Full wwPDB X-ray Structure Validation Report ⓘ

Nov 3, 2023 – 01:04 AM EDT

PDB ID	:	3V6M
Title	:	Inhibition of caspase-6 activity by single mutation outside the active site
Authors	:	Cao, Q.; Wang, X.J.; Liu, D.F.; Li, L.F.; Su, X.D.
Deposited on	:	2011-12-20
Resolution	:	2.69 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

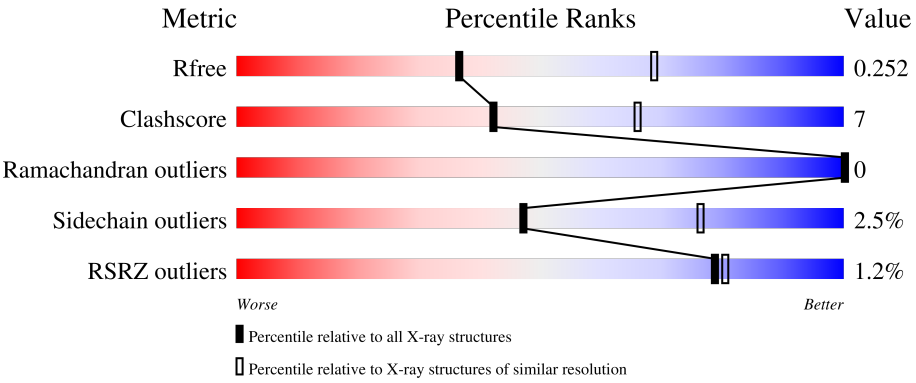
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 2.69 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=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	279	64% 9% 27%
1	B	279	66% 6% 27%
1	C	279	61% 11% 27%
1	D	279	65% 8% 27%
1	F	279	64% 9% 27%

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Mol	Chain	Length	Quality of chain
1	G	279	63% 9% • 27%
1	I	279	2% 62% 10% • 27%
1	J	279	62% 11% • 26%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 12783 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 Caspase-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	205	Total	C	N	O	S	0	0	0
			1572	1013	265	281	13			
1	B	204	Total	C	N	O	S	0	0	0
			1597	1030	270	284	13			
1	C	205	Total	C	N	O	S	0	0	0
			1555	1002	261	279	13			
1	D	204	Total	C	N	O	S	0	0	0
			1595	1025	273	284	13			
1	F	203	Total	C	N	O	S	0	0	0
			1569	1012	265	279	13			
1	G	204	Total	C	N	O	S	0	0	0
			1616	1043	275	285	13			
1	I	204	Total	C	N	O	S	1	0	0
			1576	1017	263	283	13			
1	J	206	Total	C	N	O	S	0	0	0
			1638	1056	281	288	13			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	23	MET	-	expression tag	UNP P55212
A	257	GLU	SER	SEE REMARK 999	UNP P55212
A	294	LEU	-	expression tag	UNP P55212
A	295	GLU	-	expression tag	UNP P55212
A	296	HIS	-	expression tag	UNP P55212
A	297	HIS	-	expression tag	UNP P55212
A	298	HIS	-	expression tag	UNP P55212
A	299	HIS	-	expression tag	UNP P55212
A	300	HIS	-	expression tag	UNP P55212
A	301	HIS	-	expression tag	UNP P55212
B	23	MET	-	expression tag	UNP P55212
B	257	GLU	SER	SEE REMARK 999	UNP P55212
B	294	LEU	-	expression tag	UNP P55212

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Chain	Residue	Modelled	Actual	Comment	Reference
B	295	GLU	-	expression tag	UNP P55212
B	296	HIS	-	expression tag	UNP P55212
B	297	HIS	-	expression tag	UNP P55212
B	298	HIS	-	expression tag	UNP P55212
B	299	HIS	-	expression tag	UNP P55212
B	300	HIS	-	expression tag	UNP P55212
B	301	HIS	-	expression tag	UNP P55212
C	23	MET	-	expression tag	UNP P55212
C	257	GLU	SER	SEE REMARK 999	UNP P55212
C	294	LEU	-	expression tag	UNP P55212
C	295	GLU	-	expression tag	UNP P55212
C	296	HIS	-	expression tag	UNP P55212
C	297	HIS	-	expression tag	UNP P55212
C	298	HIS	-	expression tag	UNP P55212
C	299	HIS	-	expression tag	UNP P55212
C	300	HIS	-	expression tag	UNP P55212
C	301	HIS	-	expression tag	UNP P55212
D	23	MET	-	expression tag	UNP P55212
D	257	GLU	SER	SEE REMARK 999	UNP P55212
D	294	LEU	-	expression tag	UNP P55212
D	295	GLU	-	expression tag	UNP P55212
D	296	HIS	-	expression tag	UNP P55212
D	297	HIS	-	expression tag	UNP P55212
D	298	HIS	-	expression tag	UNP P55212
D	299	HIS	-	expression tag	UNP P55212
D	300	HIS	-	expression tag	UNP P55212
D	301	HIS	-	expression tag	UNP P55212
F	23	MET	-	expression tag	UNP P55212
F	257	GLU	SER	SEE REMARK 999	UNP P55212
F	294	LEU	-	expression tag	UNP P55212
F	295	GLU	-	expression tag	UNP P55212
F	296	HIS	-	expression tag	UNP P55212
F	297	HIS	-	expression tag	UNP P55212
F	298	HIS	-	expression tag	UNP P55212
F	299	HIS	-	expression tag	UNP P55212
F	300	HIS	-	expression tag	UNP P55212
F	301	HIS	-	expression tag	UNP P55212
G	23	MET	-	expression tag	UNP P55212
G	257	GLU	SER	SEE REMARK 999	UNP P55212
G	294	LEU	-	expression tag	UNP P55212
G	295	GLU	-	expression tag	UNP P55212
G	296	HIS	-	expression tag	UNP P55212

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Chain	Residue	Modelled	Actual	Comment	Reference
G	297	HIS	-	expression tag	UNP P55212
G	298	HIS	-	expression tag	UNP P55212
G	299	HIS	-	expression tag	UNP P55212
G	300	HIS	-	expression tag	UNP P55212
G	301	HIS	-	expression tag	UNP P55212
I	23	MET	-	expression tag	UNP P55212
I	257	GLU	SER	SEE REMARK 999	UNP P55212
I	294	LEU	-	expression tag	UNP P55212
I	295	GLU	-	expression tag	UNP P55212
I	296	HIS	-	expression tag	UNP P55212
I	297	HIS	-	expression tag	UNP P55212
I	298	HIS	-	expression tag	UNP P55212
I	299	HIS	-	expression tag	UNP P55212
I	300	HIS	-	expression tag	UNP P55212
I	301	HIS	-	expression tag	UNP P55212
J	23	MET	-	expression tag	UNP P55212
J	257	GLU	SER	SEE REMARK 999	UNP P55212
J	294	LEU	-	expression tag	UNP P55212
J	295	GLU	-	expression tag	UNP P55212
J	296	HIS	-	expression tag	UNP P55212
J	297	HIS	-	expression tag	UNP P55212
J	298	HIS	-	expression tag	UNP P55212
J	299	HIS	-	expression tag	UNP P55212
J	300	HIS	-	expression tag	UNP P55212
J	301	HIS	-	expression tag	UNP P55212

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	8	Total O 8 8	0	0
2	B	12	Total O 12 12	0	0
2	C	5	Total O 5 5	0	0
2	D	12	Total O 12 12	0	0
2	F	4	Total O 4 4	0	0
2	G	13	Total O 13 13	0	0
2	I	3	Total O 3 3	0	0

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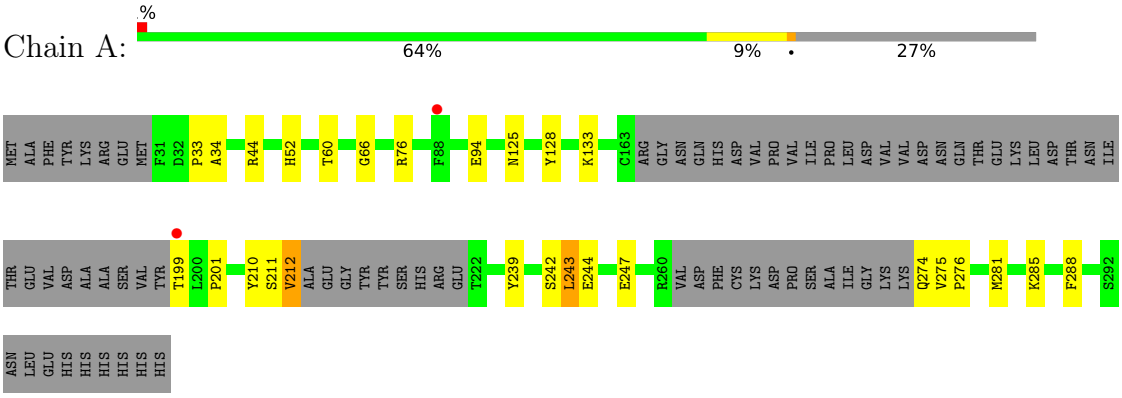
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	J	8	Total O 8 8	0	0

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.

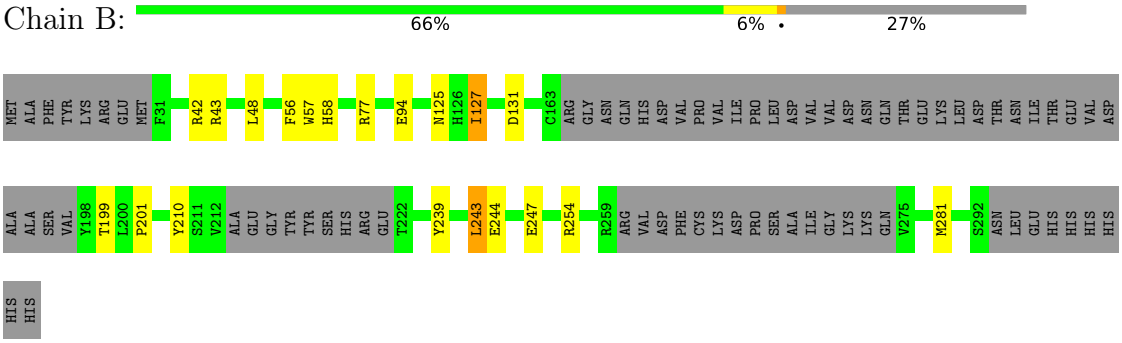
• Molecule 1: Caspase-6

Chain A:



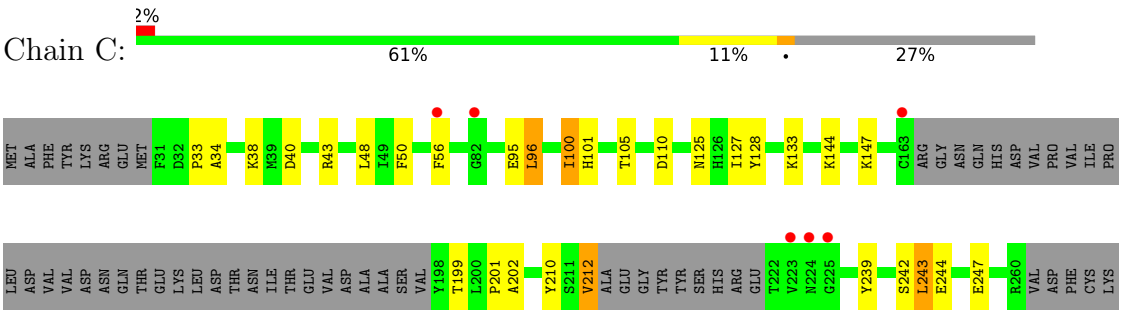
• Molecule 1: Caspase-6

Chain B:



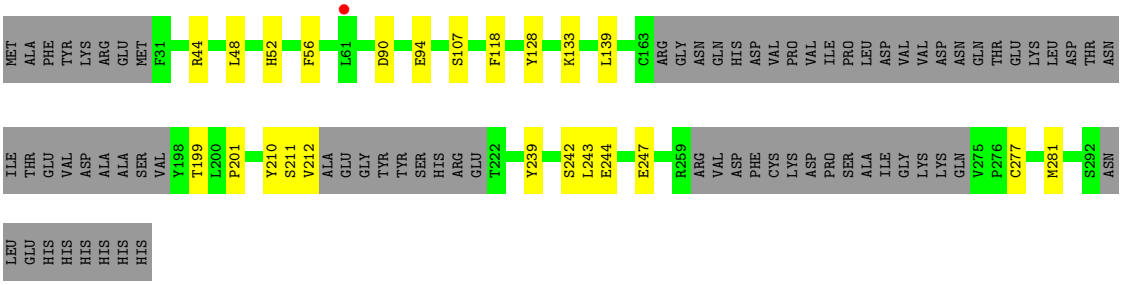
• Molecule 1: Caspase-6

Chain C:



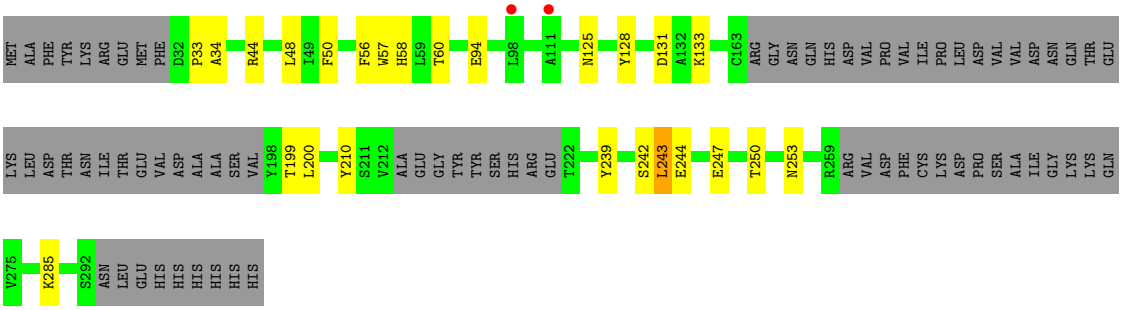
• Molecule 1: Caspase-6

Chain D:



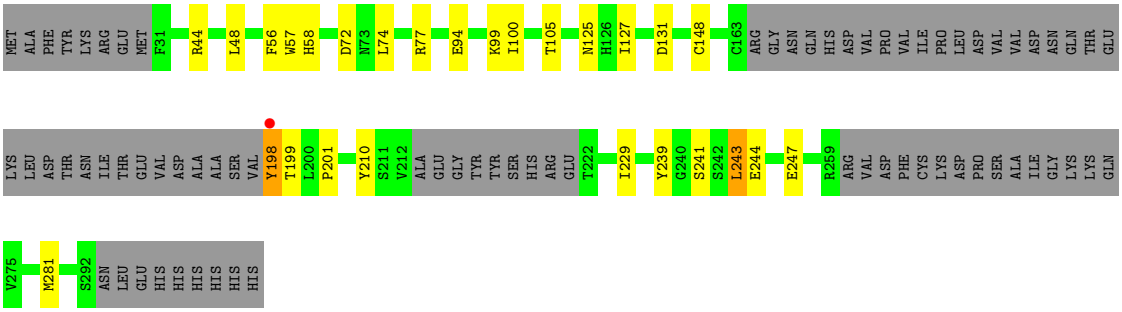
• Molecule 1: Caspase-6

Chain F:



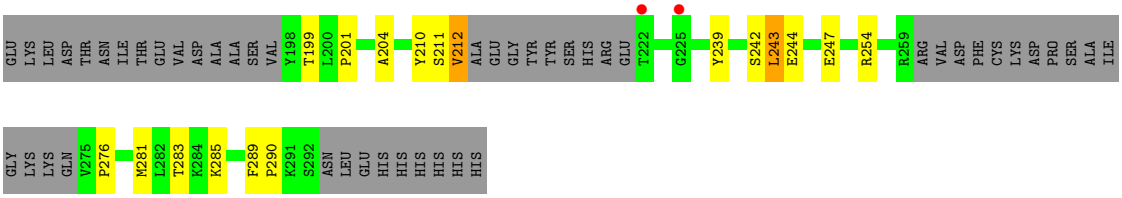
• Molecule 1: Caspase-6

Chain G:



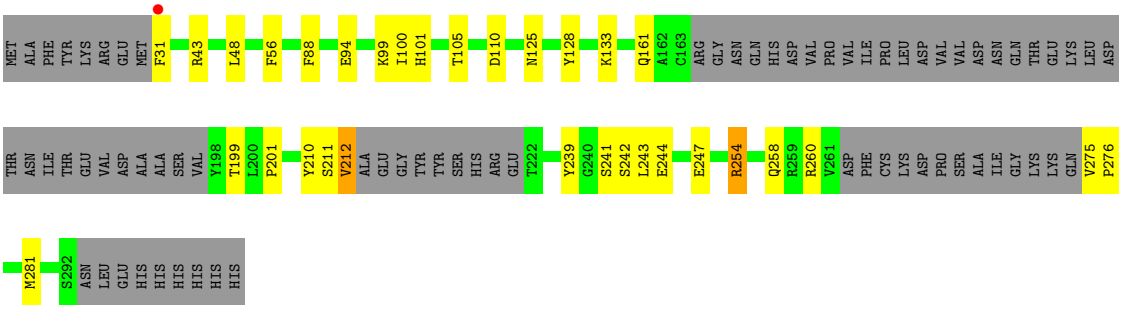
• Molecule 1: Caspase-6

Chain I:



• Molecule 1: Caspase-6

Chain J:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	81.15Å 162.63Å 89.15Å 90.00° 95.01° 90.00°	Depositor
Resolution (Å)	19.99 – 2.69 39.24 – 2.69	Depositor EDS
% Data completeness (in resolution range)	92.9 (19.99-2.69) 92.9 (39.24-2.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	8.80 (at 2.69Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.215 , 0.259 0.211 , 0.252	Depositor DCC
R_{free} test set	2983 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	46.7	Xtriage
Anisotropy	0.306	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 52.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	12783	wwPDB-VP
Average B, all atoms (Å^2)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.99% 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

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	0.72	0/1604	0.70	0/2161
1	B	0.69	0/1633	0.73	0/2199
1	C	0.70	0/1587	0.69	0/2141
1	D	0.69	1/1629 (0.1%)	0.75	0/2191
1	F	0.75	0/1604	0.72	0/2165
1	G	0.74	1/1653 (0.1%)	0.74	1/2224 (0.0%)
1	I	0.74	0/1610	0.67	0/2170
1	J	0.69	0/1676	0.73	0/2254
All	All	0.72	2/12996 (0.0%)	0.72	1/17505 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	148	CYS	CB-SG	-5.92	1.72	1.81
1	D	277	CYS	CB-SG	-5.14	1.73	1.81

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	G	77	ARG	NE-CZ-NH1	-5.40	117.60	120.30

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	1572	0	1497	28	0
1	B	1597	0	1530	18	0
1	C	1555	0	1472	24	0
1	D	1595	0	1538	17	1
1	F	1569	0	1489	25	0
1	G	1616	0	1560	22	1
1	I	1576	0	1504	29	0
1	J	1638	0	1586	28	0
2	A	8	0	0	4	0
2	B	12	0	0	1	0
2	C	5	0	0	0	0
2	D	12	0	0	0	0
2	F	4	0	0	0	0
2	G	13	0	0	0	0
2	I	3	0	0	0	0
2	J	8	0	0	0	0
All	All	12783	0	12176	171	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 7.

All (171) 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:C:239:TYR:HB3	1:C:243:LEU:HD22	1.55	0.88
1:A:274:GLN:O	1:A:275:VAL:HG22	1.81	0.81
1:A:212:VAL:HG13	1:A:276:PRO:HA	1.64	0.79
1:F:239:TYR:HB3	1:F:243:LEU:HD22	1.64	0.78
1:C:101:HIS:O	1:C:105:THR:HG22	1.84	0.78
1:F:94:GLU:HG2	1:I:56:PHE:CE1	2.18	0.78
1:A:239:TYR:HB3	1:A:243:LEU:HD22	1.66	0.78
1:A:274:GLN:O	1:A:275:VAL:CG2	2.31	0.77
1:D:239:TYR:HB3	1:D:243:LEU:HD22	1.67	0.77
1:B:239:TYR:HB3	1:B:243:LEU:HD22	1.66	0.75
1:J:212:VAL:HG13	1:J:276:PRO:HA	1.69	0.72
1:J:239:TYR:HB3	1:J:243:LEU:HD22	1.71	0.72
1:B:57:TRP:CD1	1:B:58:HIS:CE1	2.78	0.71
1:I:239:TYR:HB3	1:I:243:LEU:HD22	1.73	0.71
1:A:76:ARG:NH1	1:G:72:ASP:OD2	2.23	0.71
1:G:57:TRP:CE3	1:G:58:HIS:CE1	2.80	0.69
1:G:239:TYR:HB3	1:G:243:LEU:HD22	1.74	0.68
1:B:57:TRP:HD1	1:B:58:HIS:CE1	2.12	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:43:ARG:NH2	1:J:110:ASP:OD1	2.23	0.66
1:I:204:ALA:HB2	1:J:275:VAL:HG21	1.78	0.65
1:C:96:LEU:HD12	1:C:96:LEU:O	1.95	0.65
1:C:277:CYS:HB2	1:D:281:MET:HG2	1.79	0.64
1:F:94:GLU:HG2	1:I:56:PHE:CZ	2.32	0.63
1:F:56:PHE:CE1	1:I:94:GLU:HG2	2.33	0.63
1:F:34:ALA:HA	1:F:285:LYS:NZ	2.12	0.63
1:F:34:ALA:HA	1:F:285:LYS:HZ3	1.62	0.63
1:A:34:ALA:HA	1:A:285:LYS:NZ	2.15	0.62
1:J:212:VAL:CG1	1:J:276:PRO:HA	2.29	0.62
1:I:33:PRO:O	1:I:285:LYS:NZ	2.33	0.61
1:F:33:PRO:O	1:F:285:LYS:NZ	2.34	0.60
1:A:52:HIS:HD2	2:A:401:HOH:O	1.84	0.60
1:C:43:ARG:NH2	1:C:110:ASP:OD1	2.29	0.59
1:A:125:ASN:OD1	1:A:125:ASN:N	2.30	0.58
1:F:200:LEU:CB	1:G:198:TYR:CE1	2.87	0.58
1:C:212:VAL:HG13	1:C:276:PRO:HA	1.86	0.58
1:J:125:ASN:OD1	1:J:125:ASN:N	2.30	0.57
1:B:201:PRO:HG2	1:B:281:MET:HG3	1.86	0.57
1:J:199:THR:O	1:J:210:TYR:OH	2.21	0.57
1:B:199:THR:O	1:B:210:TYR:OH	2.21	0.57
1:D:199:THR:O	1:D:210:TYR:OH	2.23	0.56
1:G:57:TRP:HE3	1:G:58:HIS:CE1	2.22	0.56
1:D:201:PRO:HB2	1:D:281:MET:HG3	1.86	0.56
1:I:34:ALA:HA	1:I:285:LYS:NZ	2.21	0.56
1:A:201:PRO:HB2	1:A:281:MET:HG3	1.86	0.56
1:I:34:ALA:HA	1:I:285:LYS:HZ3	1.71	0.55
1:F:199:THR:O	1:F:210:TYR:OH	2.22	0.55
1:B:125:ASN:OD1	1:B:125:ASN:N	2.37	0.55
1:C:96:LEU:HD12	1:C:96:LEU:C	2.27	0.55
1:A:274:GLN:C	1:A:275:VAL:HG23	2.27	0.55
1:C:33:PRO:O	1:C:285:LYS:NZ	2.40	0.55
1:A:199:THR:O	1:A:210:TYR:OH	2.25	0.54
1:G:199:THR:O	1:G:210:TYR:OH	2.25	0.54
1:I:212:VAL:HG13	1:I:276:PRO:HA	1.88	0.54
1:A:33:PRO:O	1:A:285:LYS:NZ	2.40	0.54
1:J:211:SER:C	1:J:212:VAL:HG13	2.28	0.54
1:I:33:PRO:HG3	1:J:239:TYR:CE1	2.43	0.54
1:A:212:VAL:CG1	1:A:276:PRO:HA	2.34	0.53
1:B:94:GLU:HG2	1:D:56:PHE:CE1	2.43	0.53
1:C:34:ALA:HA	1:C:285:LYS:NZ	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:274:GLN:C	1:A:275:VAL:CG2	2.74	0.53
1:B:57:TRP:CD1	1:B:58:HIS:ND1	2.77	0.52
1:C:199:THR:O	1:C:210:TYR:OH	2.26	0.52
1:G:94:GLU:HG2	1:J:56:PHE:CE1	2.44	0.52
1:C:277:CYS:SG	1:C:278:PHE:N	2.82	0.52
1:F:244:GLU:O	1:F:247:GLU:HG2	2.08	0.52
1:B:56:PHE:CE1	1:D:94:GLU:HG2	2.45	0.52
1:G:244:GLU:O	1:G:247:GLU:HG2	2.10	0.52
1:D:52:HIS:HD2	1:D:90:ASP:HA	1.75	0.52
1:I:199:THR:O	1:I:210:TYR:OH	2.28	0.52
1:F:200:LEU:CB	1:G:198:TYR:CZ	2.93	0.51
1:A:44:ARG:NH2	1:A:288:PHE:O	2.44	0.51
1:G:201:PRO:HB2	1:G:281:MET:HG3	1.93	0.51
1:I:254:ARG:HG2	1:J:31:PHE:HZ	1.75	0.51
1:J:88:PHE:CE1	1:J:99:LYS:HE3	2.46	0.51
1:F:57:TRP:CH2	1:F:58:HIS:HE1	2.30	0.50
1:A:94:GLU:HG2	1:C:56:PHE:CE1	2.47	0.50
1:A:244:GLU:O	1:A:247:GLU:HG2	2.12	0.50
1:J:244:GLU:O	1:J:247:GLU:HG2	2.12	0.50
1:G:57:TRP:CZ3	1:G:58:HIS:HE1	2.29	0.49
1:A:201:PRO:HG2	1:A:281:MET:HG3	1.92	0.49
1:J:201:PRO:HG2	1:J:281:MET:HG3	1.94	0.49
1:B:244:GLU:O	1:B:247:GLU:HG2	2.12	0.49
1:J:258:GLN:O	1:J:260:ARG:HG2	2.13	0.49
1:C:239:TYR:CB	1:C:243:LEU:HD22	2.33	0.48
1:A:66:GLY:HA2	2:A:404:HOH:O	2.13	0.48
1:I:125:ASN:OD1	1:I:125:ASN:N	2.35	0.48
1:G:125:ASN:OD1	1:G:125:ASN:N	2.36	0.48
1:I:244:GLU:O	1:I:247:GLU:HG2	2.13	0.48
1:A:34:ALA:HA	1:A:285:LYS:HZ3	1.77	0.48
1:F:57:TRP:CZ3	1:F:58:HIS:HE1	2.33	0.47
1:G:74:LEU:HD11	1:G:229:ILE:HD12	1.97	0.47
1:C:201:PRO:HB2	1:C:281:MET:HG3	1.95	0.47
1:I:201:PRO:HG2	1:I:281:MET:HG3	1.96	0.47
1:B:94:GLU:HG2	1:D:56:PHE:CZ	2.50	0.47
1:D:201:PRO:HG2	1:D:281:MET:HG3	1.97	0.47
1:F:250:THR:O	1:F:253:ASN:HB2	2.15	0.47
1:F:57:TRP:CZ2	1:F:58:HIS:CE1	3.02	0.46
1:J:101:HIS:CE1	1:J:105:THR:HG21	2.51	0.46
1:A:52:HIS:CD2	2:A:401:HOH:O	2.65	0.46
1:A:239:TYR:CB	1:A:243:LEU:HD22	2.43	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:96:LEU:O	1:C:100:ILE:HG22	2.15	0.46
1:C:50:PHE:CE1	1:C:96:LEU:HD13	2.50	0.46
1:B:43:ARG:HD2	2:B:412:HOH:O	2.16	0.46
1:C:244:GLU:O	1:C:247:GLU:HG2	2.15	0.46
1:F:128:TYR:CE1	1:F:133:LYS:HG2	2.51	0.46
1:J:201:PRO:HB2	1:J:281:MET:HG3	1.98	0.46
1:A:201:PRO:CB	1:A:281:MET:HG3	2.45	0.46
1:G:127:ILE:HD12	1:G:127:ILE:HA	1.79	0.46
1:B:131:ASP:OD2	1:B:131:ASP:N	2.50	0.45
1:D:201:PRO:CB	1:D:281:MET:HG3	2.46	0.45
1:G:57:TRP:CE3	1:G:58:HIS:HE1	2.30	0.45
1:C:125:ASN:OD1	1:C:125:ASN:N	2.49	0.45
1:C:48:LEU:HA	1:C:48:LEU:HD23	1.69	0.45
1:B:201:PRO:HB2	1:B:281:MET:HG3	1.99	0.45
1:B:239:TYR:CB	1:B:243:LEU:HD22	2.40	0.45
1:G:57:TRP:CZ3	1:G:58:HIS:CE1	3.04	0.45
1:I:48:LEU:HD23	1:I:48:LEU:HA	1.65	0.45
1:A:34:ALA:HA	1:A:285:LYS:HZ1	1.81	0.45
1:G:99:LYS:HD3	1:G:99:LYS:HA	1.70	0.45
1:B:48:LEU:HD23	1:B:48:LEU:HA	1.77	0.45
1:J:101:HIS:O	1:J:105:THR:HG23	2.15	0.45
1:B:127:ILE:HD12	1:B:127:ILE:HA	1.73	0.45
1:G:56:PHE:CE1	1:J:94:GLU:HG2	2.52	0.45
1:J:48:LEU:HA	1:J:48:LEU:HD23	1.74	0.44
1:I:55:PHE:O	1:I:56:PHE:C	2.55	0.44
1:I:201:PRO:HB2	1:I:281:MET:HG3	1.99	0.44
1:D:44:ARG:HA	1:D:44:ARG:HD3	1.89	0.44
1:I:97:LEU:O	1:I:101:HIS:HB2	2.18	0.44
1:A:211:SER:O	1:A:212:VAL:C	2.54	0.44
1:D:48:LEU:HD23	1:D:48:LEU:HA	1.77	0.44
1:G:48:LEU:HA	1:G:48:LEU:HD23	1.73	0.44
1:I:283:THR:O	1:J:254:ARG:HB2	2.18	0.44
1:F:57:TRP:CE2	1:F:58:HIS:CE1	3.06	0.43
1:F:239:TYR:CB	1:F:243:LEU:HD22	2.39	0.43
1:I:101:HIS:CE1	1:I:142:LEU:HD11	2.52	0.43
1:I:254:ARG:HG2	1:J:31:PHE:CZ	2.52	0.43
1:A:274:GLN:O	1:A:275:VAL:HG23	2.13	0.43
1:I:127:ILE:HA	1:I:127:ILE:HD12	1.78	0.43
1:J:161:GLN:O	1:J:161:GLN:HG3	2.18	0.43
1:D:118:PHE:CZ	1:D:139:LEU:HD13	2.54	0.43
1:G:131:ASP:OD2	1:G:131:ASP:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:211:SER:O	1:D:212:VAL:HB	2.19	0.42
1:D:244:GLU:O	1:D:247:GLU:HG2	2.19	0.42
1:J:99:LYS:HA	1:J:99:LYS:HD3	1.92	0.42
1:B:201:PRO:HB2	1:B:281:MET:SD	2.59	0.42
1:C:201:PRO:HG2	1:C:281:MET:HG3	2.01	0.42
1:I:108:HIS:ND1	1:I:151:LEU:HD11	2.35	0.42
1:D:128:TYR:CE1	1:D:133:LYS:HG2	2.55	0.42
1:F:131:ASP:OD2	1:F:131:ASP:N	2.53	0.42
1:J:211:SER:C	1:J:212:VAL:CG1	2.88	0.42
1:I:211:SER:O	1:I:212:VAL:C	2.59	0.41
1:I:239:TYR:CB	1:I:243:LEU:HD22	2.47	0.41
1:C:128:TYR:CE1	1:C:133:LYS:HG2	2.55	0.41
1:F:56:PHE:CZ	1:I:94:GLU:HG2	2.55	0.41
1:G:44:ARG:HA	1:G:44:ARG:HD3	1.89	0.41
1:C:127:ILE:HD12	1:C:127:ILE:HA	1.83	0.41
1:F:48:LEU:HA	1:F:48:LEU:HD23	1.75	0.41
1:F:125:ASN:OD1	1:F:125:ASN:N	2.52	0.41
1:F:48:LEU:HD13	1:F:50:PHE:CE2	2.56	0.41
1:A:128:TYR:CE1	1:A:133:LYS:HG2	2.56	0.41
1:F:57:TRP:CH2	1:F:58:HIS:CE1	3.09	0.41
1:D:239:TYR:CB	1:D:243:LEU:HD22	2.43	0.41
1:C:38:LYS:HG3	1:C:40:ASP:OD1	2.21	0.40
1:I:33:PRO:HG3	1:J:239:TYR:CZ	2.55	0.40
1:J:128:TYR:CE1	1:J:133:LYS:HG2	2.56	0.40
1:J:239:TYR:CB	1:J:243:LEU:HD22	2.46	0.40
1:C:144:LYS:HD2	1:C:202:ALA:HB1	2.03	0.40
1:G:201:PRO:HG2	1:G:281:MET:HG3	2.03	0.40
1:A:94:GLU:HB2	2:A:403:HOH:O	2.22	0.40
1:F:44:ARG:HA	1:F:44:ARG:HD3	1.92	0.40
1:I:289:PHE:HA	1:I:290:PRO:HD3	1.98	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:107:SER:OG	1:G:105:THR:OG1[2_555]	2.17	0.03

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	197/279 (71%)	190 (96%)	7 (4%)	0	100	100
1	B	196/279 (70%)	191 (97%)	5 (3%)	0	100	100
1	C	197/279 (71%)	193 (98%)	4 (2%)	0	100	100
1	D	196/279 (70%)	188 (96%)	8 (4%)	0	100	100
1	F	195/279 (70%)	187 (96%)	8 (4%)	0	100	100
1	G	196/279 (70%)	189 (96%)	7 (4%)	0	100	100
1	I	196/279 (70%)	192 (98%)	4 (2%)	0	100	100
1	J	198/279 (71%)	190 (96%)	8 (4%)	0	100	100
All	All	1571/2232 (70%)	1520 (97%)	51 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	158/247 (64%)	154 (98%)	4 (2%)	47	76
1	B	164/247 (66%)	159 (97%)	5 (3%)	41	70
1	C	156/247 (63%)	148 (95%)	8 (5%)	24	50
1	D	165/247 (67%)	164 (99%)	1 (1%)	86	95
1	F	159/247 (64%)	156 (98%)	3 (2%)	57	82
1	G	167/247 (68%)	163 (98%)	4 (2%)	49	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	I	162/247 (66%)	159 (98%)	3 (2%)	57 82
1	J	171/247 (69%)	166 (97%)	5 (3%)	42 71
All	All	1302/1976 (66%)	1269 (98%)	33 (2%)	47 76

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	THR
1	A	212	VAL
1	A	242	SER
1	A	243	LEU
1	B	42	ARG
1	B	77	ARG
1	B	127	ILE
1	B	243	LEU
1	B	254	ARG
1	C	95	GLU
1	C	96	LEU
1	C	100	ILE
1	C	147	LYS
1	C	212	VAL
1	C	242	SER
1	C	243	LEU
1	C	277	CYS
1	D	242	SER
1	F	60	THR
1	F	242	SER
1	F	243	LEU
1	G	100	ILE
1	G	198	TYR
1	G	241	SER
1	G	243	LEU
1	I	212	VAL
1	I	242	SER
1	I	243	LEU
1	J	100	ILE
1	J	212	VAL
1	J	241	SER
1	J	242	SER
1	J	254	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	52	HIS
1	B	287	HIS
1	C	52	HIS
1	C	258	GLN
1	F	52	HIS
1	F	58	HIS
1	G	58	HIS
1	I	52	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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	205/279 (73%)	-0.20	2 (0%) 82 83	36, 51, 79, 118	0
1	B	204/279 (73%)	-0.35	0 100 100	29, 47, 78, 105	0
1	C	205/279 (73%)	-0.06	6 (2%) 51 52	36, 55, 80, 119	1 (0%)
1	D	204/279 (73%)	-0.22	1 (0%) 91 92	28, 47, 78, 105	0
1	F	203/279 (72%)	-0.02	2 (0%) 82 83	40, 55, 80, 105	0
1	G	204/279 (73%)	-0.20	1 (0%) 91 92	26, 47, 79, 106	0
1	I	204/279 (73%)	-0.06	6 (2%) 51 52	39, 57, 79, 106	1 (0%)
1	J	206/279 (73%)	-0.24	1 (0%) 91 92	25, 46, 79, 123	0
All	All	1635/2232 (73%)	-0.17	19 (1%) 79 80	25, 51, 80, 123	2 (0%)

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	223	VAL	5.0
1	F	98	LEU	2.9
1	C	225	GLY	2.8
1	C	82	GLY	2.7
1	I	225	GLY	2.6
1	A	88	PHE	2.6
1	A	199	THR	2.4
1	C	163	CYS	2.4
1	F	111	ALA	2.4
1	C	56	PHE	2.4
1	J	31	PHE	2.4
1	I	58	HIS	2.3
1	I	56	PHE	2.2
1	C	224	ASN	2.2
1	D	61	LEU	2.2
1	G	198	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
1	I	78	PHE	2.1
1	I	222	THR	2.1
1	I	61	LEU	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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.