Full wwPDB X-ray Structure Validation Report ⓘ

Sep 19, 2016 – 10:48 PM EDT

PDB ID	:	5CHW
Title	:	Structure of ISG15 in space group P212121
Authors	:	Fritz, G.; Basters, A.
Deposited on	:	2015-07-10
Resolution	:	2.10 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

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

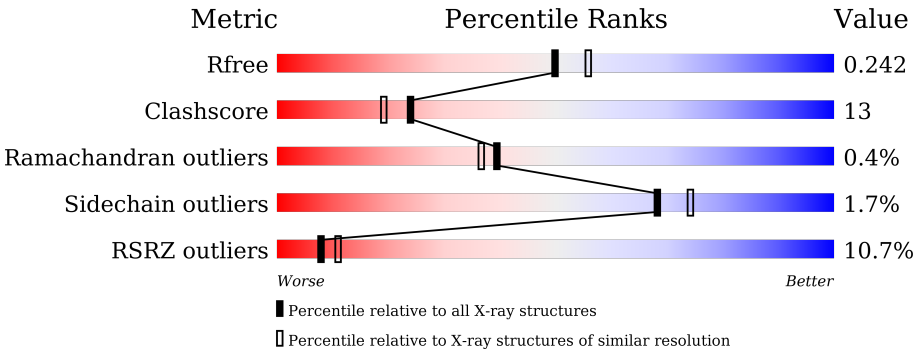
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20027939
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027939

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 2.10 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}	91344	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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	155	5% 85% 14%
1	B	155	6% 81% 17%
1	C	155	3% 81% 15%
1	D	155	2% 83% 15%
1	E	155	4% 78% 20%
1	F	155	26% 61% 30% 5%

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Mol	Chain	Length	Quality of chain
1	G	155	4% 86% 12%
1	H	155	10% 73% 23%
1	I	155	19% 67% 28%
1	J	155	27% 68% 27%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	H	201	-	-	X	-
3	GOL	A	202	-	-	-	X
3	GOL	A	203	-	-	-	X
3	GOL	B	203	-	-	-	X
3	GOL	B	204	-	-	-	X
3	GOL	D	205	-	-	-	X
3	GOL	G	203	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12085 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 Ubiquitin-like protein ISG15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	154	Total	C	N	O	S	0	0	0
			1210	764	213	228	5			
1	B	151	Total	C	N	O	S	0	0	0
			1190	754	207	224	5			
1	C	150	Total	C	N	O	S	0	0	0
			1172	743	203	221	5			
1	D	154	Total	C	N	O	S	0	0	0
			1200	759	210	226	5			
1	E	154	Total	C	N	O	S	0	0	0
			1204	761	210	228	5			
1	F	147	Total	C	N	O	S	0	0	0
			1150	729	200	218	3			
1	G	154	Total	C	N	O	S	0	0	0
			1195	756	208	226	5			
1	H	150	Total	C	N	O	S	0	0	0
			1178	746	206	221	5			
1	I	149	Total	C	N	O	S	0	0	0
			1154	733	197	219	5			
1	J	149	Total	C	N	O	S	0	0	0
			1160	736	197	222	5			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	76	SER	CYS	engineered mutation	UNP Q64339
B	76	SER	CYS	engineered mutation	UNP Q64339
C	76	SER	CYS	engineered mutation	UNP Q64339
D	76	SER	CYS	engineered mutation	UNP Q64339
E	76	SER	CYS	engineered mutation	UNP Q64339
F	76	SER	CYS	engineered mutation	UNP Q64339
G	76	SER	CYS	engineered mutation	UNP Q64339
H	76	SER	CYS	engineered mutation	UNP Q64339
I	76	SER	CYS	engineered mutation	UNP Q64339

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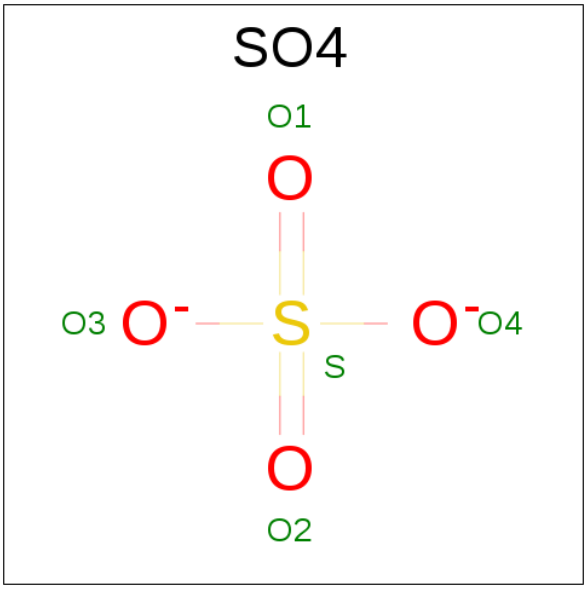
Chain	Residue	Modelled	Actual	Comment	Reference
J	76	SER	CYS	engineered mutation	UNP Q64339

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	E	1	Total O S 5 4 1	0	0
2	E	1	Total O S 5 4 1	0	0
2	E	1	Total O S 5 4 1	0	0
2	G	1	Total O S 5 4 1	0	0

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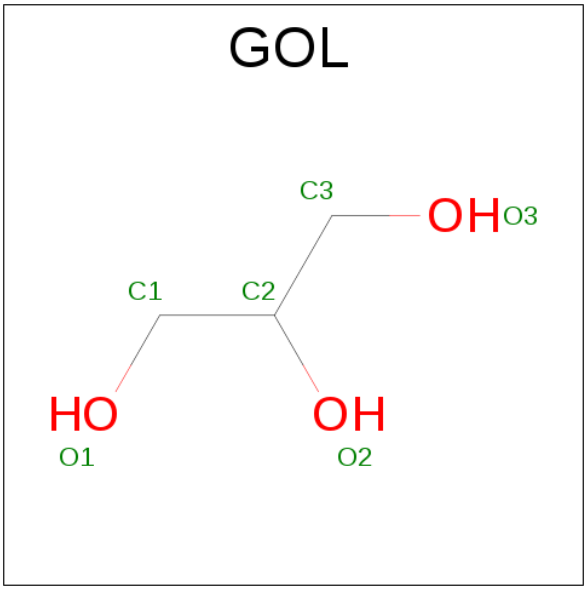
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	1	Total O S 5 4 1	0	0
2	H	1	Total O S 5 4 1	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0
3	D	1	Total C O 6 3 3	0	0
3	G	1	Total C O 6 3 3	0	0
3	G	1	Total C O 6 3 3	0	0
3	I	1	Total C O 6 3 3	0	0

- Molecule 4 is water.

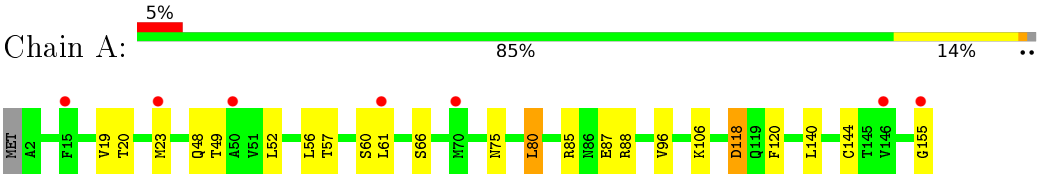
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	23	Total O 23 23	0	0
4	B	15	Total O 15 15	0	0
4	C	18	Total O 18 18	0	0
4	D	20	Total O 20 20	0	0
4	E	24	Total O 24 24	0	0
4	F	6	Total O 6 6	0	0
4	G	33	Total O 33 33	0	0
4	H	7	Total O 7 7	0	0
4	I	3	Total O 3 3	0	0
4	J	4	Total O 4 4	0	0

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 errors 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.

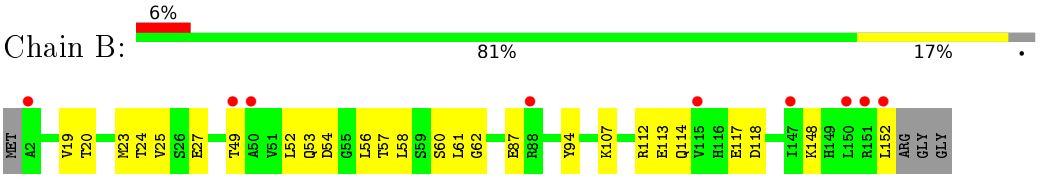
- Molecule 1: Ubiquitin-like protein ISG15

Chain A:



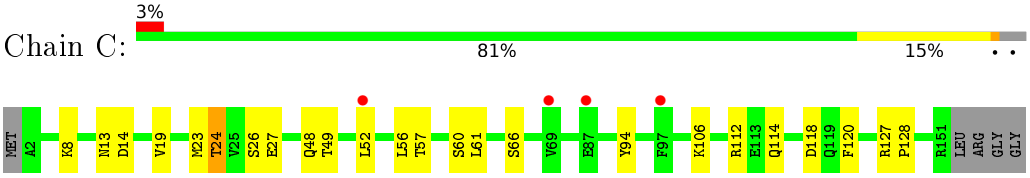
- Molecule 1: Ubiquitin-like protein ISG15

Chain B:



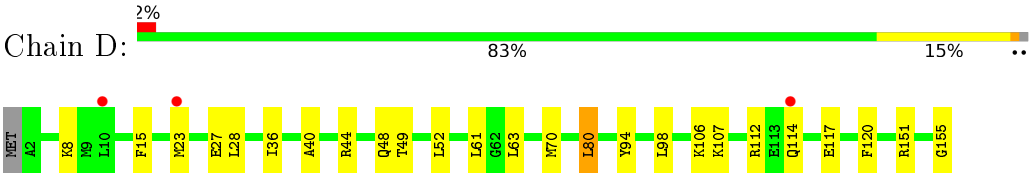
- Molecule 1: Ubiquitin-like protein ISG15

Chain C:



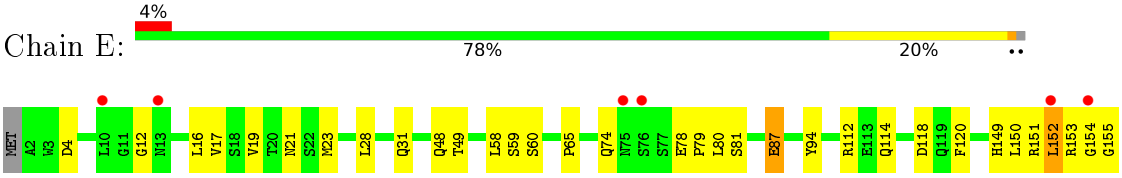
- Molecule 1: Ubiquitin-like protein ISG15

Chain D:



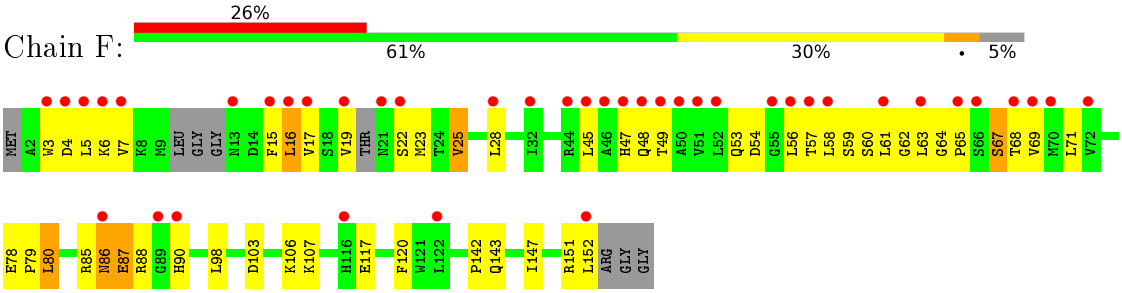
- Molecule 1: Ubiquitin-like protein ISG15

Chain E:



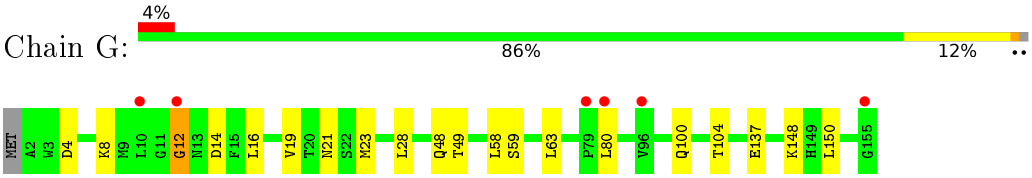
- Molecule 1: Ubiquitin-like protein ISG15

Chain F:



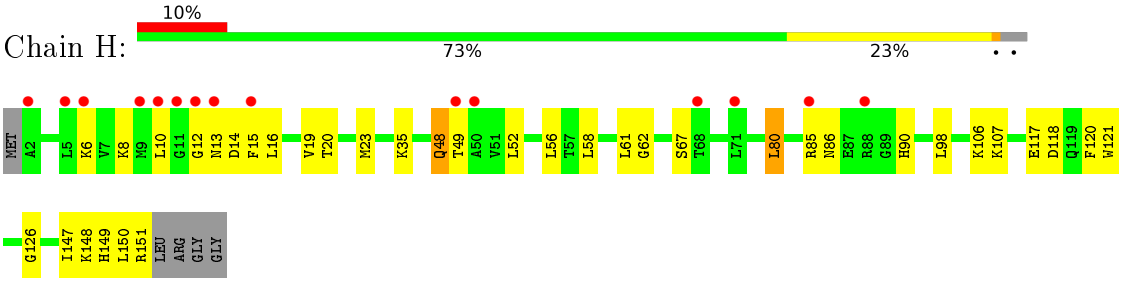
• Molecule 1: Ubiquitin-like protein ISG15

Chain G:



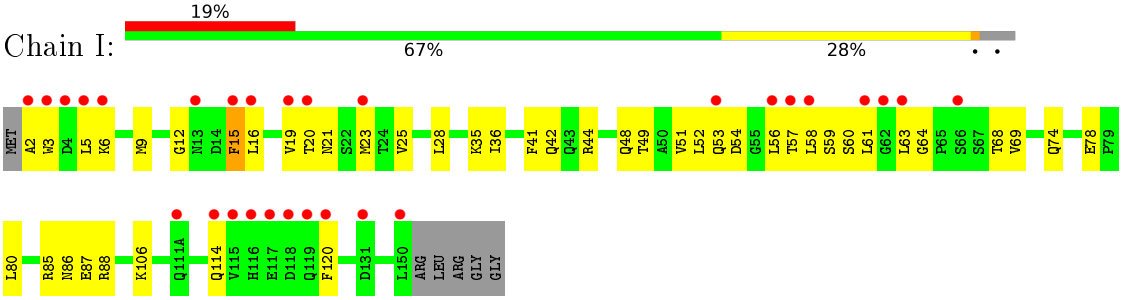
• Molecule 1: Ubiquitin-like protein ISG15

Chain H:



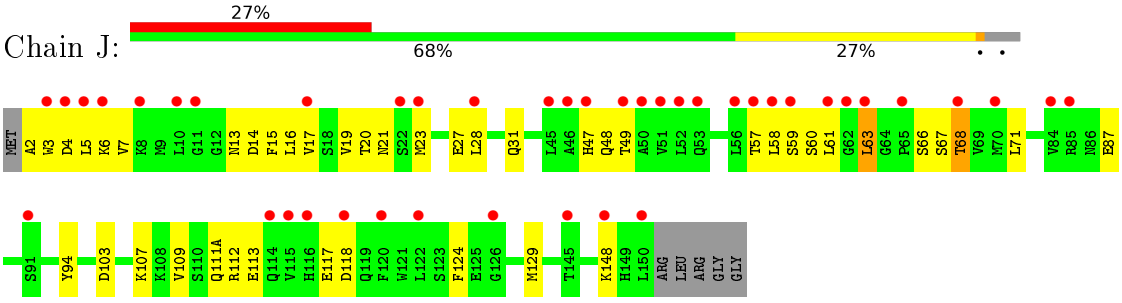
• Molecule 1: Ubiquitin-like protein ISG15

Chain I:



• Molecule 1: Ubiquitin-like protein ISG15

Chain J:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	102.85Å 103.96Å 192.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.69 – 2.10 49.69 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.69-2.10) 99.9 (49.69-2.00)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.03 (at 2.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.198 , 0.242 0.198 , 0.242	Depositor DCC
R_{free} test set	5878 reflections (4.87%)	DCC
Wilson B-factor (Å^2)	49.3	Xtriage
Anisotropy	0.561	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 62.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.017 for k,h,-l	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	12085	wwPDB-VP
Average B, all atoms (Å^2)	88.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.03% 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: GOL, SO4

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	0.70	0/1229	0.73	1/1656 (0.1%)
1	B	0.66	0/1209	0.71	0/1632
1	C	0.63	0/1191	0.71	0/1609
1	D	0.62	0/1219	0.71	0/1644
1	E	0.67	0/1223	0.74	0/1649
1	F	0.41	0/1167	0.63	1/1577 (0.1%)
1	G	0.70	0/1213	0.78	0/1636
1	H	0.52	0/1197	0.65	0/1616
1	I	0.41	0/1173	0.60	0/1587
1	J	0.35	0/1178	0.55	0/1592
All	All	0.58	0/11999	0.69	2/16198 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	F	64	GLY	N-CA-C	-6.07	97.92	113.10
1	A	155	GLY	N-CA-C	5.43	126.67	113.10

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	1210	0	1240	18	0
1	B	1190	0	1221	28	0
1	C	1172	0	1195	22	0
1	D	1200	0	1225	18	1
1	E	1204	0	1229	39	0
1	F	1150	0	1155	61	0
1	G	1195	0	1220	17	0
1	H	1178	0	1206	42	0
1	I	1154	0	1167	51	0
1	J	1160	0	1181	52	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	1	0
2	D	20	0	0	1	0
2	E	15	0	0	2	0
2	G	10	0	0	0	0
2	H	5	0	0	2	0
3	A	12	0	16	0	0
3	B	18	0	24	1	0
3	D	6	0	8	1	0
3	G	12	0	16	0	0
3	I	6	0	8	0	0
4	A	23	0	0	1	0
4	B	15	0	0	0	0
4	C	18	0	0	0	0
4	D	20	0	0	0	0
4	E	24	0	0	0	0
4	F	6	0	0	0	0
4	G	33	0	0	0	0
4	H	7	0	0	1	0
4	I	3	0	0	0	0
4	J	4	0	0	1	0
All	All	12085	0	12111	315	1

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 13.

All (315) 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:E:153:ARG:HD2	1:H:85:ARG:HH12	1.19	1.06
1:F:63:LEU:HG	1:F:67:SER:HB3	1.37	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:53:GLN:HB2	1:I:56:LEU:HD13	1.43	1.00
1:E:153:ARG:HB2	1:H:85:ARG:HH22	1.28	0.98
1:F:61:LEU:HD23	1:F:62:GLY:H	1.29	0.97
1:B:53:GLN:HB3	1:B:56:LEU:HD13	1.48	0.92
1:H:85:ARG:HH21	1:H:147:ILE:HD11	1.33	0.91
1:I:25:VAL:HG13	1:I:54:ASP:HA	1.55	0.89
1:I:9:MET:HE3	1:I:12:GLY:HA3	1.54	0.88
1:E:153:ARG:HD2	1:H:85:ARG:NH1	1.88	0.88
1:E:153:ARG:HB2	1:H:85:ARG:NH2	1.87	0.87
1:J:103:ASP:OD2	1:J:107:LYS:HE3	1.75	0.86
1:F:47:HIS:CG	1:F:63:LEU:HD11	2.11	0.84
1:F:47:HIS:CD2	1:F:63:LEU:HD11	2.13	0.84
1:E:154:GLY:HA3	1:H:147:ILE:HG13	1.59	0.83
1:I:19:VAL:HG12	1:I:23:MET:HE1	1.58	0.83
1:D:8:LYS:HD2	1:D:70:MET:HE1	1.64	0.79
1:A:56:LEU:HD13	1:A:61:LEU:HD21	1.65	0.78
1:F:19:VAL:HG13	1:F:58:LEU:HD13	1.65	0.78
1:A:52:LEU:HD22	1:A:61:LEU:HD13	1.65	0.78
1:F:61:LEU:CD2	1:F:62:GLY:H	1.98	0.76
1:A:85:ARG:NH2	1:D:63:LEU:O	2.18	0.74
1:H:85:ARG:HH21	1:H:147:ILE:CD1	2.00	0.74
1:H:85:ARG:NH2	1:H:147:ILE:HD11	2.03	0.73
1:C:24:THR:CG2	1:C:27:GLU:H	2.03	0.72
1:B:53:GLN:HB3	1:B:56:LEU:CD1	2.19	0.72
1:H:52:LEU:HD22	1:H:61:LEU:HD13	1.73	0.71
1:B:24:THR:HG23	1:B:27:GLU:H	1.55	0.70
1:J:17:VAL:HG11	1:J:31:GLN:HB3	1.73	0.70
1:H:121:TRP:HB2	1:I:53:GLN:HE22	1.57	0.69
1:J:6:LYS:HE3	1:J:68:THR:HB	1.74	0.69
1:H:151:ARG:NH1	1:I:56:LEU:HG	2.08	0.69
1:E:153:ARG:CD	1:H:85:ARG:HH12	2.03	0.69
1:F:25:VAL:HG11	1:F:53:GLN:O	1.94	0.68
1:H:151:ARG:HH12	1:I:56:LEU:HG	1.58	0.68
1:B:107:LYS:HG2	1:B:117:GLU:OE2	1.94	0.68
1:C:24:THR:HG22	1:C:27:GLU:HG3	1.75	0.67
1:E:153:ARG:CB	1:H:85:ARG:HH22	2.04	0.67
1:B:87:GLU:OE1	1:B:87:GLU:N	2.26	0.66
1:F:22:SER:HB2	1:F:57:THR:CG2	2.25	0.66
1:B:20:THR:H	1:B:23:MET:HE3	1.61	0.66
1:I:21:ASN:HB3	1:I:59:SER:HB3	1.77	0.66
1:J:107:LYS:HG2	1:J:117:GLU:OE2	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:20:THR:HG22	1:J:23:MET:HB2	1.78	0.66
1:C:56:LEU:HD13	1:C:61:LEU:HD21	1.78	0.65
1:F:5:LEU:HD21	1:F:69:VAL:HG11	1.77	0.65
1:F:63:LEU:CG	1:F:67:SER:HB3	2.22	0.65
1:I:25:VAL:HG11	1:I:53:GLN:O	1.96	0.65
1:J:23:MET:HB3	1:J:58:LEU:HD12	1.77	0.65
1:F:86:ASN:O	1:F:87:GLU:HG3	1.96	0.65
1:D:151:ARG:NH2	2:D:201:SO4:O4	2.23	0.65
1:F:53:GLN:HB2	1:F:56:LEU:CD1	2.27	0.65
1:A:20:THR:H	1:A:23:MET:HE3	1.62	0.64
1:F:151:ARG:HG2	1:F:152:LEU:HD12	1.79	0.64
1:E:155:GLY:C	1:H:126:GLY:HA2	2.17	0.64
1:F:19:VAL:HG13	1:F:58:LEU:CD1	2.26	0.64
1:B:24:THR:CG2	1:B:27:GLU:HG3	2.27	0.64
1:D:23:MET:HE2	1:D:27:GLU:C	2.17	0.64
1:F:58:LEU:O	1:F:59:SER:OG	2.12	0.64
1:B:57:THR:HG23	1:B:60:SER:H	1.62	0.64
1:E:74:GLN:HG3	1:E:74:GLN:O	1.97	0.64
1:H:106:LYS:HE2	4:H:302:HOH:O	1.97	0.64
1:I:9:MET:CE	1:I:12:GLY:HA3	2.27	0.63
1:J:17:VAL:CG1	1:J:31:GLN:HB3	2.28	0.63
1:C:60:SER:HA	1:E:152:LEU:O	1.99	0.63
1:E:23:MET:HE3	1:E:28:LEU:HB2	1.80	0.63
1:I:44:ARG:NH2	1:I:51:VAL:HG21	2.14	0.62
1:J:20:THR:O	1:J:58:LEU:HD12	1.99	0.62
1:E:114:GLN:HG3	1:G:12:GLY:HA2	1.82	0.62
1:J:23:MET:HB3	1:J:58:LEU:CD1	2.28	0.62
1:F:107:LYS:HG2	1:F:117:GLU:OE2	1.99	0.62
1:D:23:MET:HE1	1:D:28:LEU:HA	1.81	0.61
1:F:53:GLN:HB2	1:F:56:LEU:HD13	1.82	0.61
1:C:24:THR:HG22	1:C:27:GLU:CG	2.30	0.61
1:H:106:LYS:NZ	1:H:120:PHE:O	2.34	0.60
1:F:23:MET:O	1:F:58:LEU:HG	2.01	0.60
1:G:23:MET:HE3	1:G:28:LEU:HB2	1.83	0.60
1:F:5:LEU:HD21	1:F:69:VAL:CG1	2.31	0.60
1:F:86:ASN:HD22	1:F:88:ARG:HH21	1.49	0.60
1:I:53:GLN:HB2	1:I:56:LEU:CD1	2.26	0.60
1:J:48:GLN:O	1:J:49:THR:OG1	2.19	0.60
1:C:94:TYR:CE2	1:C:112:ARG:HD3	2.35	0.60
1:J:3:TRP:HH2	1:J:5:LEU:HD13	1.67	0.60
1:J:87:GLU:OE1	1:J:87:GLU:N	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:86:ASN:ND2	1:F:88:ARG:HH21	2.00	0.59
1:G:8:LYS:HG3	1:G:14:ASP:OD1	2.02	0.59
1:I:53:GLN:OE1	1:I:56:LEU:HD11	2.02	0.59
1:J:94:TYR:OH	1:J:112:ARG:HD3	2.03	0.59
1:A:60:SER:O	1:B:152:LEU:HB2	2.03	0.59
1:J:124:PHE:HB2	1:J:129:MET:CE	2.33	0.59
2:C:201:SO4:O3	1:I:44:ARG:NH1	2.35	0.59
1:C:24:THR:HG23	1:C:27:GLU:H	1.68	0.59
1:A:88:ARG:HH12	3:B:203:GOL:H31	1.68	0.59
1:G:4:ASP:HB3	1:G:16:LEU:HD22	1.85	0.58
1:I:52:LEU:HD22	1:I:61:LEU:HD13	1.85	0.58
1:J:57:THR:HG23	1:J:60:SER:H	1.67	0.58
1:F:19:VAL:CG1	1:F:58:LEU:HD13	2.31	0.58
1:C:52:LEU:HD22	1:C:61:LEU:HD13	1.85	0.58
1:E:21:ASN:HB3	1:E:59:SER:HB3	1.84	0.58
1:F:63:LEU:HA	1:F:67:SER:HB2	1.85	0.58
1:I:48:GLN:O	1:I:49:THR:OG1	2.20	0.58
1:G:48:GLN:O	1:G:49:THR:OG1	2.21	0.58
1:C:24:THR:HG22	1:C:27:GLU:H	1.69	0.57
1:C:118:ASP:OD1	1:C:118:ASP:N	2.37	0.57
1:F:3:TRP:CZ3	1:F:65:PRO:HA	2.39	0.57
1:C:57:THR:O	1:C:60:SER:HB3	2.05	0.57
1:E:60:SER:OG	2:E:202:SO4:O3	2.15	0.57
1:B:24:THR:HG22	1:B:27:GLU:CG	2.35	0.56
1:D:94:TYR:CZ	1:D:112:ARG:HD3	2.40	0.56
1:I:20:THR:HG22	1:I:23:MET:HB2	1.87	0.56
1:A:56:LEU:CD1	1:A:61:LEU:HD21	2.34	0.56
1:C:48:GLN:O	1:C:49:THR:OG1	2.20	0.55
1:H:86:ASN:HD21	1:H:90:HIS:HB2	1.71	0.55
1:B:24:THR:HG22	1:B:27:GLU:HG3	1.88	0.55
1:A:87:GLU:OE1	1:A:87:GLU:N	2.27	0.55
1:I:106:LYS:NZ	1:I:120:PHE:O	2.40	0.55
1:A:80:LEU:HD11	1:A:96:VAL:HG23	1.88	0.55
1:D:23:MET:CE	1:D:28:LEU:HA	2.36	0.55
1:H:15:PHE:CD2	1:H:35:LYS:HD3	2.42	0.55
1:I:19:VAL:HG12	1:I:23:MET:CE	2.35	0.55
1:F:23:MET:H	1:F:58:LEU:HB2	1.72	0.55
1:G:19:VAL:CG1	1:G:23:MET:HE2	2.37	0.55
1:G:19:VAL:HB	1:G:23:MET:HE2	1.89	0.55
1:E:19:VAL:HG12	1:E:23:MET:CE	2.37	0.54
1:J:113:GLU:OE1	1:J:148:LYS:NZ	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:124:PHE:HB2	1:J:129:MET:HE3	1.90	0.54
1:I:6:LYS:HE3	1:I:68:THR:OG1	2.07	0.54
1:F:57:THR:HG22	1:F:58:LEU:O	2.07	0.54
1:J:23:MET:HE2	1:J:27:GLU:C	2.28	0.54
1:I:2:ALA:HA	1:I:19:VAL:O	2.06	0.54
1:H:23:MET:O	1:H:58:LEU:HD13	2.07	0.54
1:H:48:GLN:O	1:H:49:THR:OG1	2.21	0.53
1:E:87:GLU:OE1	1:E:87:GLU:N	2.41	0.53
1:A:48:GLN:O	1:A:49:THR:OG1	2.22	0.53
1:F:22:SER:HB2	1:F:57:THR:HG21	1.90	0.53
1:H:67:SER:HA	2:H:201:SO4:O2	2.08	0.53
1:B:25:VAL:HG21	1:B:52:LEU:HB3	1.91	0.53
1:J:20:THR:CG2	1:J:23:MET:HB2	2.39	0.53
1:B:57:THR:HG22	1:B:60:SER:HB3	1.91	0.53
1:E:23:MET:HE2	1:E:58:LEU:HD11	1.91	0.53
1:A:19:VAL:HA	1:A:23:MET:CE	2.40	0.52
1:J:94:TYR:CZ	1:J:112:ARG:HD3	2.43	0.52
1:J:21:ASN:HB3	1:J:59:SER:HB2	1.90	0.52
1:H:107:LYS:HG2	1:H:117:GLU:OE2	2.09	0.52
1:G:100:GLN:HB3	1:G:104:THR:OG1	2.10	0.52
1:D:48:GLN:O	1:D:49:THR:OG1	2.25	0.52
1:H:118:ASP:O	1:H:151:ARG:HD2	2.09	0.52
1:F:23:MET:O	1:F:58:LEU:N	2.42	0.52
1:I:35:LYS:HE3	1:J:111(A):GLN:NE2	2.24	0.52
1:D:107:LYS:HG2	1:D:117:GLU:OE2	2.09	0.52
1:E:155:GLY:HA3	1:H:126:GLY:HA2	1.92	0.51
1:F:61:LEU:HD23	1:F:62:GLY:N	2.12	0.51
1:I:35:LYS:HE3	1:J:111(A):GLN:OE1	2.10	0.51
1:I:25:VAL:CG1	1:I:53:GLN:O	2.58	0.51
1:E:155:GLY:CA	1:H:126:GLY:HA2	2.41	0.51
1:G:21:ASN:HB3	1:G:59:SER:HB3	1.92	0.51
1:I:36:ILE:O	1:J:112:ARG:HD2	2.10	0.51
1:J:19:VAL:HB	1:J:58:LEU:CD1	2.41	0.51
1:E:153:ARG:HB2	1:H:85:ARG:CZ	2.39	0.51
1:F:106:LYS:NZ	1:F:120:PHE:O	2.44	0.51
1:E:17:VAL:CG1	1:E:31:GLN:HB3	2.40	0.51
1:F:4:ASP:HA	1:F:17:VAL:O	2.10	0.51
1:I:56:LEU:CD2	1:I:61:LEU:HD21	2.41	0.51
1:J:67:SER:HA	4:J:202:HOH:O	2.10	0.51
1:D:94:TYR:OH	1:D:112:ARG:HD3	2.11	0.50
1:F:7:VAL:HG22	1:F:69:VAL:HG13	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:57:THR:CG2	1:B:60:SER:HB3	2.42	0.50
1:E:118:ASP:O	1:E:151:ARG:HD3	2.11	0.50
1:J:3:TRP:CH2	1:J:5:LEU:HD13	2.46	0.50
1:A:75:ASN:HB2	4:A:319:HOH:O	2.12	0.50
1:G:58:LEU:HD22	1:G:63:LEU:HD12	1.92	0.50
1:F:3:TRP:CG	1:F:65:PRO:HG3	2.46	0.50
1:I:25:VAL:CG1	1:I:54:ASP:HA	2.35	0.50
1:B:113:GLU:OE1	1:B:148:LYS:HE2	2.12	0.49
1:J:47:HIS:ND1	1:J:48:GLN:HG3	2.27	0.49
1:E:81:SER:HB3	1:G:137:GLU:HG3	1.93	0.49
1:I:3:TRP:CH2	1:I:64:GLY:O	2.65	0.49
1:D:8:LYS:HB3	1:D:70:MET:HE2	1.92	0.49
1:E:65:PRO:HG2	2:E:201:SO4:O2	2.12	0.49
1:B:19:VAL:HA	1:B:23:MET:CE	2.43	0.49
1:B:24:THR:HG22	1:B:27:GLU:CD	2.32	0.49
1:F:47:HIS:CE1	1:F:63:LEU:HD11	2.48	0.49
1:J:15:PHE:C	1:J:16:LEU:HD12	2.32	0.49
1:J:17:VAL:HG11	1:J:31:GLN:CB	2.42	0.49
1:E:19:VAL:HG12	1:E:23:MET:HE1	1.94	0.49
1:F:62:GLY:O	1:F:63:LEU:HB2	2.11	0.48
1:G:19:VAL:HG12	1:G:23:MET:CE	2.43	0.48
1:B:19:VAL:HA	1:B:23:MET:HE1	1.95	0.48
1:H:80:LEU:HD21	1:H:98:LEU:HG	1.95	0.48
1:F:49:THR:O	1:F:49:THR:HG22	2.13	0.48
1:A:118:ASP:N	1:A:118:ASP:OD1	2.45	0.48
1:F:47:HIS:CD2	1:F:48:GLN:HG3	2.48	0.48
1:A:140:LEU:HD22	1:A:144:CYS:SG	2.54	0.48
1:E:19:VAL:CG1	1:E:23:MET:HE2	2.44	0.48
1:J:23:MET:O	1:J:58:LEU:HG	2.13	0.48
1:F:7:VAL:HA	1:F:69:VAL:O	2.14	0.48
1:F:22:SER:HB2	1:F:57:THR:HG23	1.96	0.48
1:I:86:ASN:C	1:I:88:ARG:H	2.16	0.48
1:J:4:ASP:HB3	1:J:16:LEU:HB3	1.94	0.48
1:J:47:HIS:CE1	1:J:48:GLN:HG3	2.49	0.48
1:J:118:ASP:OD1	1:J:118:ASP:N	2.46	0.48
1:F:16:LEU:HD22	1:F:16:LEU:H	1.79	0.47
1:I:58:LEU:O	1:I:61:LEU:N	2.44	0.47
1:J:16:LEU:N	1:J:16:LEU:HD12	2.29	0.47
1:C:8:LYS:HG3	1:C:14:ASP:OD1	2.14	0.47
1:F:103:ASP:O	1:F:107:LYS:HG3	2.14	0.47
1:F:47:HIS:CD2	1:F:63:LEU:CD1	2.93	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:57:THR:O	1:F:60:SER:OG	2.20	0.47
1:B:94:TYR:OH	1:B:112:ARG:HD3	2.14	0.47
1:F:3:TRP:CE3	1:F:65:PRO:HA	2.50	0.47
1:B:52:LEU:HD22	1:B:61:LEU:HD13	1.96	0.47
1:B:114:GLN:NE2	1:C:13:ASN:HB3	2.30	0.46
1:C:127:ARG:HA	1:C:128:PRO:HD2	1.72	0.46
1:E:23:MET:CE	1:E:28:LEU:HA	2.45	0.46
1:J:61:LEU:O	1:J:63:LEU:HD13	2.14	0.46
1:D:40:ALA:HB3	3:D:205:GOL:H12	1.98	0.46
1:I:19:VAL:HB	1:I:23:MET:HE2	1.96	0.46
1:B:56:LEU:CD2	1:B:61:LEU:HD21	2.45	0.46
1:H:148:LYS:NZ	1:H:150:LEU:HD11	2.29	0.46
1:I:25:VAL:HG13	1:I:54:ASP:CA	2.37	0.46
1:J:3:TRP:HZ3	1:J:5:LEU:HA	1.79	0.46
1:D:23:MET:HE2	1:D:28:LEU:N	2.31	0.46
1:F:85:ARG:HH21	1:F:147:ILE:HD11	1.81	0.46
1:B:56:LEU:HD23	1:B:61:LEU:HD21	1.97	0.46
1:F:16:LEU:N	1:F:16:LEU:HD13	2.29	0.46
1:D:114:GLN:OE1	1:D:114:GLN:HA	2.16	0.46
1:J:94:TYR:CZ	1:J:109:VAL:HG22	2.51	0.46
1:I:44:ARG:HG3	1:I:74:GLN:CG	2.45	0.45
1:B:20:THR:N	1:B:23:MET:HE3	2.30	0.45
1:I:25:VAL:HA	1:I:28:LEU:HB3	1.98	0.45
1:C:24:THR:HG23	1:C:26:SER:N	2.31	0.45
1:H:20:THR:HG22	1:H:23:MET:HB2	1.97	0.45
1:B:118:ASP:N	1:B:118:ASP:OD1	2.45	0.45
1:H:10:LEU:C	1:H:12:GLY:H	2.20	0.45
1:I:15:PHE:N	1:I:15:PHE:CD1	2.85	0.45
1:I:20:THR:CG2	1:I:23:MET:HB2	2.46	0.45
1:J:4:ASP:HA	1:J:17:VAL:O	2.16	0.45
1:H:120:PHE:HB2	1:H:149:HIS:O	2.17	0.45
1:I:85:ARG:HG2	1:I:87:GLU:H	1.80	0.45
1:C:106:LYS:NZ	1:C:120:PHE:O	2.49	0.45
1:A:20:THR:N	1:A:23:MET:HE3	2.29	0.45
1:A:80:LEU:CD1	1:A:96:VAL:HG23	2.47	0.45
1:B:49:THR:O	1:B:49:THR:HG22	2.16	0.45
1:E:78:GLU:HB3	1:E:79:PRO:HD2	1.99	0.45
1:F:71:LEU:C	1:F:71:LEU:HD23	2.38	0.45
1:F:78:GLU:HB3	1:F:79:PRO:HD2	1.99	0.45
1:E:81:SER:HB3	1:G:137:GLU:CG	2.46	0.44
1:H:19:VAL:HA	1:H:23:MET:CE	2.46	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:24:THR:CG2	1:C:27:GLU:HG3	2.46	0.44
1:D:80:LEU:HD21	1:D:98:LEU:HG	1.98	0.44
1:E:19:VAL:CG1	1:E:23:MET:CE	2.95	0.44
1:I:35:LYS:HE3	1:J:111(A):GLN:HE22	1.82	0.44
1:I:35:LYS:HE3	1:J:111(A):GLN:CD	2.37	0.44
1:E:4:ASP:HB3	1:E:16:LEU:HD22	2.00	0.44
1:F:25:VAL:O	1:F:28:LEU:HB3	2.17	0.44
1:G:23:MET:HE1	1:G:28:LEU:HA	2.00	0.44
1:J:63:LEU:HD12	1:J:67:SER:OG	2.17	0.44
1:F:63:LEU:HA	1:F:67:SER:CB	2.46	0.44
1:E:114:GLN:CG	1:G:12:GLY:HA2	2.47	0.44
1:J:23:MET:HE1	1:J:28:LEU:HA	1.99	0.44
1:F:151:ARG:O	1:F:152:LEU:HD12	2.17	0.44
1:J:124:PHE:HB2	1:J:129:MET:HE2	1.99	0.44
1:F:6:LYS:HA	1:F:15:PHE:O	2.18	0.43
1:H:13:ASN:CG	1:I:114:GLN:HG3	2.39	0.43
1:G:19:VAL:CB	1:G:23:MET:HE2	2.48	0.43
1:I:5:LEU:HD21	1:I:69:VAL:HG21	2.00	0.43
1:J:47:HIS:CD2	1:J:63:LEU:HD11	2.54	0.43
1:I:15:PHE:CZ	1:I:36:ILE:HD13	2.54	0.43
1:I:25:VAL:HG11	1:I:53:GLN:C	2.38	0.43
1:I:21:ASN:CB	1:I:59:SER:HB3	2.44	0.43
1:I:78:GLU:N	1:I:78:GLU:OE1	2.32	0.43
1:J:71:LEU:HD23	1:J:71:LEU:C	2.38	0.43
1:I:36:ILE:HB	1:J:112:ARG:HB2	2.01	0.43
1:F:25:VAL:HG13	1:F:54:ASP:O	2.19	0.43
1:C:114:GLN:CD	1:E:12:GLY:HA2	2.40	0.43
1:F:80:LEU:HD21	1:F:98:LEU:HG	2.01	0.42
1:A:57:THR:O	1:A:60:SER:HB3	2.19	0.42
1:H:20:THR:H	1:H:23:MET:HE3	1.85	0.42
1:J:63:LEU:HA	1:J:63:LEU:HD12	1.77	0.42
1:F:63:LEU:N	1:F:63:LEU:HD12	2.35	0.42
1:I:41:PHE:CE1	1:I:42:GLN:HG3	2.55	0.42
1:A:106:LYS:NZ	1:A:120:PHE:O	2.53	0.42
1:J:57:THR:O	1:J:61:LEU:HG	2.19	0.42
1:B:58:LEU:HA	1:B:58:LEU:HD23	1.81	0.42
1:H:121:TRP:HB2	1:I:53:GLN:NE2	2.31	0.42
1:I:57:THR:O	1:I:60:SER:HB3	2.20	0.42
1:J:3:TRP:CZ3	1:J:5:LEU:HA	2.55	0.42
1:E:23:MET:HE3	1:E:28:LEU:CB	2.47	0.42
1:F:45:LEU:CD2	1:F:71:LEU:HB2	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:88:ARG:C	1:F:90:HIS:H	2.23	0.42
1:H:48:GLN:NE2	2:H:201:SO4:O1	2.53	0.42
1:E:120:PHE:HB2	1:E:149:HIS:O	2.20	0.42
1:F:53:GLN:O	1:F:56:LEU:HD13	2.20	0.42
1:H:80:LEU:CD2	1:H:98:LEU:HG	2.50	0.42
1:E:48:GLN:O	1:E:49:THR:OG1	2.33	0.41
1:I:63:LEU:HD23	1:I:63:LEU:HA	1.91	0.41
1:J:2:ALA:HA	1:J:19:VAL:O	2.20	0.41
1:D:52:LEU:HD22	1:D:61:LEU:HD13	2.02	0.41
1:C:60:SER:O	1:E:152:LEU:HD12	2.20	0.41
1:D:15:PHE:CE1	1:D:36:ILE:HD13	2.55	0.41
1:F:45:LEU:HD23	1:F:71:LEU:HA	2.02	0.41
1:J:7:VAL:O	1:J:14:ASP:HA	2.21	0.41
1:B:24:THR:OG1	1:B:54:ASP:O	2.38	0.41
1:C:19:VAL:HA	1:C:23:MET:CE	2.50	0.41
1:F:142:PRO:O	1:F:143:GLN:HB2	2.20	0.41
1:H:56:LEU:CD1	1:H:61:LEU:HD21	2.51	0.41
1:I:15:PHE:C	1:I:16:LEU:HD12	2.40	0.41
1:H:6:LYS:HG2	1:H:16:LEU:CD2	2.51	0.41
1:H:98:LEU:HA	1:H:98:LEU:HD23	1.74	0.41
1:C:56:LEU:CD2	1:E:151:ARG:HE	2.34	0.41
1:H:8:LYS:HG3	1:H:14:ASP:OD1	2.21	0.41
1:F:47:HIS:NE2	1:F:63:LEU:HD11	2.34	0.40
1:E:94:TYR:CE2	1:E:112:ARG:HD3	2.57	0.40
1:G:148:LYS:NZ	1:G:150:LEU:HD21	2.36	0.40
1:D:106:LYS:NZ	1:D:120:PHE:O	2.54	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:44:ARG:NH1	1:D:155:GLY:O[3_555]	2.04	0.16

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	152/155 (98%)	148 (97%)	4 (3%)	0	100 100
1	B	149/155 (96%)	144 (97%)	4 (3%)	1 (1%)	26 21
1	C	148/155 (96%)	145 (98%)	3 (2%)	0	100 100
1	D	152/155 (98%)	150 (99%)	2 (1%)	0	100 100
1	E	152/155 (98%)	151 (99%)	0	1 (1%)	26 21
1	F	141/155 (91%)	135 (96%)	4 (3%)	2 (1%)	14 7
1	G	152/155 (98%)	148 (97%)	3 (2%)	1 (1%)	26 21
1	H	148/155 (96%)	145 (98%)	2 (1%)	1 (1%)	26 21
1	I	147/155 (95%)	143 (97%)	4 (3%)	0	100 100
1	J	147/155 (95%)	141 (96%)	6 (4%)	0	100 100
All	All	1488/1550 (96%)	1450 (97%)	32 (2%)	6 (0%)	39 37

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	62	GLY
1	E	87	GLU
1	H	62	GLY
1	F	87	GLU
1	G	12	GLY
1	F	86	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	137/138 (99%)	134 (98%)	3 (2%)	60 64
1	B	136/138 (99%)	136 (100%)	0	100 100
1	C	133/138 (96%)	131 (98%)	2 (2%)	72 78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	D	135/138 (98%)	134 (99%)	1 (1%)	88 92
1	E	136/138 (99%)	133 (98%)	3 (2%)	60 64
1	F	129/138 (94%)	124 (96%)	5 (4%)	39 39
1	G	134/138 (97%)	133 (99%)	1 (1%)	88 92
1	H	134/138 (97%)	132 (98%)	2 (2%)	72 78
1	I	130/138 (94%)	128 (98%)	2 (2%)	72 78
1	J	132/138 (96%)	128 (97%)	4 (3%)	48 51
All	All	1336/1380 (97%)	1313 (98%)	23 (2%)	68 74

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	66	SER
1	A	80	LEU
1	A	118	ASP
1	C	24	THR
1	C	66	SER
1	D	80	LEU
1	E	80	LEU
1	E	150	LEU
1	E	152	LEU
1	F	16	LEU
1	F	25	VAL
1	F	67	SER
1	F	68	THR
1	F	80	LEU
1	G	80	LEU
1	H	48	GLN
1	H	80	LEU
1	I	15	PHE
1	I	80	LEU
1	J	13	ASN
1	J	63	LEU
1	J	66	SER
1	J	68	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	GLN
1	E	114	GLN
1	F	47	HIS
1	F	48	GLN
1	F	86	ASN
1	I	13	ASN

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)

22 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	SO4	A	201	-	4,4,4	0.24	0	6,6,6	0.22	0
3	GOL	A	202	-	5,5,5	0.40	0	5,5,5	0.42	0
3	GOL	A	203	-	5,5,5	0.41	0	5,5,5	0.56	0
2	SO4	B	201	-	4,4,4	0.24	0	6,6,6	0.31	0
3	GOL	B	202	-	5,5,5	0.27	0	5,5,5	0.34	0
3	GOL	B	203	-	5,5,5	0.43	0	5,5,5	0.41	0
3	GOL	B	204	-	5,5,5	0.49	0	5,5,5	0.54	0
2	SO4	C	201	-	4,4,4	0.28	0	6,6,6	0.16	0
2	SO4	D	201	-	4,4,4	0.29	0	6,6,6	0.14	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	SO4	D	202	-	4,4,4	0.25	0	6,6,6	0.18	0
2	SO4	D	203	-	4,4,4	0.37	0	6,6,6	0.69	0
2	SO4	D	204	-	4,4,4	0.13	0	6,6,6	0.29	0
3	GOL	D	205	-	5,5,5	0.37	0	5,5,5	0.50	0
2	SO4	E	201	-	4,4,4	0.20	0	6,6,6	0.19	0
2	SO4	E	202	-	4,4,4	0.25	0	6,6,6	0.49	0
2	SO4	E	203	-	4,4,4	0.30	0	6,6,6	0.15	0
2	SO4	G	201	-	4,4,4	0.28	0	6,6,6	0.23	0
2	SO4	G	202	-	4,4,4	0.31	0	6,6,6	0.15	0
3	GOL	G	203	-	5,5,5	0.28	0	5,5,5	0.32	0
3	GOL	G	204	-	5,5,5	0.48	0	5,5,5	0.25	0
2	SO4	H	201	-	4,4,4	0.16	0	6,6,6	0.11	0
3	GOL	I	201	-	5,5,5	0.41	0	5,5,5	0.36	0

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	SO4	A	201	-	-	0/0/0/0	0/0/0/0
3	GOL	A	202	-	-	0/4/4/4	0/0/0/0
3	GOL	A	203	-	-	0/4/4/4	0/0/0/0
2	SO4	B	201	-	-	0/0/0/0	0/0/0/0
3	GOL	B	202	-	-	0/4/4/4	0/0/0/0
3	GOL	B	203	-	-	0/4/4/4	0/0/0/0
3	GOL	B	204	-	-	0/4/4/4	0/0/0/0
2	SO4	C	201	-	-	0/0/0/0	0/0/0/0
2	SO4	D	201	-	-	0/0/0/0	0/0/0/0
2	SO4	D	202	-	-	0/0/0/0	0/0/0/0
2	SO4	D	203	-	-	0/0/0/0	0/0/0/0
2	SO4	D	204	-	-	0/0/0/0	0/0/0/0
3	GOL	D	205	-	-	0/4/4/4	0/0/0/0
2	SO4	E	201	-	-	0/0/0/0	0/0/0/0
2	SO4	E	202	-	-	0/0/0/0	0/0/0/0
2	SO4	E	203	-	-	0/0/0/0	0/0/0/0
2	SO4	G	201	-	-	0/0/0/0	0/0/0/0
2	SO4	G	202	-	-	0/0/0/0	0/0/0/0
3	GOL	G	203	-	-	0/4/4/4	0/0/0/0
3	GOL	G	204	-	-	0/4/4/4	0/0/0/0
2	SO4	H	201	-	-	0/0/0/0	0/0/0/0
3	GOL	I	201	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	203	GOL	1	0
2	C	201	SO4	1	0
2	D	201	SO4	1	0
3	D	205	GOL	1	0
2	E	201	SO4	1	0
2	E	202	SO4	1	0
2	H	201	SO4	2	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	154/155 (99%)	0.65	7 (4%) 37 46	46, 68, 121, 148	0
1	B	151/155 (97%)	0.55	9 (5%) 25 33	45, 74, 115, 169	0
1	C	150/155 (96%)	0.58	4 (2%) 58 65	51, 78, 109, 153	0
1	D	154/155 (99%)	0.50	3 (1%) 70 75	52, 69, 113, 142	0
1	E	154/155 (99%)	0.55	6 (3%) 43 52	50, 67, 121, 155	0
1	F	147/155 (94%)	1.62	41 (27%) 1 1	62, 100, 190, 220	0
1	G	154/155 (99%)	0.53	6 (3%) 43 52	48, 65, 103, 151	0
1	H	150/155 (96%)	0.75	15 (10%) 9 13	57, 85, 140, 178	0
1	I	149/155 (96%)	1.11	29 (19%) 1 2	72, 108, 154, 176	0
1	J	149/155 (96%)	1.52	42 (28%) 1 1	74, 122, 181, 192	0
All	All	1512/1550 (97%)	0.83	162 (10%) 8 11	45, 80, 153, 220	0

All (162) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	11	GLY	8.2
1	J	63	LEU	7.9
1	F	50	ALA	7.7
1	F	46	ALA	7.3
1	I	63	LEU	7.2
1	I	61	LEU	7.1
1	F	68	THR	6.8
1	H	10	LEU	6.7
1	I	62	GLY	6.7
1	F	89	GLY	6.7
1	J	50	ALA	6.7
1	F	56	LEU	6.6
1	J	3	TRP	6.6

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Mol	Chain	Res	Type	RSRZ
1	F	152	LEU	6.3
1	B	2	ALA	6.2
1	I	23	MET	6.2
1	F	49	THR	5.9
1	J	10	LEU	5.7
1	F	70	MET	5.7
1	J	56	LEU	5.7
1	F	3	TRP	5.5
1	F	15	PHE	5.5
1	G	12	GLY	5.3
1	J	58	LEU	5.1
1	F	57	THR	5.0
1	E	154	GLY	5.0
1	J	115	VAL	4.9
1	B	152	LEU	4.8
1	I	3	TRP	4.8
1	F	69	VAL	4.8
1	F	4	ASP	4.8
1	J	5	LEU	4.6
1	H	2	ALA	4.5
1	F	21	ASN	4.5
1	F	6	LYS	4.4
1	H	49	THR	4.4
1	J	11	GLY	4.3
1	I	115	VAL	4.2
1	J	150	LEU	4.2
1	I	56	LEU	4.2
1	F	66	SER	4.1
1	F	63	LEU	4.0
1	F	17	VAL	4.0
1	J	116	HIS	4.0
1	J	59	SER	4.0
1	J	84	VAL	4.0
1	F	5	LEU	3.9
1	I	53	GLN	3.9
1	I	120	PHE	3.9
1	E	75	ASN	3.7
1	J	61	LEU	3.7
1	F	58	LEU	3.7
1	J	62	GLY	3.6
1	F	13	ASN	3.6
1	D	10	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
1	I	114	GLN	3.5
1	F	48	GLN	3.4
1	J	148	LYS	3.4
1	H	68	THR	3.4
1	I	58	LEU	3.4
1	J	52	LEU	3.4
1	J	51	VAL	3.3
1	J	22	SER	3.3
1	F	52	LEU	3.3
1	F	45	LEU	3.2
1	F	86	ASN	3.2
1	F	47	HIS	3.2
1	J	122	LEU	3.2
1	J	65	PRO	3.1
1	J	23	MET	3.1
1	J	70	MET	3.1
1	J	91	SER	3.1
1	F	72	VAL	3.1
1	J	53	GLN	3.1
1	E	152	LEU	3.1
1	J	49	THR	3.0
1	J	45	LEU	3.0
1	I	118	ASP	3.0
1	F	32	ILE	3.0
1	E	10	LEU	3.0
1	F	65	PRO	3.0
1	B	115	VAL	2.9
1	J	114	GLN	2.9
1	A	61	LEU	2.9
1	I	19	VAL	2.9
1	J	17	VAL	2.9
1	J	85	ARG	2.9
1	F	22	SER	2.9
1	B	150	LEU	2.9
1	B	49	THR	2.8
1	G	155	GLY	2.8
1	I	5	LEU	2.8
1	E	76	SER	2.8
1	A	50	ALA	2.7
1	B	151	ARG	2.7
1	J	120	PHE	2.7
1	A	23	MET	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	87	GLU	2.7
1	I	119	GLN	2.7
1	H	15	PHE	2.7
1	F	55	GLY	2.7
1	I	66	SER	2.6
1	J	4	ASP	2.6
1	F	51	VAL	2.6
1	H	50	ALA	2.6
1	J	68	THR	2.6
1	A	155	GLY	2.6
1	I	15	PHE	2.6
1	F	44	ARG	2.5
1	I	16	LEU	2.6
1	I	6	LYS	2.5
1	J	6	LYS	2.5
1	I	117	GLU	2.5
1	I	57	THR	2.5
1	D	114	GLN	2.5
1	I	150	LEU	2.5
1	F	116	HIS	2.5
1	H	13	ASN	2.4
1	C	52	LEU	2.4
1	G	80	LEU	2.4
1	H	12	GLY	2.3
1	J	8	LYS	2.3
1	J	145	THR	2.3
1	H	88	ARG	2.3
1	H	5	LEU	2.3
1	J	118	ASP	2.3
1	G	10	LEU	2.2
1	H	71	LEU	2.2
1	F	7	VAL	2.2
1	I	4	ASP	2.2
1	F	16	LEU	2.2
1	J	28	LEU	2.2
1	C	97	PHE	2.2
1	I	20	THR	2.2
1	I	13	ASN	2.2
1	B	50	ALA	2.2
1	I	111(A)	GLN	2.2
1	B	88	ARG	2.2
1	H	85	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	147	ILE	2.1
1	H	6	LYS	2.1
1	F	61	LEU	2.1
1	C	69	VAL	2.1
1	I	2	ALA	2.1
1	J	57	THR	2.1
1	E	13	ASN	2.1
1	I	116	HIS	2.1
1	A	15	PHE	2.1
1	D	23	MET	2.1
1	A	70	MET	2.1
1	F	19	VAL	2.1
1	F	90	HIS	2.1
1	I	131	ASP	2.0
1	A	146	VAL	2.0
1	J	46	ALA	2.0
1	G	79	PRO	2.0
1	F	28	LEU	2.0
1	F	122	LEU	2.0
1	J	47	HIS	2.0
1	H	9	MET	2.0
1	G	96	VAL	2.0
1	J	126	GLY	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å^2)	Q<0.9
3	GOL	A	202	6/6	0.69	0.24	10.20	90,93,103,103	0
3	GOL	A	203	6/6	0.79	0.35	8.39	106,110,115,130	0
3	GOL	G	203	6/6	0.81	0.34	5.79	93,101,115,116	0
3	GOL	D	205	6/6	0.54	0.23	4.10	66,96,103,104	0
3	GOL	B	204	6/6	0.68	0.24	3.27	84,102,109,112	0
3	GOL	B	203	6/6	0.86	0.26	2.64	100,101,103,108	0
3	GOL	G	204	6/6	0.83	0.23	0.68	92,97,98,101	0
2	SO4	D	204	5/5	0.95	0.14	0.33	73,90,93,98	0
2	SO4	E	201	5/5	0.88	0.15	0.30	131,133,137,142	0
2	SO4	D	203	5/5	0.97	0.18	0.25	65,76,88,106	0
2	SO4	E	202	5/5	0.95	0.15	0.24	84,88,91,106	0
2	SO4	G	201	5/5	0.93	0.14	0.11	87,101,114,121	0
2	SO4	B	201	5/5	0.87	0.13	-0.22	97,111,119,121	0
2	SO4	D	201	5/5	0.95	0.17	-0.26	110,113,127,131	0
3	GOL	I	201	6/6	0.80	0.18	-0.35	98,102,103,106	0
2	SO4	D	202	5/5	0.94	0.17	-0.45	97,104,112,114	0
2	SO4	C	201	5/5	0.99	0.16	-0.70	84,89,92,98	0
2	SO4	A	201	5/5	0.83	0.13	-	93,113,116,120	0
2	SO4	E	203	5/5	0.96	0.09	-	92,93,102,109	0
2	SO4	G	202	5/5	0.95	0.15	-	88,99,108,110	0
3	GOL	B	202	6/6	0.81	0.14	-	87,104,112,112	0
2	SO4	H	201	5/5	0.90	0.22	-	130,130,134,135	0

6.5 Other polymers (i)

There are no such residues in this entry.