Full wwPDB X-ray Structure Validation Report (i)

Jan 28, 2019 – 07:45 PM EST

PDB ID	:	5Q03
Title	:	Human liver fructose-1,6-bisphosphatase 1 (fructose 1,6-bisphosphate 1-phosphatase, E.C.3.1.3.11) complexed with the allosteric inhibitor 1-(5-bromo-1,3-thiazol-2-yl)-3-[5-(2-methylpropyl)thiophen-2-yl]sulfonylurea
Authors	:	Ruf, A.; Joseph, C.; Alker, A.; Banner, D.; Tetaz, T.; Benz, J.; Kuhn, B.; Rudolph, M.G.; Yang, H.; Shao, C.; Burley, S.K.
Deposited on	:	2017-04-18
Resolution	:	2.31 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 (i) symbol.

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

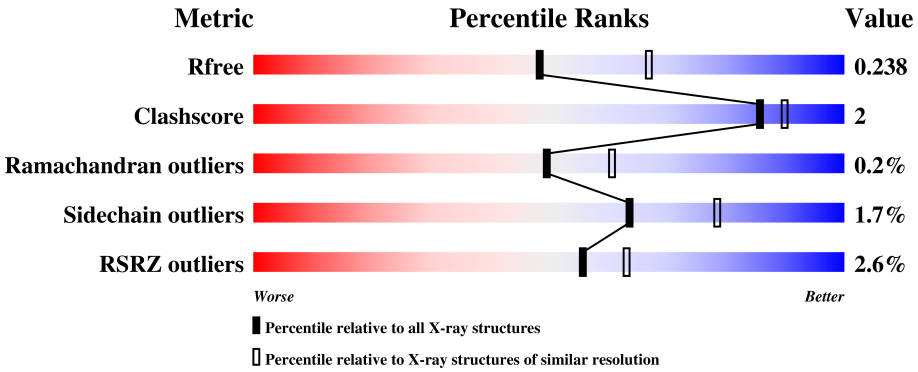
MolProbity	:	4.02b-467
Mogul	:	1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix)	:	1.13
EDS	:	rb-20031633
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac	:	5.8.0158
CCP4	:	7.0 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20031633

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.31 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}	111664	5225 (2.34-2.30)
Clashscore	122126	5849 (2.34-2.30)
Ramachandran outliers	120053	5790 (2.34-2.30)
Sidechain outliers	120020	5789 (2.34-2.30)
RSRZ outliers	108989	5109 (2.34-2.30)

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 on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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 <=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	338	2% 86% 8% • 6%
1	B	338	3% 90% • 6%
1	C	338	2% 88% 5% 6%
1	D	338	% 88% 6% 6%
1	E	338	4% 86% 7% • 6%

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Mol	Chain	Length	Quality of chain
1	F	338	5% 87% 7% 6%
1	G	338	2% 86% 7% 6%
1	H	338	% 87% 6% 6%

2 Entry composition (i)

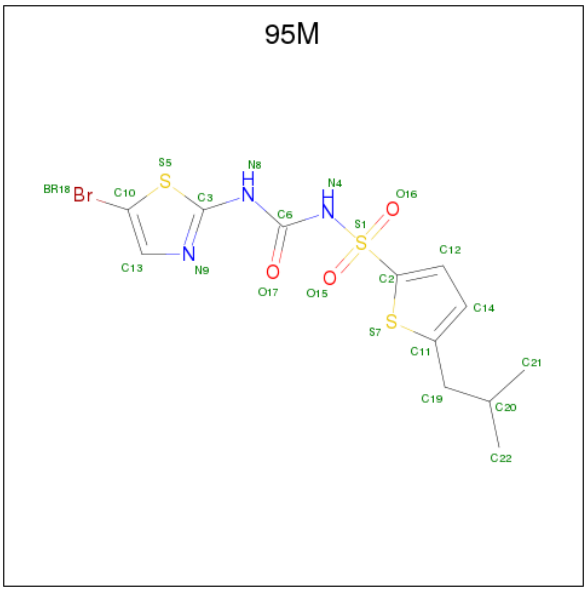
There are 3 unique types of molecules in this entry. The entry contains 20723 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Fructose-1,6-bisphosphatase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	319	Total	C	N	O	S	0	1	0
			2446	1558	412	459	17			
1	B	317	Total	C	N	O	S	0	2	0
			2437	1551	410	458	18			
1	C	317	Total	C	N	O	S	0	1	0
			2431	1548	407	458	18			
1	D	317	Total	C	N	O	S	0	1	0
			2431	1548	409	457	17			
1	E	319	Total	C	N	O	S	0	1	0
			2447	1559	412	459	17			
1	F	317	Total	C	N	O	S	0	1	0
			2430	1547	409	457	17			
1	G	317	Total	C	N	O	S	0	1	0
			2430	1547	409	457	17			
1	H	317	Total	C	N	O	S	0	0	0
			2425	1545	406	457	17			

- Molecule 2 is N-[(5-bromo-1,3-thiazol-2-yl)carbamoyl]-5-(2-methylpropyl)thiophene-2-sulfonamide (three-letter code: 95M) (formula: $C_{12}H_{14}BrN_3O_3S_3$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	Br	C	N	O	S	0	0
			22	1	12	3	3	3		
2	B	1	Total	Br	C	N	O	S	0	0
			22	1	12	3	3	3		
2	C	1	Total	Br	C	N	O	S	0	0
			22	1	12	3	3	3		
2	D	1	Total	Br	C	N	O	S	0	0
			22	1	12	3	3	3		
2	E	1	Total	Br	C	N	O	S	0	0
			22	1	12	3	3	3		
2	F	1	Total	Br	C	N	O	S	0	0
			22	1	12	3	3	3		
2	G	1	Total	Br	C	N	O	S	0	0
			22	1	12	3	3	3		
2	H	1	Total	Br	C	N	O	S	0	0
			22	1	12	3	3	3		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	156	Total	O	0	0
			156	156		
3	B	111	Total	O	0	0
			111	111		
3	C	164	Total	O	0	0
			164	164		
3	D	171	Total	O	0	0
			171	171		

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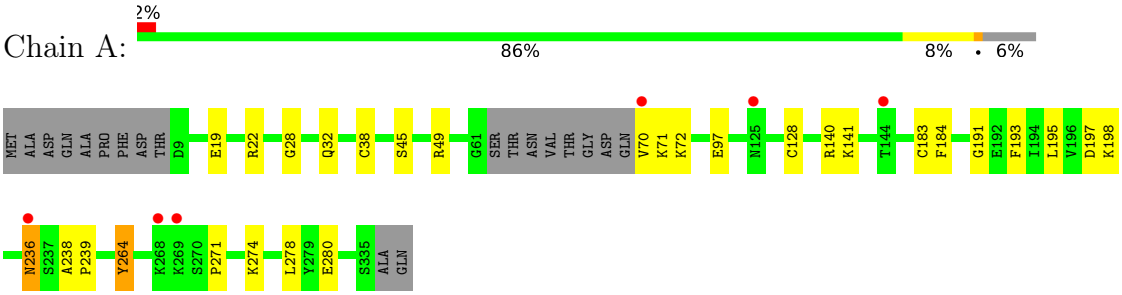
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	E	87	Total O 87 87	0	0
3	F	92	Total O 92 92	0	0
3	G	145	Total O 145 145	0	0
3	H	144	Total O 144 144	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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 geometryand 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.

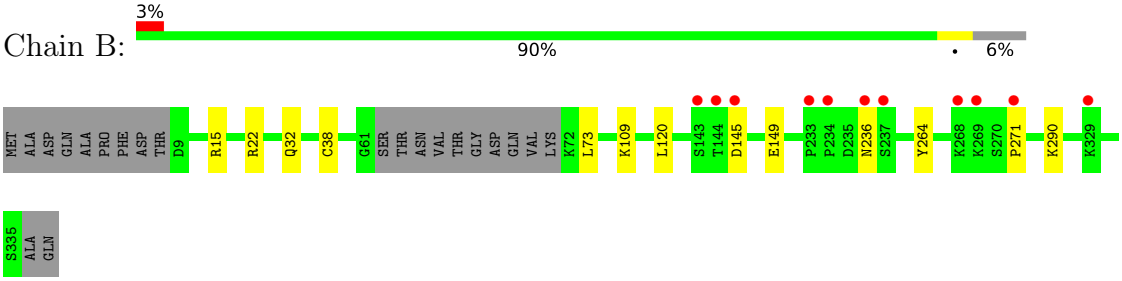
• Molecule 1: Fructose-1,6-bisphosphatase 1

Chain A:



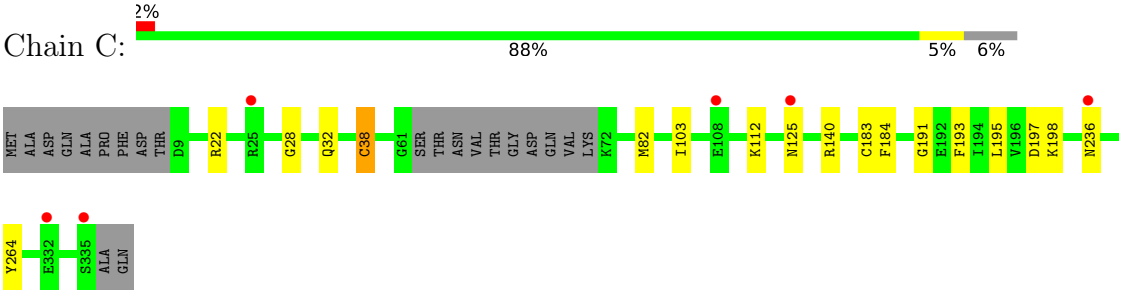
• Molecule 1: Fructose-1,6-bisphosphatase 1

Chain B:



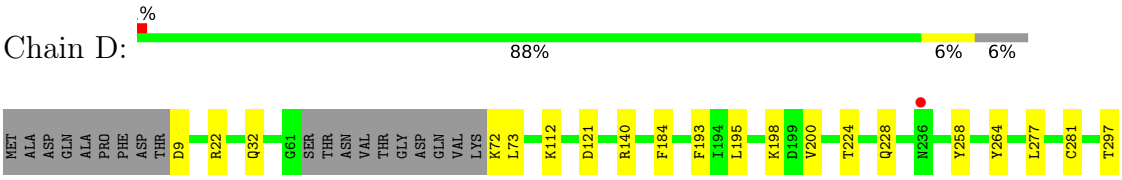
• Molecule 1: Fructose-1,6-bisphosphatase 1

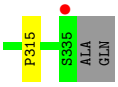
Chain C:



• Molecule 1: Fructose-1,6-bisphosphatase 1

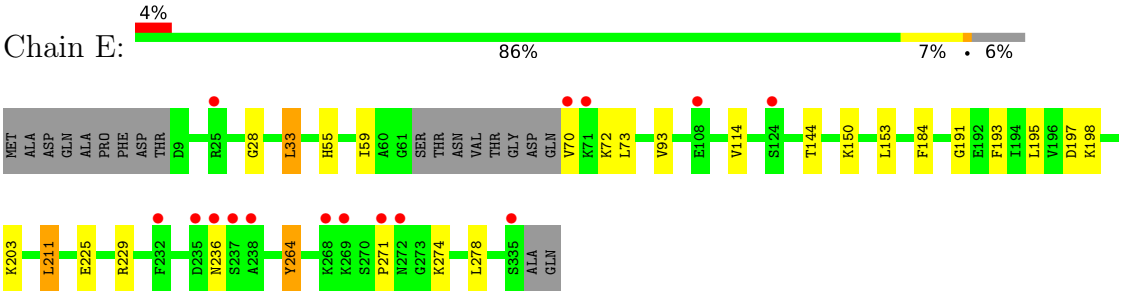
Chain D:





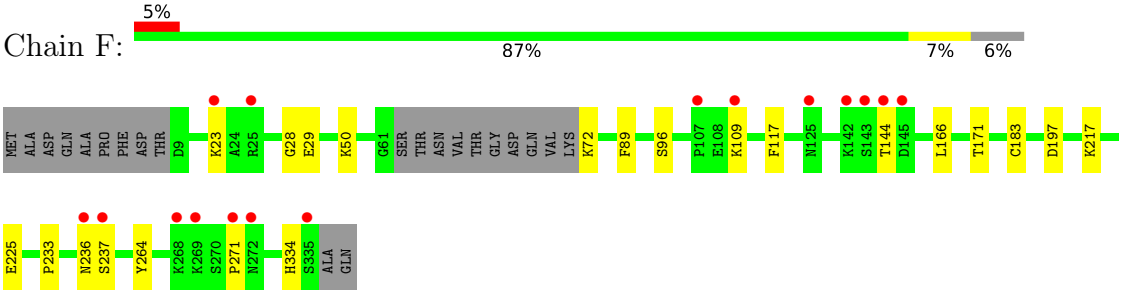
• Molecule 1: Fructose-1,6-bisphosphatase 1

Chain E:



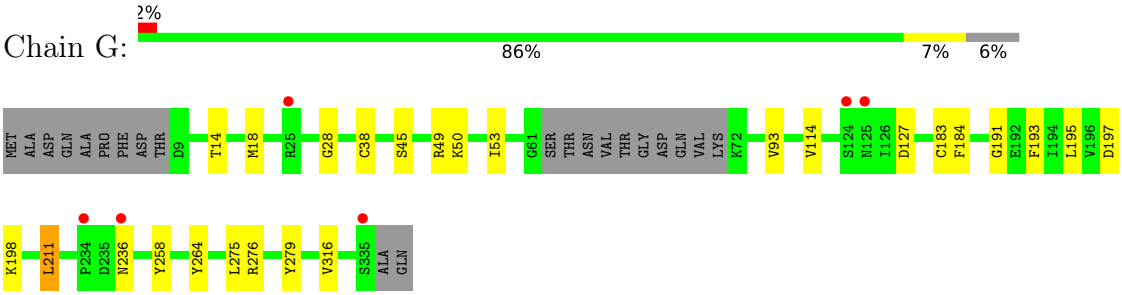
• Molecule 1: Fructose-1,6-bisphosphatase 1

Chain F:



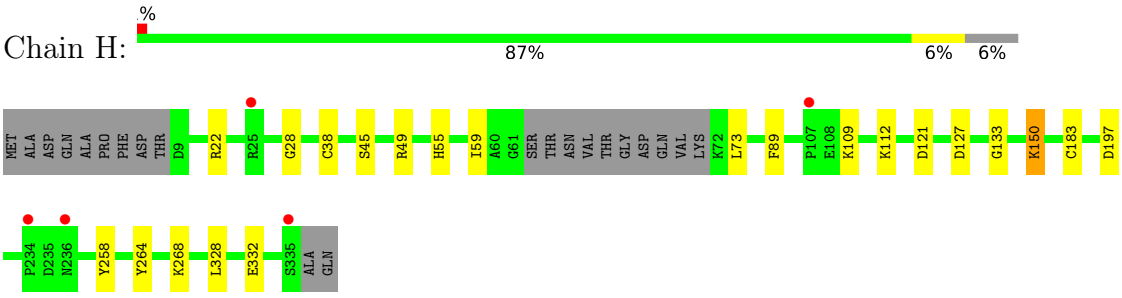
• Molecule 1: Fructose-1,6-bisphosphatase 1

Chain G:



• Molecule 1: Fructose-1,6-bisphosphatase 1

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	66.44Å 294.19Å 83.57Å 90.00° 97.56° 90.00°	Depositor
Resolution (Å)	20.37 – 2.31 20.37 – 2.31	Depositor EDS
% Data completeness (in resolution range)	96.7 (20.37-2.31) 96.7 (20.37-2.31)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.86 (at 2.30Å)	Xtriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, R_{free}	0.178 , 0.238 0.178 , 0.238	Depositor DCC
R_{free} test set	6681 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	29.3	Xtriage
Anisotropy	0.637	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 70.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	20723	wwPDB-VP
Average B, all atoms (Å^2)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.79% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 95M

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	0.46	0/2495	0.63	0/3368
1	B	0.42	0/2485	0.60	0/3355
1	C	0.49	0/2474	0.64	0/3341
1	D	0.50	0/2479	0.65	0/3347
1	E	0.41	0/2495	0.60	2/3368 (0.1%)
1	F	0.39	0/2479	0.59	0/3347
1	G	0.48	0/2479	0.64	1/3347 (0.0%)
1	H	0.46	0/2468	0.63	0/3333
All	All	0.45	0/19854	0.62	3/26806 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	211	LEU	CA-CB-CG	6.49	130.22	115.30
1	G	211	LEU	CA-CB-CG	5.82	128.69	115.30
1	E	33	LEU	CA-CB-CG	5.81	128.66	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2446	0	2496	20	0
1	B	2437	0	2482	7	0
1	C	2431	0	2473	12	0
1	D	2431	0	2478	11	0
1	E	2447	0	2500	14	0
1	F	2430	0	2474	11	0
1	G	2430	0	2474	14	0
1	H	2425	0	2469	12	0
2	A	22	0	0	2	0
2	B	22	0	0	0	0
2	C	22	0	0	2	0
2	D	22	0	0	0	0
2	E	22	0	0	3	0
2	F	22	0	0	1	0
2	G	22	0	0	3	0
2	H	22	0	0	1	0
3	A	156	0	0	8	0
3	B	111	0	0	2	0
3	C	164	0	0	1	0
3	D	171	0	0	2	0
3	E	87	0	0	2	0
3	F	92	0	0	1	0
3	G	145	0	0	4	0
3	H	144	0	0	2	0
All	All	20723	0	19846	94	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 2.

All (94) 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)
2:G:401:95M:S5	3:G:582:HOH:O	2.21	0.99
2:E:401:95M:BR18	3:G:582:HOH:O	2.51	0.82
1:B:22:ARG:NH1	1:D:32:GLN:OE1	2.28	0.66
3:A:619:HOH:O	1:C:38[A]:CYS:SG	2.52	0.66
1:B:109:LYS:NZ	1:D:9:ASP:OD2	2.25	0.66
1:D:121:ASP:OD2	3:D:501:HOH:O	2.14	0.65
1:H:183:CYS:HB2	1:H:197:ASP:HB2	1.82	0.62
1:H:328:LEU:O	1:H:332:GLU:HG2	2.00	0.61
1:G:50:LYS:HD2	1:G:53:ILE:HD12	1.81	0.61
1:G:28:GLY:HA2	2:G:401:95M:O17	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:82:MET:HE1	1:C:103:ILE:HG21	1.84	0.59
1:G:198:LYS:NZ	3:G:504:HOH:O	2.34	0.57
1:C:28:GLY:HA2	2:C:401:95M:O17	2.06	0.55
1:F:28:GLY:HA2	2:F:401:95M:O17	2.05	0.55
1:A:183:CYS:HB2	1:A:197:ASP:HB2	1.90	0.54
1:A:140[B]:ARG:NH1	1:A:141:LYS:O	2.40	0.53
1:A:264:TYR:CE1	1:A:274:LYS:HB2	2.43	0.52
1:A:191:GLY:HA3	1:C:191:GLY:HA3	1.90	0.52
1:E:28:GLY:HA2	2:E:401:95M:O17	2.07	0.52
1:B:32:GLN:OE1	1:D:22:ARG:NH1	2.42	0.52
1:E:28:GLY:HA2	2:E:401:95M:C6	2.40	0.52
1:C:125:ASN:ND2	3:C:505:HOH:O	2.30	0.51
1:F:233:PRO:HG2	1:F:237:SER:O	2.11	0.51
1:B:290:LYS:NZ	3:B:501:HOH:O	2.22	0.51
1:C:184:PHE:HB3	1:C:193:PHE:HB3	1.93	0.50
1:A:19:GLU:OE1	3:A:501:HOH:O	2.20	0.50
1:E:93:VAL:HB	1:E:114:VAL:HG13	1.94	0.49
1:F:183:CYS:HB2	1:F:197:ASP:HB2	1.94	0.49
1:A:32:GLN:OE1	1:C:22:ARG:NH1	2.43	0.49
1:E:225:GLU:O	1:E:229:ARG:HG3	2.13	0.49
1:A:28:GLY:HA2	2:A:401:95M:O17	2.11	0.48
1:G:183:CYS:HB2	1:G:197:ASP:HB2	1.94	0.48
1:G:184:PHE:HB3	1:G:193:PHE:HB3	1.95	0.48
1:H:55:HIS:HA	1:H:59:ILE:HG22	1.94	0.48
1:E:264:TYR:CE1	1:E:274:LYS:HB3	2.48	0.48
1:E:150:LYS:HD3	1:E:153:LEU:HD12	1.96	0.48
1:H:121:ASP:N	1:H:133:GLY:O	2.43	0.48
1:D:112:LYS:HD2	1:D:140[B]:ARG:NH2	2.29	0.47
1:F:89:PHE:CD1	1:F:109:LYS:HA	2.49	0.47
2:G:401:95M:C10	3:G:582:HOH:O	2.56	0.47
1:B:73:LEU:HD12	1:B:73:LEU:HA	1.80	0.47
1:C:28:GLY:HA2	2:C:401:95M:C6	2.45	0.47
1:H:28:GLY:HA2	2:H:401:95M:C6	2.44	0.47
1:F:225:GLU:OE1	1:F:334:HIS:NE2	2.45	0.46
1:E:73:LEU:HA	1:E:73:LEU:HD12	1.79	0.46
1:G:93:VAL:HB	1:G:114:VAL:HG13	1.97	0.46
1:G:276:ARG:NH1	1:G:279:TYR:OH	2.49	0.46
1:H:112:LYS:NZ	3:H:504:HOH:O	2.30	0.46
1:F:166:LEU:O	1:F:171:THR:HA	2.16	0.45
1:A:280:GLU:OE2	3:A:503:HOH:O	2.21	0.45
1:D:297:THR:HB	1:D:315:PRO:HG2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:184:PHE:HB3	1:E:193:PHE:HB3	1.99	0.45
1:B:15:ARG:HD3	3:B:506:HOH:O	2.17	0.45
1:G:275:LEU:HD12	1:G:316:VAL:HG11	2.00	0.44
1:C:112:LYS:HB2	1:C:140:ARG:NH1	2.32	0.44
1:A:22:ARG:NH1	1:C:32:GLN:OE1	2.47	0.44
1:D:258:TYR:O	3:D:502:HOH:O	2.21	0.44
1:E:191:GLY:HA3	1:G:191:GLY:HA3	1.98	0.44
1:A:28:GLY:HA2	2:A:401:95M:C6	2.48	0.44
1:G:45:SER:O	1:G:49:ARG:HD3	2.18	0.44
1:A:72:LYS:HA	1:A:72:LYS:HD3	1.65	0.43
1:E:195:LEU:HD21	1:E:198:LYS:HG2	2.00	0.43
1:E:278:LEU:HG	3:E:512:HOH:O	2.18	0.43
1:C:183:CYS:HB2	1:C:197:ASP:HB2	2.00	0.43
1:G:258:TYR:OH	1:H:127:ASP:HB2	2.18	0.43
1:D:224:THR:O	1:D:228:GLN:HG2	2.18	0.43
1:E:72:LYS:HG3	1:E:73:LEU:N	2.34	0.43
1:F:23:LYS:NZ	3:F:516:HOH:O	2.49	0.43
1:G:127:ASP:HB2	1:H:258:TYR:OH	2.18	0.43
1:A:19:GLU:HG3	3:A:515:HOH:O	2.17	0.43
1:H:89:PHE:CD1	1:H:109:LYS:HA	2.54	0.43
1:A:71:LYS:NZ	3:A:507:HOH:O	2.30	0.43
1:G:195:LEU:HD21	1:G:198:LYS:HG2	2.01	0.43
1:D:277:LEU:HA	1:D:281:CYS:HB2	2.01	0.42
1:E:55:HIS:HA	1:E:59:ILE:HG22	2.01	0.42
1:E:203:LYS:NZ	3:E:506:HOH:O	2.52	0.42
1:F:96:SER:HB2	1:F:117:PHE:CZ	2.54	0.42
1:C:195:LEU:HD21	1:C:198:LYS:HG2	2.01	0.41
1:A:195:LEU:HD21	1:A:198:LYS:HG2	2.02	0.41
1:A:278:LEU:HG	3:A:564:HOH:O	2.19	0.41
1:H:150:LYS:HD2	3:H:529:HOH:O	2.19	0.41
1:B:120:LEU:HD12	1:B:120:LEU:HA	1.86	0.41
1:A:184:PHE:HB3	1:A:193:PHE:HB3	2.02	0.41
1:F:29:GLU:HG3	1:H:22:ARG:HH12	1.86	0.41
1:A:128:CYS:O	3:A:504:HOH:O	2.21	0.41
1:A:45:SER:O	1:A:49:ARG:HD3	2.21	0.41
1:A:236:ASN:ND2	3:A:520:HOH:O	2.54	0.41
1:D:195:LEU:HD21	1:D:198:LYS:HG2	2.03	0.41
1:F:50:LYS:HA	1:F:50:LYS:HD3	1.79	0.41
1:H:45:SER:O	1:H:49:ARG:HD3	2.21	0.40
1:A:238:ALA:HA	1:A:239:PRO:HD3	1.99	0.40
1:D:184:PHE:HB3	1:D:193:PHE:HB3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:89:PHE:CE1	1:F:109:LYS:HA	2.55	0.40
1:G:14:THR:HG22	1:G:18:MET:CE	2.51	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	316/338 (94%)	307 (97%)	8 (2%)	1 (0%)	43 53
1	B	315/338 (93%)	306 (97%)	7 (2%)	2 (1%)	27 32
1	C	314/338 (93%)	304 (97%)	9 (3%)	1 (0%)	43 53
1	D	314/338 (93%)	306 (98%)	8 (2%)	0	100 100
1	E	316/338 (94%)	307 (97%)	9 (3%)	0	100 100
1	F	314/338 (93%)	303 (96%)	10 (3%)	1 (0%)	43 53
1	G	314/338 (93%)	304 (97%)	9 (3%)	1 (0%)	43 53
1	H	313/338 (93%)	306 (98%)	7 (2%)	0	100 100
All	All	2516/2704 (93%)	2443 (97%)	67 (3%)	6 (0%)	49 61

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	145	ASP
1	B	236	ASN
1	C	236	ASN
1	F	236	ASN
1	A	236	ASN
1	G	236	ASN

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	267/281 (95%)	262 (98%)	5 (2%)	60	76
1	B	266/281 (95%)	261 (98%)	5 (2%)	60	76
1	C	265/281 (94%)	262 (99%)	3 (1%)	76	87
1	D	265/281 (94%)	261 (98%)	4 (2%)	67	81
1	E	267/281 (95%)	259 (97%)	8 (3%)	44	60
1	F	265/281 (94%)	260 (98%)	5 (2%)	60	76
1	G	265/281 (94%)	262 (99%)	3 (1%)	76	87
1	H	264/281 (94%)	259 (98%)	5 (2%)	60	76
All	All	2124/2248 (94%)	2086 (98%)	38 (2%)	63	77

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	CYS
1	A	70	VAL
1	A	97	GLU
1	A	264	TYR
1	A	271	PRO
1	B	38[A]	CYS
1	B	38[B]	CYS
1	B	149	GLU
1	B	264	TYR
1	B	271	PRO
1	C	38[A]	CYS
1	C	38[B]	CYS
1	C	264	TYR
1	D	72	LYS
1	D	73	LEU
1	D	200	VAL
1	D	264	TYR
1	E	33	LEU
1	E	70	VAL

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Mol	Chain	Res	Type
1	E	144	THR
1	E	197	ASP
1	E	211	LEU
1	E	236	ASN
1	E	264	TYR
1	E	271	PRO
1	F	72	LYS
1	F	144	THR
1	F	217	LYS
1	F	264	TYR
1	F	271	PRO
1	G	38	CYS
1	G	211	LEU
1	G	264	TYR
1	H	38	CYS
1	H	73	LEU
1	H	150	LYS
1	H	264	TYR
1	H	268	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 carbohydrates in this entry.

5.6 Ligand geometry (i)

8 ligands are modelled in this entry.

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	$\#\|Z\| > 2$
2	95M	A	401	-	18,23,23	1.28	3 (16%)	15,33,33	1.46	2 (13%)
2	95M	B	401	-	18,23,23	1.31	2 (11%)	15,33,33	1.06	1 (6%)
2	95M	C	401	-	18,23,23	1.45	2 (11%)	15,33,33	1.62	5 (33%)
2	95M	D	401	-	18,23,23	1.61	2 (11%)	15,33,33	1.30	2 (13%)
2	95M	E	401	-	18,23,23	1.36	2 (11%)	15,33,33	1.62	3 (20%)
2	95M	F	401	-	18,23,23	0.99	1 (5%)	15,33,33	1.19	2 (13%)
2	95M	G	401	-	18,23,23	1.18	2 (11%)	15,33,33	2.01	5 (33%)
2	95M	H	401	-	18,23,23	1.02	1 (5%)	15,33,33	1.31	2 (13%)

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
2	95M	A	401	-	-	0/10/19/19	0/2/2/2
2	95M	B	401	-	-	0/10/19/19	0/2/2/2
2	95M	C	401	-	-	0/10/19/19	0/2/2/2
2	95M	D	401	-	-	0/10/19/19	0/2/2/2
2	95M	E	401	-	-	0/10/19/19	0/2/2/2
2	95M	F	401	-	-	0/10/19/19	0/2/2/2
2	95M	G	401	-	-	0/10/19/19	0/2/2/2
2	95M	H	401	-	-	0/10/19/19	0/2/2/2

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	95M	C2-S7	-3.65	1.65	1.72
2	D	401	95M	C2-S1	-3.47	1.71	1.76
2	C	401	95M	C2-S1	-2.82	1.72	1.76
2	A	401	95M	C2-S7	-2.77	1.67	1.72
2	F	401	95M	C2-S7	-2.48	1.68	1.72
2	A	401	95M	C2-S1	-2.32	1.73	1.76
2	E	401	95M	C2-S1	-2.24	1.73	1.76
2	G	401	95M	C2-S7	-2.21	1.68	1.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	95M	C14-C11	-2.14	1.26	1.39
2	B	401	95M	C19-C20	2.43	1.63	1.51
2	G	401	95M	C19-C20	2.54	1.63	1.51
2	H	401	95M	C19-C20	2.60	1.63	1.51
2	E	401	95M	C19-C20	3.44	1.67	1.51
2	C	401	95M	C19-C20	3.96	1.70	1.51
2	D	401	95M	C19-C20	4.34	1.72	1.51

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	G	401	95M	C2-S1-N4	-4.44	101.96	107.18
2	G	401	95M	C11-C19-C20	-3.03	107.68	114.43
2	E	401	95M	O15-S1-N4	-2.75	98.92	106.75
2	C	401	95M	O16-S1-O15	-2.55	116.36	119.56
2	C	401	95M	O15-S1-C2	-2.38	103.66	107.61
2	G	401	95M	N4-C6-N8	2.06	117.73	114.74
2	C	401	95M	N4-C6-N8	2.07	117.75	114.74
2	B	401	95M	BR18-C10-C13	2.35	127.98	124.38
2	H	401	95M	BR18-C10-C13	2.38	128.03	124.38
2	C	401	95M	BR18-C10-C13	2.41	128.07	124.38
2	D	401	95M	BR18-C10-C13	2.42	128.08	124.38
2	F	401	95M	BR18-C10-C13	2.49	128.19	124.38
2	A	401	95M	BR18-C10-C13	2.53	128.26	124.38
2	G	401	95M	BR18-C10-C13	2.55	128.28	124.38
2	E	401	95M	BR18-C10-C13	2.55	128.29	124.38
2	F	401	95M	O16-S1-N4	2.58	114.09	106.75
2	D	401	95M	O16-S1-N4	2.64	114.24	106.75
2	C	401	95M	O16-S1-N4	3.12	115.61	106.75
2	G	401	95M	O16-S1-N4	3.32	116.18	106.75
2	H	401	95M	C2-S1-N4	3.37	111.15	107.18
2	A	401	95M	O16-S1-N4	3.52	116.75	106.75
2	E	401	95M	O16-S1-N4	3.99	118.07	106.75

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	95M	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	401	95M	2	0
2	E	401	95M	3	0
2	F	401	95M	1	0
2	G	401	95M	3	0
2	H	401	95M	1	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

6.1 Protein, DNA and RNA chains

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, 95^{th} 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	319/338 (94%)	-0.36	6 (1%)	66	73	16, 32, 65, 106	0
1	B	317/338 (93%)	-0.21	11 (3%)	44	51	19, 35, 70, 112	0
1	C	317/338 (93%)	-0.42	6 (1%)	66	73	17, 29, 55, 122	0
1	D	317/338 (93%)	-0.50	2 (0%)	89	92	14, 27, 49, 71	0
1	E	319/338 (94%)	-0.06	15 (4%)	31	39	24, 42, 79, 117	0
1	F	317/338 (93%)	-0.03	16 (5%)	29	36	23, 43, 83, 127	0
1	G	317/338 (93%)	-0.40	6 (1%)	66	73	20, 33, 57, 98	0
1	H	317/338 (93%)	-0.36	5 (1%)	72	77	22, 35, 67, 93	0
All	All	2540/2704 (93%)	-0.29	67 (2%)	56	63	14, 35, 68, 127	0

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	70	VAL	9.6
1	A	70	VAL	6.7
1	C	236	ASN	6.1
1	F	236	ASN	6.1
1	B	144	THR	4.9
1	F	269	LYS	4.9
1	E	236	ASN	4.9
1	B	234	PRO	4.7
1	H	335	SER	4.7
1	B	269	LYS	4.4
1	F	145	ASP	4.4
1	G	335	SER	4.4
1	E	335	SER	4.3
1	E	268	LYS	4.2
1	E	269	LYS	4.2
1	E	237	SER	4.1

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Mol	Chain	Res	Type	RSRZ
1	B	236	ASN	3.9
1	H	236	ASN	3.8
1	G	236	ASN	3.8
1	F	144	THR	3.8
1	F	143	SER	3.7
1	F	237	SER	3.6
1	E	238	ALA	3.6
1	A	268	LYS	3.5
1	F	107	PRO	3.4
1	B	271	PRO	3.3
1	F	271	PRO	3.3
1	A	144	THR	3.2
1	C	335	SER	3.1
1	F	125	ASN	3.1
1	F	109	LYS	3.0
1	F	268	LYS	3.0
1	F	142	LYS	2.9
1	E	25	ARG	2.9
1	B	237	SER	2.9
1	E	124	SER	2.8
1	F	25	ARG	2.8
1	D	335	SER	2.8
1	H	25	ARG	2.8
1	D	236	ASN	2.8
1	E	232	PHE	2.7
1	G	234	PRO	2.6
1	A	125	ASN	2.6
1	C	25	ARG	2.5
1	C	108	GLU	2.5
1	B	268	LYS	2.5
1	B	329	LYS	2.5
1	A	236	ASN	2.5
1	G	25	ARG	2.4
1	E	108	GLU	2.4
1	B	145	ASP	2.4
1	E	235	ASP	2.3
1	F	272	ASN	2.3
1	H	234	PRO	2.3
1	F	335	SER	2.3
1	E	272	ASN	2.2
1	G	125	ASN	2.2
1	B	233	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	G	124	SER	2.2
1	F	23	LYS	2.1
1	C	332	GLU	2.1
1	C	125	ASN	2.1
1	H	107	PRO	2.1
1	B	143	SER	2.1
1	E	71	LYS	2.1
1	E	271	PRO	2.0
1	A	269	LYS	2.0

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 carbohydrates 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, 95^{th} 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(Å^2)	Q<0.9
2	95M	F	401	22/22	0.96	0.14	42,62,72,81	1
2	95M	B	401	22/22	0.96	0.13	36,48,56,60	1
2	95M	E	401	22/22	0.96	0.13	24,44,60,70	1
2	95M	D	401	22/22	0.97	0.10	7,41,48,51	1
2	95M	G	401	22/22	0.97	0.12	21,46,70,74	1
2	95M	H	401	22/22	0.97	0.10	20,57,69,79	1
2	95M	C	401	22/22	0.97	0.12	15,43,58,68	1
2	95M	A	401	22/22	0.97	0.12	15,44,52,58	1

6.5 Other polymers (i)

There are no such residues in this entry.