118.20	113.05
3	C	1479	CIT	O1-C1-C2	-2.64	115.22	122.94
3	C	1479	CIT	O4-C5-C4	2.50	122.37	114.35
3	C	1479	CIT	O4-C5-O3	-2.04	118.22	123.30

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	1479	CIT	C1-C2-C3-C4
3	C	1479	CIT	C1-C2-C3-C6
3	C	1479	CIT	C1-C2-C3-O7
3	C	1479	CIT	O2-C1-C2-C3
3	A	1479	CIT	C1-C2-C3-C6
3	C	1479	CIT	O1-C1-C2-C3
3	A	1479	CIT	O1-C1-C2-C3

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1479	CIT	3	0
3	C	1479	CIT	2	0

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](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	478/481 (99%)	-0.20	4 (0%) 86 87	14, 23, 35, 44	0
1	C	478/481 (99%)	-0.09	6 (1%) 77 79	15, 26, 39, 50	0
2	B	519/519 (100%)	-0.32	3 (0%) 89 90	13, 20, 34, 46	0
2	D	519/519 (100%)	-0.39	3 (0%) 89 90	12, 20, 34, 44	0
All	All	1994/2000 (99%)	-0.25	16 (0%) 86 87	12, 22, 35, 50	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	122	VAL	4.4
2	D	4	ILE	4.0
2	D	5	ASP	3.6
1	C	315	ASP	3.5
1	A	1	THR	3.1
2	D	122	VAL	3.0
1	A	124	PHE	2.9
1	A	213	PRO	2.9
1	C	124	PHE	2.7
2	B	4	ILE	2.7
1	C	1	THR	2.5
1	A	212	GLN	2.4
1	C	93	ALA	2.3
2	B	121	ALA	2.2
1	C	213	PRO	2.2
1	C	42	GLY	2.1

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	MG	A	3001	1/1	0.82	0.10	28,28,28,28	0
5	MG	A	3003	1/1	0.86	0.20	37,37,37,37	0
3	CIT	C	1479	13/13	0.88	0.51	14,16,21,22	13
3	CIT	A	1479	13/13	0.93	0.53	12,16,17,18	13
5	MG	B	1522	1/1	0.98	0.12	23,23,23,23	0
7	CL	B	1521	1/1	0.98	0.04	26,26,26,26	0
4	CFM	A	1480	17/17	0.99	0.11	12,15,17,17	0
5	MG	B	1523	1/1	0.99	0.06	21,21,21,21	0
6	CLF	B	1520	15/15	0.99	0.08	14,16,19,22	0
6	CLF	D	1521	15/15	0.99	0.10	14,16,18,20	0
4	CFM	C	1480	17/17	0.99	0.08	13,18,19,20	0
7	CL	D	1520	1/1	1.00	0.07	23,23,23,23	0

6.5 Other polymers [i](#)

There are no such residues in this entry.