Full wwPDB X-ray Structure Validation Report (i)

Mar 9, 2024 – 06:26 PM EST

PDB ID	:	3GXA
Title	:	Crystal structure of GNA1946
Authors	:	Yang, X.; Shen, Y.
Deposited on	:	2009-04-02
Resolution	:	2.25 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

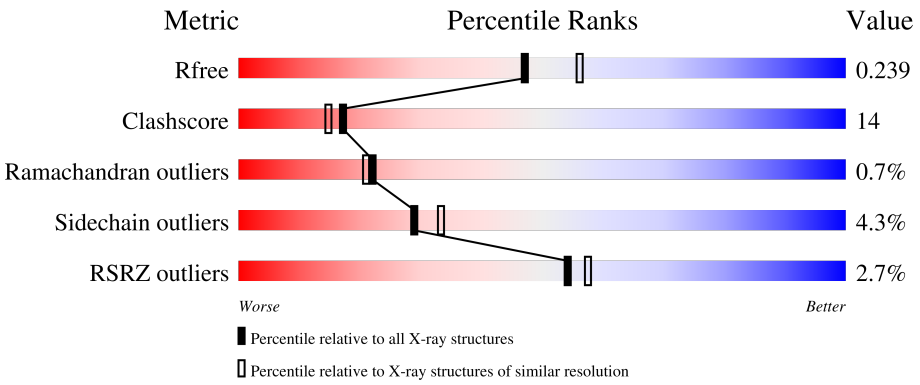
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.25 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	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

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 <=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	275	64% 20% • 13%
1	B	275	2% 66% 19% • 13%
1	C	275	7% 59% 27% • 11%
1	D	275	2% 67% 18% • 13%
1	E	275	% 63% 21% • 13%

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Mol	Chain	Length	Quality of chain
1	F	275	2% 64% 21% 11%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 12179 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 Outer membrane lipoprotein GNA1946.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	239	1884	1211	305	365	3	0	0	0
1	B	239	1884	1211	305	365	3	0	0	0
1	C	244	1915	1228	311	373	3	0	0	0
1	D	239	1884	1211	305	365	3	0	0	0
1	E	239	1884	1211	305	365	3	0	0	0
1	F	244	1915	1228	311	373	3	0	0	0

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	21	MET	-	expression tag	UNP Q7BMQ8
A	288	LEU	-	expression tag	UNP Q7BMQ8
A	289	GLU	-	expression tag	UNP Q7BMQ8
A	290	HIS	-	expression tag	UNP Q7BMQ8
A	291	HIS	-	expression tag	UNP Q7BMQ8
A	292	HIS	-	expression tag	UNP Q7BMQ8
A	293	HIS	-	expression tag	UNP Q7BMQ8
A	294	HIS	-	expression tag	UNP Q7BMQ8
A	295	HIS	-	expression tag	UNP Q7BMQ8
B	21	MET	-	expression tag	UNP Q7BMQ8
B	288	LEU	-	expression tag	UNP Q7BMQ8
B	289	GLU	-	expression tag	UNP Q7BMQ8
B	290	HIS	-	expression tag	UNP Q7BMQ8
B	291	HIS	-	expression tag	UNP Q7BMQ8
B	292	HIS	-	expression tag	UNP Q7BMQ8
B	293	HIS	-	expression tag	UNP Q7BMQ8
B	294	HIS	-	expression tag	UNP Q7BMQ8

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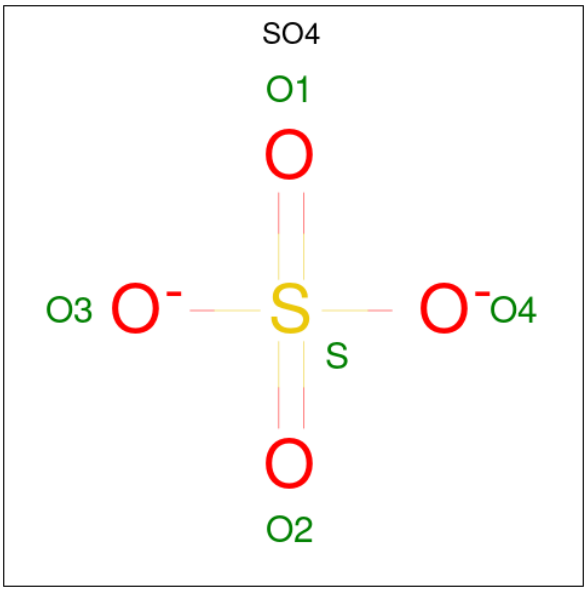
Chain	Residue	Modelled	Actual	Comment	Reference
B	295	HIS	-	expression tag	UNP Q7BMQ8
C	21	MET	-	expression tag	UNP Q7BMQ8
C	288	LEU	-	expression tag	UNP Q7BMQ8
C	289	GLU	-	expression tag	UNP Q7BMQ8
C	290	HIS	-	expression tag	UNP Q7BMQ8
C	291	HIS	-	expression tag	UNP Q7BMQ8
C	292	HIS	-	expression tag	UNP Q7BMQ8
C	293	HIS	-	expression tag	UNP Q7BMQ8
C	294	HIS	-	expression tag	UNP Q7BMQ8
C	295	HIS	-	expression tag	UNP Q7BMQ8
D	21	MET	-	expression tag	UNP Q7BMQ8
D	288	LEU	-	expression tag	UNP Q7BMQ8
D	289	GLU	-	expression tag	UNP Q7BMQ8
D	290	HIS	-	expression tag	UNP Q7BMQ8
D	291	HIS	-	expression tag	UNP Q7BMQ8
D	292	HIS	-	expression tag	UNP Q7BMQ8
D	293	HIS	-	expression tag	UNP Q7BMQ8
D	294	HIS	-	expression tag	UNP Q7BMQ8
D	295	HIS	-	expression tag	UNP Q7BMQ8
E	21	MET	-	expression tag	UNP Q7BMQ8
E	288	LEU	-	expression tag	UNP Q7BMQ8
E	289	GLU	-	expression tag	UNP Q7BMQ8
E	290	HIS	-	expression tag	UNP Q7BMQ8
E	291	HIS	-	expression tag	UNP Q7BMQ8
E	292	HIS	-	expression tag	UNP Q7BMQ8
E	293	HIS	-	expression tag	UNP Q7BMQ8
E	294	HIS	-	expression tag	UNP Q7BMQ8
E	295	HIS	-	expression tag	UNP Q7BMQ8
F	21	MET	-	expression tag	UNP Q7BMQ8
F	288	LEU	-	expression tag	UNP Q7BMQ8
F	289	GLU	-	expression tag	UNP Q7BMQ8
F	290	HIS	-	expression tag	UNP Q7BMQ8
F	291	HIS	-	expression tag	UNP Q7BMQ8
F	292	HIS	-	expression tag	UNP Q7BMQ8
F	293	HIS	-	expression tag	UNP Q7BMQ8
F	294	HIS	-	expression tag	UNP Q7BMQ8
F	295	HIS	-	expression tag	UNP Q7BMQ8

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



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

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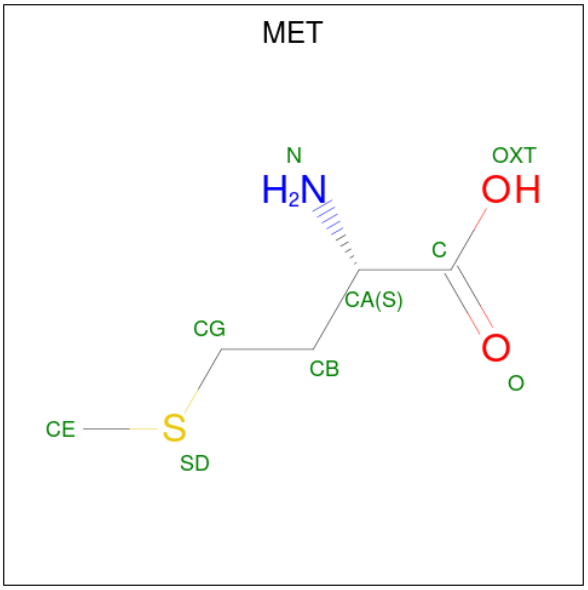
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	O	S			
2	F	1	5	4	1		0	0
			Total	O	S			
2	F	1	5	4	1		0	0

- Molecule 3 is METHIONINE (three-letter code: MET) (formula: $C_5H_{11}NO_2S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
3	A	1	9	5	1	2	1	0	0
			Total	C	N	O	S		
3	B	1	9	5	1	2	1	0	0
			Total	C	N	O	S		
3	C	1	9	5	1	2	1	0	0
			Total	C	N	O	S		
3	D	1	9	5	1	2	1	0	0
			Total	C	N	O	S		
3	E	1	9	5	1	2	1	0	0
			Total	C	N	O	S		
3	F	1	9	5	1	2	1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	128	128	128	0	0

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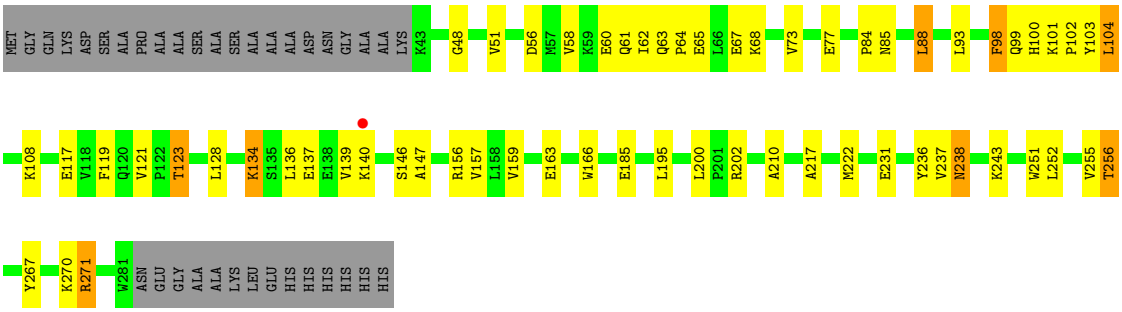
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	B	111	111	111	0	0
			Total	O		
4	C	100	100	100	0	0
			Total	O		
4	D	136	136	136	0	0
			Total	O		
4	E	105	105	105	0	0
			Total	O		
4	F	99	99	99	0	0

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.

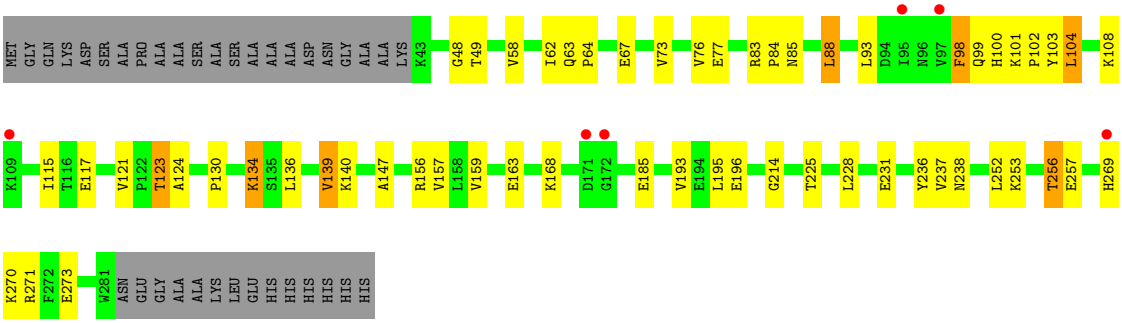
• Molecule 1: Outer membrane lipoprotein GNA1946

Chain A: 64% 20% • 13%



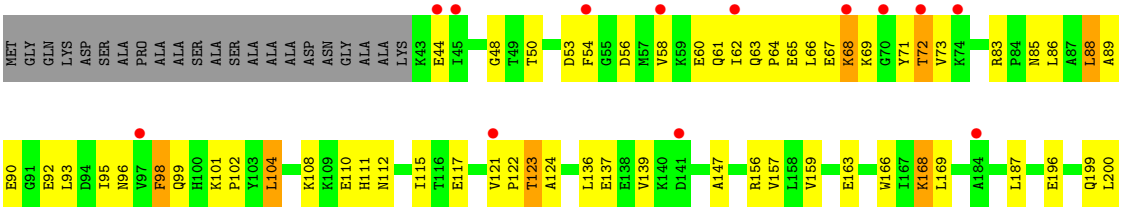
• Molecule 1: Outer membrane lipoprotein GNA1946

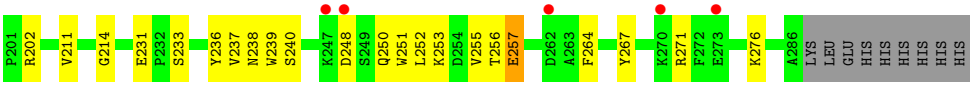
Chain B: 2% 66% 19% • 13%



• Molecule 1: Outer membrane lipoprotein GNA1946

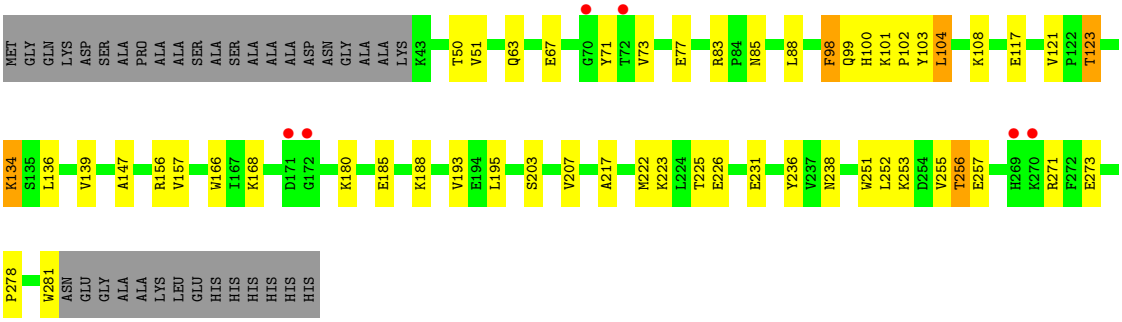
Chain C: 7% 59% 27% • 11%





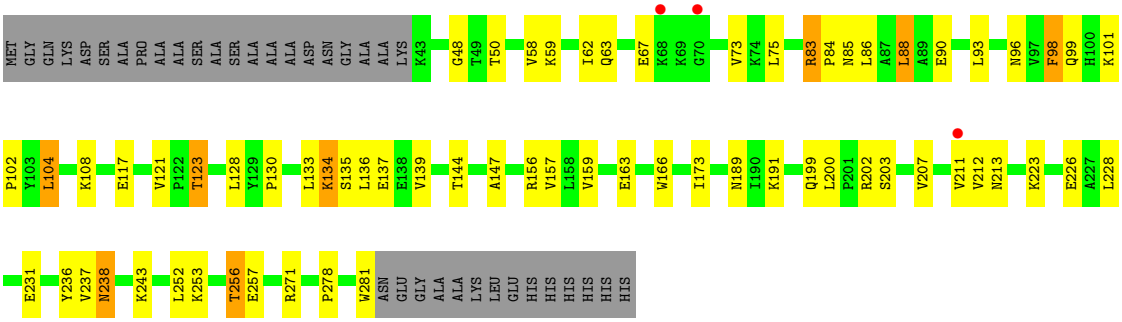
• Molecule 1: Outer membrane lipoprotein GNA1946

Chain D:



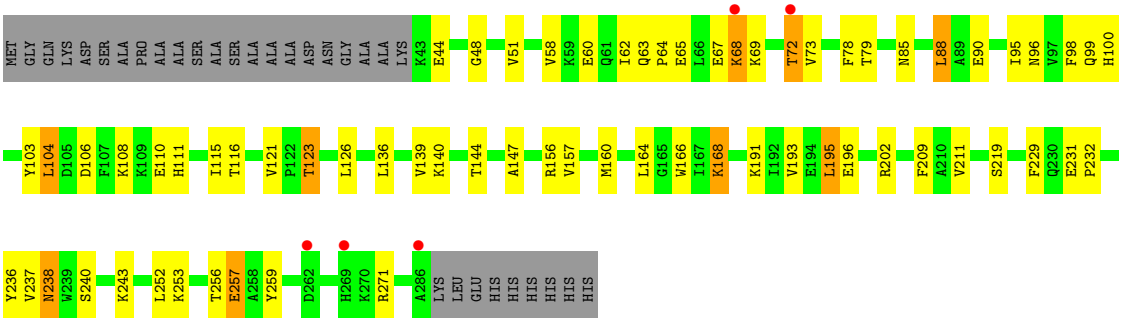
• Molecule 1: Outer membrane lipoprotein GNA1946

Chain E:



• Molecule 1: Outer membrane lipoprotein GNA1946

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	108.39Å 122.81Å 160.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	21.55 – 2.25 21.55 – 2.25	Depositor EDS
% Data completeness (in resolution range)	94.4 (21.55-2.25) 94.5 (21.55-2.25)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$< I/\sigma(I) >$ [1]	2.67 (at 2.26Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.206 , 0.239 0.206 , 0.239	Depositor DCC
R_{free} test set	5130 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	24.2	Xtriage
Anisotropy	0.521	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 41.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	12179	wwPDB-VP
Average B, all atoms (Å^2)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.66% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.41	0/1927	0.67	0/2615
1	B	0.38	0/1927	0.66	0/2615
1	C	0.36	0/1958	0.61	0/2657
1	D	0.37	0/1927	0.63	0/2615
1	E	0.37	0/1927	0.65	0/2615
1	F	0.37	0/1958	0.65	0/2657
All	All	0.38	0/11624	0.64	0/15774

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1884	0	1855	49	0
1	B	1884	0	1855	54	0
1	C	1915	0	1880	67	0
1	D	1884	0	1855	49	0
1	E	1884	0	1855	53	0
1	F	1915	0	1880	60	0
2	A	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	30	0	0	1	0
2	C	5	0	0	1	0
2	D	20	0	0	1	0
2	E	5	0	0	0	0
2	F	10	0	0	0	0
3	A	9	0	8	1	0
3	B	9	0	8	1	0
3	C	9	0	8	1	0
3	D	9	0	8	1	0
3	E	9	0	8	1	0
3	F	9	0	8	1	0
4	A	128	0	0	2	0
4	B	111	0	0	3	0
4	C	100	0	0	8	0
4	D	136	0	0	0	0
4	E	105	0	0	0	0
4	F	99	0	0	2	0
All	All	12179	0	11228	316	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 14.

All (316) 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:B:123:THR:HG21	1:B:238:ASN:H	1.12	1.12
1:E:123:THR:HG21	1:E:238:ASN:H	1.14	1.11
1:A:123:THR:HG21	1:A:238:ASN:H	1.16	1.05
1:C:123:THR:HG21	1:C:238:ASN:H	1.16	1.05
1:D:123:THR:HG21	1:D:238:ASN:H	1.17	1.04
1:F:139:VAL:HG21	1:F:166:TRP:CZ2	1.94	1.02
1:A:85:ASN:HD21	1:A:99:GLN:HE22	1.05	0.99
1:E:136:LEU:O	1:E:139:VAL:HG23	1.66	0.93
1:C:85:ASN:HD21	1:C:99:GLN:HE22	1.14	0.93
1:C:139:VAL:HG21	1:C:166:TRP:CZ2	2.04	0.92
1:F:123:THR:HG21	1:F:238:ASN:H	1.34	0.91
1:F:85:ASN:HD21	1:F:99:GLN:HE22	1.17	0.91
1:D:85:ASN:HD21	1:D:99:GLN:HE22	1.22	0.87
1:E:85:ASN:HD21	1:E:99:GLN:HE22	1.21	0.85
1:B:123:THR:HG21	1:B:238:ASN:N	1.93	0.84
1:A:123:THR:HG21	1:A:238:ASN:N	1.93	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:168:LYS:HB3	1:B:185:GLU:HG3	1.58	0.83
1:D:168:LYS:HB3	1:D:185:GLU:HG3	1.61	0.82
1:C:63:GLN:HB3	1:C:64:PRO:HD3	1.62	0.82
1:B:85:ASN:HD21	1:B:99:GLN:HE22	1.26	0.81
1:D:136:LEU:O	1:D:139:VAL:HG23	1.79	0.81
1:C:233:SER:O	1:C:276:LYS:HE2	1.82	0.79
1:C:121:VAL:O	1:C:123:THR:HG22	1.83	0.79
1:D:253:LYS:O	1:D:257:GLU:HG3	1.82	0.79
1:E:123:THR:HG21	1:E:238:ASN:N	1.95	0.78
1:A:136:LEU:O	1:A:139:VAL:HG23	1.84	0.78
1:C:123:THR:HG21	1:C:238:ASN:N	1.98	0.78
1:C:168:LYS:HE2	1:C:169:LEU:O	1.82	0.77
1:D:123:THR:HG21	1:D:238:ASN:N	1.98	0.77
1:A:252:LEU:O	1:A:256:THR:HG23	1.84	0.77
1:F:136:LEU:O	1:F:139:VAL:HG23	1.84	0.77
1:F:108:LYS:HD3	1:F:115:ILE:O	1.85	0.77
1:F:156:ARG:HD2	1:F:231:GLU:OE2	1.83	0.76
1:D:156:ARG:HD2	1:D:231:GLU:OE2	1.86	0.76
1:A:156:ARG:HD2	1:A:231:GLU:OE2	1.86	0.76
1:E:139:VAL:HG21	1:E:166:TRP:CZ2	2.22	0.75
1:B:273:GLU:OE2	1:C:202:ARG:HD2	1.87	0.75
1:F:252:LEU:O	1:F:256:THR:HG23	1.86	0.75
1:F:63:GLN:HB3	1:F:64:PRO:HD3	1.70	0.73
1:B:130:PRO:HG3	1:B:228:LEU:HD21	1.71	0.73
1:E:156:ARG:HD2	1:E:231:GLU:OE2	1.88	0.73
1:D:121:VAL:O	1:D:123:THR:HG22	1.88	0.72
1:F:44:GLU:HG3	1:F:72:THR:HB	1.71	0.71
1:F:90:GLU:O	1:F:90:GLU:HG2	1.89	0.70
1:F:123:THR:HG21	1:F:238:ASN:N	2.04	0.70
1:C:251:TRP:O	1:C:255:VAL:HG23	1.91	0.70
1:D:273:GLU:OE2	1:E:202:ARG:HG2	1.92	0.69
1:C:85:ASN:HD21	1:C:99:GLN:NE2	1.89	0.69
1:F:63:GLN:HG3	1:F:73:VAL:HB	1.75	0.69
1:F:121:VAL:O	1:F:123:THR:HG22	1.93	0.69
1:C:65:GLU:HA	1:C:68:LYS:HE2	1.74	0.69
1:D:252:LEU:O	1:D:256:THR:HG23	1.93	0.69
1:C:108:LYS:HD3	1:C:115:ILE:O	1.93	0.68
1:D:156:ARG:HD3	1:D:236:TYR:CD2	2.27	0.68
1:E:86:LEU:O	1:E:90:GLU:HG3	1.94	0.68
1:F:156:ARG:HD3	1:F:236:TYR:CG	2.29	0.68
1:E:156:ARG:HD3	1:E:236:TYR:CD2	2.29	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:86:LEU:O	1:C:90:GLU:HB2	1.95	0.67
1:C:252:LEU:O	1:C:256:THR:HG23	1.95	0.67
1:C:156:ARG:HD3	1:C:236:TYR:CG	2.29	0.66
1:A:63:GLN:HB3	1:A:64:PRO:HD3	1.75	0.66
1:A:139:VAL:HG21	1:A:166:TRP:CZ2	2.31	0.66
1:D:139:VAL:HG21	1:D:166:TRP:CZ2	2.30	0.66
1:E:63:GLN:O	1:E:67:GLU:HG3	1.95	0.66
1:A:85:ASN:HD21	1:A:99:GLN:NE2	1.86	0.66
1:F:157:VAL:HG22	1:F:211:VAL:HG11	1.78	0.66
1:F:253:LYS:O	1:F:257:GLU:HG2	1.96	0.65
1:E:139:VAL:CG2	1:E:166:TRP:CZ2	2.79	0.65
1:C:253:LYS:O	1:C:257:GLU:HG2	1.96	0.65
1:E:252:LEU:O	1:E:256:THR:HG23	1.97	0.65
1:F:65:GLU:HA	1:F:68:LYS:HE2	1.78	0.64
1:B:136:LEU:O	1:B:139:VAL:HG22	1.97	0.63
1:A:238:ASN:N	1:A:238:ASN:HD22	1.97	0.63
1:F:85:ASN:HD21	1:F:99:GLN:NE2	1.95	0.63
1:B:104:LEU:HD22	1:B:108:LYS:HG3	1.79	0.63
1:E:159:VAL:O	1:E:163:GLU:HG3	1.98	0.63
1:E:85:ASN:HD21	1:E:99:GLN:NE2	1.93	0.62
1:C:104:LEU:HD22	1:C:108:LYS:HG3	1.80	0.62
1:C:156:ARG:HD3	1:C:236:TYR:CD2	2.35	0.62
1:E:134:LYS:N	1:E:134:LYS:HD2	2.13	0.62
1:B:253:LYS:O	1:B:257:GLU:HG3	1.99	0.61
1:D:134:LYS:HD2	1:D:134:LYS:N	2.15	0.61
1:E:101:LYS:HB3	1:E:102:PRO:HD3	1.82	0.61
1:D:63:GLN:HG3	1:D:73:VAL:HB	1.83	0.61
1:E:147:ALA:HB1	1:E:157:VAL:HG21	1.83	0.61
1:B:99:GLN:HE21	1:B:103:TYR:HD1	1.47	0.60
1:F:238:ASN:N	1:F:238:ASN:HD22	2.00	0.60
1:A:195:LEU:HD23	1:B:77:GLU:O	2.01	0.60
1:E:121:VAL:O	1:E:123:THR:HG22	2.00	0.60
1:F:156:ARG:HD3	1:F:236:TYR:CD2	2.36	0.60
1:E:253:LYS:O	1:E:257:GLU:HG3	2.02	0.60
1:F:139:VAL:HG22	1:F:209:PHE:CE2	2.37	0.60
1:E:133:LEU:C	1:E:134:LYS:HD2	2.22	0.60
1:F:144:THR:HG22	1:F:191:LYS:HG3	1.84	0.60
1:B:121:VAL:O	1:B:123:THR:HG22	2.02	0.59
1:A:156:ARG:HD3	1:A:236:TYR:CG	2.37	0.59
1:C:147:ALA:HB1	1:C:157:VAL:HG21	1.83	0.59
1:F:51:VAL:HG23	1:F:78:PHE:O	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:147:ALA:HB1	1:A:157:VAL:HG21	1.83	0.59
1:B:63:GLN:HG3	1:B:73:VAL:HB	1.84	0.59
1:E:48:GLY:HA3	1:E:93:LEU:HD13	1.85	0.59
1:C:95:ILE:HD11	1:C:240:SER:HB2	1.84	0.58
1:C:156:ARG:HD2	1:C:231:GLU:OE2	2.04	0.58
1:A:156:ARG:HD3	1:A:236:TYR:CD2	2.38	0.58
1:A:159:VAL:O	1:A:163:GLU:HG3	2.03	0.58
1:A:63:GLN:HG3	1:A:73:VAL:HB	1.84	0.58
1:C:88:LEU:C	1:C:90:GLU:H	2.06	0.58
1:E:173:ILE:C	1:E:173:ILE:HD12	2.24	0.57
1:E:63:GLN:HG3	1:E:73:VAL:HB	1.85	0.57
1:E:156:ARG:HD3	1:E:236:TYR:CG	2.39	0.57
1:C:256:THR:HG21	4:C:345:HOH:O	2.03	0.57
1:C:67:GLU:C	1:C:69:LYS:H	2.07	0.57
1:B:156:ARG:HD2	1:B:231:GLU:OE2	2.04	0.57
1:C:56:ASP:O	1:C:60:GLU:HG3	2.04	0.57
1:A:48:GLY:HA3	1:A:93:LEU:HD13	1.86	0.57
1:D:271:ARG:HG2	1:D:271:ARG:HH11	1.70	0.56
1:C:63:GLN:HG3	1:C:73:VAL:HB	1.86	0.56
1:D:77:GLU:O	1:F:195:LEU:HD23	2.04	0.56
1:D:223:LYS:HB2	1:D:226:GLU:HG3	1.87	0.56
1:B:63:GLN:O	1:B:67:GLU:HG3	2.06	0.56
1:B:101:LYS:HE2	1:B:117:GLU:OE2	2.06	0.56
1:A:101:LYS:HE2	1:A:117:GLU:OE2	2.06	0.56
1:B:156:ARG:HD3	1:B:236:TYR:CD2	2.41	0.56
1:A:65:GLU:OE1	1:A:68:LYS:HE2	2.06	0.55
1:B:156:ARG:NH2	3:B:296:MET:OXT	2.40	0.55
1:F:95:ILE:HD11	1:F:240:SER:HB2	1.87	0.55
1:F:156:ARG:HD3	1:F:236:TYR:CD1	2.41	0.55
1:C:271:ARG:HH11	1:C:271:ARG:HG2	1.71	0.55
1:F:126:LEU:HD23	1:F:160:MET:HE1	1.88	0.55
1:A:51:VAL:HG13	1:A:77:GLU:OE1	2.06	0.55
1:C:156:ARG:HD3	1:C:236:TYR:CD1	2.42	0.55
1:A:84:PRO:HB2	1:A:98:PHE:CE2	2.41	0.55
1:B:252:LEU:O	1:B:256:THR:HG23	2.06	0.54
1:E:271:ARG:HG2	1:E:271:ARG:HH11	1.72	0.54
1:F:104:LEU:HD22	1:F:108:LYS:HG3	1.90	0.54
1:C:53:ASP:OD1	1:C:54:PHE:N	2.40	0.54
1:D:85:ASN:HD21	1:D:99:GLN:NE2	1.99	0.54
1:F:67:GLU:C	1:F:69:LYS:H	2.10	0.54
1:D:139:VAL:CG2	1:D:166:TRP:CZ2	2.91	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:251:TRP:O	1:D:255:VAL:HG23	2.08	0.54
1:B:156:ARG:HD3	1:B:236:TYR:CG	2.43	0.53
1:B:193:VAL:HG22	1:D:195:LEU:HD21	1.89	0.53
1:E:156:ARG:HD3	1:E:236:TYR:CE2	2.43	0.53
1:B:85:ASN:HD21	1:B:99:GLN:NE2	2.03	0.53
1:E:157:VAL:HG22	1:E:211:VAL:HG11	1.91	0.53
1:F:164:LEU:HD21	1:F:229:PHE:CG	2.44	0.53
1:C:44:GLU:HG3	1:C:72:THR:HB	1.89	0.53
1:E:144:THR:HG22	1:E:191:LYS:HB3	1.91	0.53
1:E:136:LEU:O	1:E:139:VAL:CG2	2.48	0.53
1:C:159:VAL:O	1:C:163:GLU:HG3	2.07	0.53
1:A:56:ASP:HB3	1:A:60:GLU:OE2	2.09	0.52
1:A:58:VAL:HA	1:A:62:ILE:HB	1.91	0.52
1:E:104:LEU:HD22	1:E:108:LYS:HG3	1.92	0.52
1:A:136:LEU:O	1:A:139:VAL:CG2	2.57	0.52
1:A:139:VAL:CG2	1:A:166:TRP:CZ2	2.92	0.52
1:E:58:VAL:HA	1:E:62:ILE:HB	1.92	0.52
1:A:61:GLN:O	1:A:64:PRO:HD2	2.10	0.52
1:A:270:LYS:HG2	1:A:271:ARG:N	2.24	0.52
1:F:126:LEU:HD23	1:F:160:MET:CE	2.40	0.52
1:C:104:LEU:HD22	1:C:104:LEU:O	2.10	0.52
1:B:101:LYS:HB3	1:B:102:PRO:HD3	1.92	0.52
1:B:104:LEU:O	1:B:108:LYS:HG3	2.09	0.52
1:C:257:GLU:HA	4:C:491:HOH:O	2.09	0.52
1:C:66:LEU:O	1:C:71:TYR:HB2	2.09	0.52
1:C:88:LEU:HD12	1:C:96:ASN:ND2	2.25	0.52
1:F:160:MET:HE1	1:F:231:GLU:HB2	1.92	0.51
1:B:140:LYS:HA	2:B:3:SO4:O2	2.09	0.51
1:C:136:LEU:O	1:C:139:VAL:HG23	2.11	0.51
1:E:173:ILE:HD12	1:E:173:ILE:O	2.10	0.51
1:A:63:GLN:O	1:A:67:GLU:HG3	2.11	0.51
1:D:67:GLU:HA	1:D:71:TYR:O	2.10	0.51
1:C:92:GLU:O	1:C:92:GLU:HG2	2.11	0.51
1:B:104:LEU:HD22	1:B:108:LYS:CG	2.41	0.51
1:D:238:ASN:N	1:D:238:ASN:HD22	2.07	0.51
1:A:119:PHE:CD2	1:A:256:THR:HB	2.46	0.50
1:E:48:GLY:O	1:E:96:ASN:HA	2.12	0.50
1:D:156:ARG:NH2	3:D:400:MET:OXT	2.44	0.50
1:D:156:ARG:HD3	1:D:236:TYR:CE2	2.47	0.50
1:A:121:VAL:O	1:A:123:THR:HG22	2.13	0.49
1:B:134:LYS:HD2	1:B:134:LYS:N	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:101:LYS:HE2	1:E:117:GLU:OE2	2.13	0.49
1:F:160:MET:CE	1:F:231:GLU:HB2	2.43	0.49
1:F:99:GLN:HE21	1:F:103:TYR:HD1	1.60	0.49
1:A:123:THR:HG23	1:A:237:VAL:HG13	1.95	0.49
1:F:110:GLU:HG2	1:F:111:HIS:CD2	2.47	0.49
1:E:238:ASN:N	1:E:238:ASN:HD22	2.08	0.49
4:C:486:HOH:O	1:F:60:GLU:HG2	2.11	0.49
1:E:200:LEU:HD13	1:E:211:VAL:O	2.13	0.49
1:A:104:LEU:HD22	1:A:108:LYS:HG3	1.93	0.49
1:B:136:LEU:O	1:B:139:VAL:CG2	2.61	0.49
1:D:156:ARG:HD3	1:D:236:TYR:CG	2.48	0.49
1:C:238:ASN:N	1:C:238:ASN:HD22	2.10	0.48
2:D:4:SO4:O4	1:F:202:ARG:HD2	2.13	0.48
1:B:147:ALA:HB1	1:B:157:VAL:HG21	1.96	0.48
1:D:104:LEU:HD22	1:D:108:LYS:HG3	1.95	0.48
1:C:83:ARG:HD2	4:C:710:HOH:O	2.12	0.48
1:C:101:LYS:HB3	1:C:102:PRO:HD3	1.95	0.48
1:A:252:LEU:O	1:A:256:THR:CG2	2.57	0.47
1:C:200:LEU:HD13	1:C:211:VAL:O	2.13	0.47
1:F:168:LYS:HA	1:F:168:LYS:HE2	1.96	0.47
1:A:195:LEU:HD23	1:B:77:GLU:C	2.34	0.47
1:A:251:TRP:O	1:A:255:VAL:HG23	2.13	0.47
1:D:203:SER:O	1:D:207:VAL:HG22	2.14	0.47
1:C:63:GLN:HB3	1:C:64:PRO:CD	2.40	0.47
1:A:267:TYR:O	1:A:271:ARG:HB2	2.13	0.47
1:F:62:ILE:HG13	1:F:259:TYR:CZ	2.50	0.47
1:A:99:GLN:HE21	1:A:103:TYR:HD1	1.62	0.47
1:D:147:ALA:HB1	1:D:157:VAL:HG21	1.97	0.47
1:C:117:GLU:HB2	1:C:239:TRP:HB3	1.96	0.47
1:F:48:GLY:O	1:F:96:ASN:HA	2.15	0.47
1:E:123:THR:HG23	1:E:237:VAL:HG13	1.96	0.47
1:F:115:ILE:HG22	1:F:243:LYS:HA	1.95	0.47
1:A:101:LYS:HB3	1:A:102:PRO:HD3	1.97	0.47
1:F:156:ARG:NH2	3:F:600:MET:OXT	2.47	0.47
1:D:217:ALA:O	1:D:222:MET:HB2	2.15	0.46
1:C:104:LEU:CD2	1:C:108:LYS:HG3	2.44	0.46
1:C:156:ARG:NH2	3:C:300:MET:OXT	2.48	0.46
1:D:225:THR:HA	1:E:199:GLN:NE2	2.31	0.46
1:F:110:GLU:O	1:F:110:GLU:HG3	2.13	0.46
1:E:50:THR:HG23	1:E:98:PHE:HB2	1.97	0.46
1:F:100:HIS:CE1	1:F:103:TYR:HB2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:123:THR:HG23	1:F:237:VAL:HG13	1.98	0.46
1:C:61:GLN:O	1:C:64:PRO:HD2	2.16	0.46
1:C:110:GLU:HG3	1:C:111:HIS:CD2	2.51	0.46
1:F:136:LEU:O	1:F:139:VAL:CG2	2.60	0.46
1:A:156:ARG:NH2	3:A:296:MET:OXT	2.48	0.46
1:A:217:ALA:O	1:A:222:MET:HB2	2.16	0.46
1:E:139:VAL:HG21	1:E:166:TRP:CE2	2.50	0.46
1:E:59:LYS:HG3	1:E:75:LEU:HD22	1.97	0.46
1:F:58:VAL:HA	1:F:62:ILE:HB	1.98	0.45
1:B:140:LYS:HD2	4:B:331:HOH:O	2.15	0.45
1:F:271:ARG:HG2	1:F:271:ARG:HH11	1.82	0.45
1:F:116:THR:HG22	4:F:617:HOH:O	2.15	0.45
1:B:195:LEU:HD21	1:D:193:VAL:HG22	1.98	0.45
1:B:159:VAL:O	1:B:163:GLU:HG3	2.17	0.45
1:B:238:ASN:N	1:B:238:ASN:HD22	2.15	0.44
1:C:123:THR:HG23	1:C:237:VAL:HG13	1.99	0.44
1:D:77:GLU:C	1:F:195:LEU:HD23	2.37	0.44
1:C:48:GLY:O	1:C:96:ASN:HA	2.17	0.44
1:D:50:THR:HG23	1:D:98:PHE:HB2	2.00	0.44
1:A:100:HIS:CE1	1:A:103:TYR:HB2	2.52	0.44
1:A:156:ARG:HD3	1:A:236:TYR:CD1	2.52	0.44
1:E:84:PRO:HB2	1:E:98:PHE:CE2	2.52	0.44
1:B:83:ARG:HA	1:B:83:ARG:HD2	1.87	0.44
1:D:101:LYS:HE2	1:D:117:GLU:OE2	2.18	0.44
1:B:156:ARG:HD3	1:B:236:TYR:CE2	2.53	0.43
1:C:122:PRO:HD3	4:C:316:HOH:O	2.17	0.43
1:B:269:HIS:HB2	4:B:448:HOH:O	2.18	0.43
1:C:88:LEU:C	1:C:90:GLU:N	2.70	0.43
1:F:232:PRO:HA	4:F:306:HOH:O	2.19	0.43
1:A:146:SER:OG	1:A:210:ALA:HA	2.18	0.43
1:C:202:ARG:HG3	4:C:340:HOH:O	2.18	0.43
1:D:100:HIS:CE1	1:D:103:TYR:HB2	2.53	0.43
1:E:223:LYS:HB2	1:E:226:GLU:HG3	2.00	0.43
1:F:147:ALA:HB1	1:F:157:VAL:HG21	2.00	0.43
1:A:140:LYS:HB3	1:A:140:LYS:HE3	1.83	0.43
1:B:185:GLU:OE1	1:F:219:SER:HB2	2.19	0.43
1:B:100:HIS:CE1	1:B:103:TYR:HB2	2.53	0.43
1:D:101:LYS:HB3	1:D:102:PRO:HD3	2.01	0.43
1:E:130:PRO:HG3	1:E:228:LEU:HD21	2.00	0.43
1:B:123:THR:HG23	1:B:237:VAL:HG13	2.01	0.43
1:D:63:GLN:O	1:D:67:GLU:HG3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:84:PRO:HB2	1:B:98:PHE:CE2	2.53	0.43
1:D:77:GLU:OE1	1:F:193:VAL:HG13	2.19	0.42
1:E:139:VAL:HG22	1:E:166:TRP:CZ2	2.53	0.42
1:A:200:LEU:HD12	4:A:319:HOH:O	2.19	0.42
1:F:88:LEU:HD13	1:F:115:ILE:HG21	2.00	0.42
1:C:85:ASN:HB2	4:C:456:HOH:O	2.19	0.42
1:C:264:PHE:O	1:C:267:TYR:HB3	2.19	0.42
1:B:156:ARG:HD3	1:B:236:TYR:CD1	2.55	0.42
1:C:166:TRP:CD1	1:C:166:TRP:N	2.85	0.42
1:C:248:ASP:HB2	4:C:330:HOH:O	2.18	0.42
1:A:88:LEU:HD22	1:A:243:LYS:HG3	2.01	0.42
1:A:134:LYS:HE2	4:A:314:HOH:O	2.19	0.42
1:B:48:GLY:HA3	1:B:93:LEU:HD13	2.01	0.42
1:B:196:GLU:HG2	1:D:180:LYS:HZ3	1.83	0.42
1:C:124:ALA:HB3	1:C:214:GLY:HA3	2.01	0.42
1:D:166:TRP:HA	1:D:188:LYS:HG2	2.01	0.42
1:E:156:ARG:NH2	3:E:500:MET:OXT	2.53	0.42
1:C:58:VAL:HA	1:C:62:ILE:HB	2.01	0.42
1:B:124:ALA:HB3	1:B:214:GLY:HA3	2.01	0.42
1:E:203:SER:O	1:E:207:VAL:HG22	2.19	0.42
1:A:139:VAL:HG21	1:A:166:TRP:CE2	2.55	0.42
1:B:58:VAL:HA	1:B:62:ILE:HB	2.01	0.42
1:E:271:ARG:HG2	1:E:271:ARG:NH1	2.33	0.42
1:C:64:PRO:O	1:C:67:GLU:N	2.53	0.41
1:D:271:ARG:HG2	1:D:271:ARG:O	2.20	0.41
1:B:88:LEU:HD13	1:B:115:ILE:HG21	2.03	0.41
1:D:51:VAL:HA	1:D:77:GLU:OE1	2.20	0.41
1:D:278:PRO:HD2	1:D:281:TRP:CD2	2.55	0.41
1:E:88:LEU:HD22	1:E:243:LYS:HG3	2.02	0.41
1:E:278:PRO:HD2	1:E:281:TRP:CD2	2.55	0.41
1:D:139:VAL:HG21	1:D:166:TRP:CE2	2.55	0.41
1:F:51:VAL:HG21	1:F:79:THR:HG22	2.02	0.41
1:F:88:LEU:HD22	1:F:243:LYS:HG3	2.02	0.41
1:B:225:THR:HA	1:C:199:GLN:OE1	2.20	0.41
1:C:62:ILE:HD11	1:C:264:PHE:CE1	2.56	0.41
1:F:100:HIS:HA	1:F:238:ASN:HA	2.03	0.41
1:F:238:ASN:N	1:F:238:ASN:ND2	2.69	0.41
1:A:238:ASN:N	1:A:238:ASN:ND2	2.66	0.41
1:B:48:GLY:HA2	1:B:76:VAL:O	2.21	0.41
1:C:48:GLY:HA3	1:C:93:LEU:HD13	2.03	0.41
1:C:67:GLU:O	1:C:69:LYS:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:99:GLN:HE21	1:D:103:TYR:HD1	1.68	0.41
1:B:196:GLU:HG2	1:D:180:LYS:NZ	2.36	0.41
1:B:63:GLN:HB3	1:B:64:PRO:CD	2.50	0.40
1:C:50:THR:HG23	1:C:98:PHE:HB2	2.03	0.40
1:C:250:GLN:HB3	2:C:9:SO4:O4	2.20	0.40
1:B:228:LEU:O	1:C:196:GLU:HG2	2.21	0.40
1:B:270:LYS:HD3	4:B:320:HOH:O	2.20	0.40
1:D:83:ARG:HA	1:D:83:ARG:HD2	1.92	0.40
1:E:212:VAL:HG12	1:E:213:ASN:O	2.21	0.40
1:F:67:GLU:O	1:F:69:LYS:N	2.54	0.40
1:D:225:THR:HG22	1:E:199:GLN:HE21	1.86	0.40
1:B:49:THR:O	1:B:77:GLU:HA	2.21	0.40
1:E:83:ARG:HG2	1:E:83:ARG:HH11	1.87	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	237/275 (86%)	232 (98%)	4 (2%)	1 (0%)	34	37
1	B	237/275 (86%)	231 (98%)	5 (2%)	1 (0%)	34	37
1	C	242/275 (88%)	229 (95%)	9 (4%)	4 (2%)	9	4
1	D	237/275 (86%)	229 (97%)	7 (3%)	1 (0%)	34	37
1	E	237/275 (86%)	232 (98%)	4 (2%)	1 (0%)	34	37
1	F	242/275 (88%)	235 (97%)	5 (2%)	2 (1%)	19	17
All	All	1432/1650 (87%)	1388 (97%)	34 (2%)	10 (1%)	22	21

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	98	PHE
1	C	98	PHE
1	E	98	PHE
1	B	98	PHE
1	C	68	LYS
1	D	98	PHE
1	F	68	LYS
1	F	98	PHE
1	C	187	LEU
1	C	89	ALA

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	202/225 (90%)	191 (95%)	11 (5%)	22	22
1	B	202/225 (90%)	195 (96%)	7 (4%)	36	43
1	C	204/225 (91%)	196 (96%)	8 (4%)	32	38
1	D	202/225 (90%)	197 (98%)	5 (2%)	47	56
1	E	202/225 (90%)	191 (95%)	11 (5%)	22	22
1	F	204/225 (91%)	193 (95%)	11 (5%)	22	22
All	All	1216/1350 (90%)	1163 (96%)	53 (4%)	29	32

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	88	LEU
1	A	104	LEU
1	A	123	THR
1	A	128	LEU
1	A	134	LYS
1	A	137	GLU
1	A	185	GLU
1	A	202	ARG
1	A	238	ASN

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Mol	Chain	Res	Type
1	A	256	THR
1	A	271	ARG
1	B	88	LEU
1	B	104	LEU
1	B	123	THR
1	B	134	LYS
1	B	139	VAL
1	B	256	THR
1	B	271	ARG
1	C	72	THR
1	C	88	LEU
1	C	104	LEU
1	C	112	ASN
1	C	123	THR
1	C	137	GLU
1	C	168	LYS
1	C	257	GLU
1	D	88	LEU
1	D	104	LEU
1	D	123	THR
1	D	134	LYS
1	D	256	THR
1	E	83	ARG
1	E	88	LEU
1	E	104	LEU
1	E	123	THR
1	E	128	LEU
1	E	134	LYS
1	E	135	SER
1	E	137	GLU
1	E	189	ASN
1	E	238	ASN
1	E	256	THR
1	F	72	THR
1	F	88	LEU
1	F	104	LEU
1	F	106	ASP
1	F	123	THR
1	F	140	LYS
1	F	168	LYS
1	F	195	LEU
1	F	196	GLU

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Mol	Chain	Res	Type
1	F	238	ASN
1	F	257	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	99	GLN
1	A	238	ASN
1	B	99	GLN
1	B	174	ASN
1	B	189	ASN
1	B	238	ASN
1	C	99	GLN
1	C	189	ASN
1	C	238	ASN
1	D	99	GLN
1	D	189	ASN
1	D	238	ASN
1	E	99	GLN
1	E	111	HIS
1	E	112	ASN
1	E	199	GLN
1	E	238	ASN
1	F	99	GLN
1	F	111	HIS
1	F	238	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 monosaccharides 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	F	11	-	4,4,4	0.24	0	6,6,6	0.04	0
2	SO4	B	8	-	4,4,4	0.22	0	6,6,6	0.06	0
3	MET	A	296	-	7,8,8	0.73	0	7,9,9	0.71	0
2	SO4	C	9	-	4,4,4	0.23	0	6,6,6	0.08	0
3	MET	F	600	-	7,8,8	0.73	0	7,9,9	0.78	0
3	MET	C	300	-	7,8,8	0.69	0	7,9,9	0.83	0
2	SO4	D	4	-	4,4,4	0.13	0	6,6,6	0.05	0
2	SO4	B	15	-	4,4,4	0.21	0	6,6,6	0.07	0
2	SO4	E	5	-	4,4,4	0.24	0	6,6,6	0.09	0
2	SO4	A	16	-	4,4,4	0.20	0	6,6,6	0.06	0
3	MET	E	500	-	7,8,8	0.76	0	7,9,9	0.68	0
2	SO4	F	6	-	4,4,4	0.21	0	6,6,6	0.10	0
2	SO4	D	12	-	4,4,4	0.25	0	6,6,6	0.05	0
3	MET	D	400	-	7,8,8	0.73	0	7,9,9	0.67	0
2	SO4	B	2	-	4,4,4	0.22	0	6,6,6	0.04	0
2	SO4	B	3	-	4,4,4	0.21	0	6,6,6	0.07	0
2	SO4	D	13	-	4,4,4	0.21	0	6,6,6	0.05	0
2	SO4	A	7	-	4,4,4	0.20	0	6,6,6	0.06	0
2	SO4	D	10	-	4,4,4	0.18	0	6,6,6	0.10	0
2	SO4	B	1	-	4,4,4	0.18	0	6,6,6	0.04	0
2	SO4	B	14	-	4,4,4	0.22	0	6,6,6	0.06	0
3	MET	B	296	-	7,8,8	0.83	0	7,9,9	0.71	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
3	MET	E	500	-	-	0/8/8/8	-
3	MET	C	300	-	-	2/8/8/8	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MET	A	296	-	-	1/8/8/8	-
3	MET	D	400	-	-	0/8/8/8	-
3	MET	F	600	-	-	0/8/8/8	-
3	MET	B	296	-	-	0/8/8/8	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	300	MET	OXT-C-CA-N
3	C	300	MET	O-C-CA-N
3	A	296	MET	OXT-C-CA-N

There are no ring outliers.

9 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	296	MET	1	0
2	C	9	SO4	1	0
3	F	600	MET	1	0
3	C	300	MET	1	0
2	D	4	SO4	1	0
3	E	500	MET	1	0
3	D	400	MET	1	0
2	B	3	SO4	1	0
3	B	296	MET	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 (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	239/275 (86%)	-0.31	1 (0%)	92	93	14, 22, 36, 42	0
1	B	239/275 (86%)	-0.14	6 (2%)	57	60	14, 25, 44, 50	0
1	C	244/275 (88%)	0.35	18 (7%)	14	15	18, 36, 55, 62	0
1	D	239/275 (86%)	-0.22	6 (2%)	57	60	14, 23, 43, 50	0
1	E	239/275 (86%)	-0.18	3 (1%)	77	79	16, 26, 41, 50	0
1	F	244/275 (88%)	-0.13	5 (2%)	65	68	16, 26, 47, 61	0
All	All	1444/1650 (87%)	-0.10	39 (2%)	54	57	14, 26, 46, 62	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	72	THR	4.8
1	D	269	HIS	4.3
1	F	68	LYS	4.0
1	B	172	GLY	3.7
1	F	269	HIS	3.6
1	C	247	LYS	3.6
1	C	70	GLY	3.2
1	C	270	LYS	3.2
1	C	54	PHE	3.0
1	B	171	ASP	2.9
1	C	58	VAL	2.8
1	C	68	LYS	2.8
1	C	97	VAL	2.8
1	E	68	LYS	2.8
1	A	140	LYS	2.7
1	C	141	ASP	2.7
1	B	97	VAL	2.7
1	B	269	HIS	2.6
1	C	44	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	F	286	ALA	2.5
1	D	72	THR	2.5
1	D	270	LYS	2.4
1	D	172	GLY	2.4
1	C	273	GLU	2.4
1	C	62	ILE	2.3
1	C	121	VAL	2.3
1	C	184	ALA	2.3
1	D	70	GLY	2.2
1	C	74	LYS	2.2
1	B	109	LYS	2.2
1	C	45	ILE	2.1
1	E	70	GLY	2.1
1	E	211	VAL	2.1
1	F	72	THR	2.1
1	C	262	ASP	2.1
1	F	262	ASP	2.1
1	B	95	ILE	2.0
1	D	171	ASP	2.0
1	C	248	ASP	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 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(Å^2)	Q<0.9
2	SO4	C	9	5/5	0.75	0.27	82,82,84,84	0
2	SO4	B	2	5/5	0.84	0.33	100,100,100,100	0
2	SO4	E	5	5/5	0.85	0.26	77,79,79,80	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	SO4	B	15	5/5	0.87	0.26	91,91,91,92	0
2	SO4	B	3	5/5	0.88	0.19	82,84,84,84	0
2	SO4	A	16	5/5	0.88	0.33	94,94,95,95	0
2	SO4	D	10	5/5	0.89	0.20	67,67,68,68	0
2	SO4	B	14	5/5	0.90	0.17	73,74,74,75	0
2	SO4	D	12	5/5	0.91	0.26	94,94,95,95	0
2	SO4	B	8	5/5	0.92	0.23	64,65,66,67	0
2	SO4	F	11	5/5	0.94	0.29	73,73,74,75	0
2	SO4	F	6	5/5	0.96	0.15	45,46,47,48	0
3	MET	A	296	9/9	0.97	0.14	17,17,18,19	0
3	MET	B	296	9/9	0.97	0.14	13,14,16,17	0
3	MET	E	500	9/9	0.97	0.17	15,17,20,20	0
2	SO4	A	7	5/5	0.98	0.13	33,35,35,37	0
2	SO4	B	1	5/5	0.98	0.09	36,38,39,40	0
3	MET	C	300	9/9	0.98	0.16	14,18,20,20	0
3	MET	D	400	9/9	0.98	0.15	13,14,17,17	0
2	SO4	D	13	5/5	0.98	0.15	69,69,69,69	0
2	SO4	D	4	5/5	0.99	0.09	27,28,30,30	0
3	MET	F	600	9/9	0.99	0.13	12,14,14,16	0

6.5 Other polymers (i)

There are no such residues in this entry.