



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2018 – 10:30 pm GMT

PDB ID : 4HQ0  
Title : Crystal Structure of mutant form of Caspase-7  
Authors : Lee, Y.; Kang, H.J.; Bae, K.-H.; Kim, S.J.; Chung, S.J.  
Deposited on : 2012-10-25  
Resolution : 3.00 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](mailto: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.

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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 : trunk30967  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30967

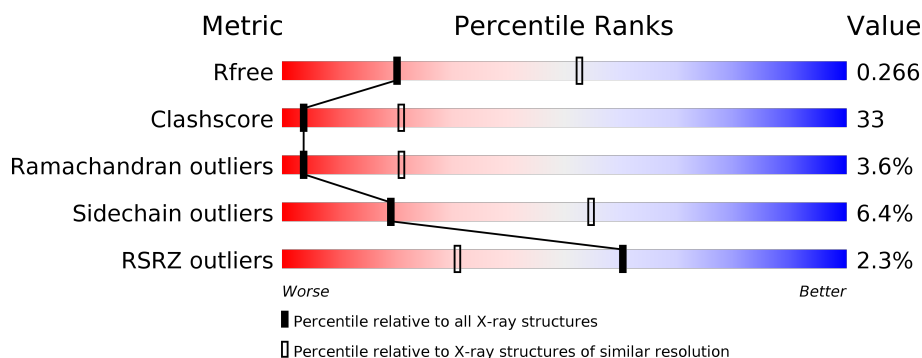
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	111664	1851 (3.00-3.00)
Clashscore	122126	2167 (3.00-3.00)
Ramachandran outliers	120053	2101 (3.00-3.00)
Sidechain outliers	120020	2104 (3.00-3.00)
RSRZ outliers	108989	1751 (3.00-3.00)

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  $\geq 3$ , 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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	272	<div> <div>%</div> <div> <div></div> <div>41%</div> <div>31%</div> <div>5%</div> <div>23%</div> </div> </div>
1	B	272	<div> <div>3%</div> <div> <div></div> <div>39%</div> <div>36%</div> <div>5%</div> <div>20%</div> </div> </div>

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3424 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-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	210	Total	C	N	O	S	0	0	0
			1681	1072	286	308	15			
1	B	217	Total	C	N	O	S	0	0	0
			1743	1110	302	316	15			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	46	MET	-	EXPRESSION TAG	UNP P55210
A	198	ALA	ASP	ENGINEERED MUTATION	UNP P55210
A	204A	LEU	-	INSERTION	UNP P55210
A	204B	VAL	-	INSERTION	UNP P55210
A	204C	PRO	-	INSERTION	UNP P55210
A	204D	ARG	-	INSERTION	UNP P55210
A	204E	GLY	-	INSERTION	UNP P55210
A	204F	SER	-	INSERTION	UNP P55210
A	304	LEU	-	EXPRESSION TAG	UNP P55210
A	305	GLU	-	EXPRESSION TAG	UNP P55210
A	306	HIS	-	EXPRESSION TAG	UNP P55210
A	307	HIS	-	EXPRESSION TAG	UNP P55210
A	308	HIS	-	EXPRESSION TAG	UNP P55210
A	309	HIS	-	EXPRESSION TAG	UNP P55210
A	310	HIS	-	EXPRESSION TAG	UNP P55210
A	311	HIS	-	EXPRESSION TAG	UNP P55210
B	46	MET	-	EXPRESSION TAG	UNP P55210
B	198	ALA	ASP	ENGINEERED MUTATION	UNP P55210
B	204A	LEU	-	INSERTION	UNP P55210
B	204B	VAL	-	INSERTION	UNP P55210
B	204C	PRO	-	INSERTION	UNP P55210
B	204D	ARG	-	INSERTION	UNP P55210
B	204E	GLY	-	INSERTION	UNP P55210
B	204F	SER	-	INSERTION	UNP P55210
B	304	LEU	-	EXPRESSION TAG	UNP P55210

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Chain	Residue	Modelled	Actual	Comment	Reference
B	305	GLU	-	EXPRESSION TAG	UNP P55210
B	306	HIS	-	EXPRESSION TAG	UNP P55210
B	307	HIS	-	EXPRESSION TAG	UNP P55210
B	308	HIS	-	EXPRESSION TAG	UNP P55210
B	309	HIS	-	EXPRESSION TAG	UNP P55210
B	310	HIS	-	EXPRESSION TAG	UNP P55210
B	311	HIS	-	EXPRESSION TAG	UNP P55210



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	89.60Å 89.60Å 182.84Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.00 – 3.00 71.43 – 3.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (40.00-3.00) 100.0 (71.43-3.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.75 (at 3.01Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.222 , 0.267 0.221 , 0.266	Depositor DCC
$R_{free}$ test set	846 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	66.9	Xtriage
Anisotropy	0.486	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 58.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.013 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	3424	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.85% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	1/1715 (0.1%)	0.63	1/2305 (0.0%)
1	B	0.71	1/1779 (0.1%)	0.69	1/2393 (0.0%)
All	All	0.71	2/3494 (0.1%)	0.66	2/4698 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	186	CYS	CB-SG	-23.68	1.42	1.82
1	B	186	CYS	CB-SG	-23.10	1.43	1.82

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	152	GLY	N-CA-C	-6.06	97.95	113.10
1	A	152	GLY	N-CA-C	-5.01	100.57	113.10

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	1681	0	1661	112	0
1	B	1743	0	1732	129	0
All	All	3424	0	3393	223	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 33.

All (223) 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:A:80:LYS:H	1:A:80:LYS:HD3	1.15	1.11
1:A:186:CYS:SG	1:A:231:SER:HB3	1.90	1.10
1:B:225:THR:HB	1:B:231:SER:HB3	1.29	1.08
1:A:215:VAL:HB	1:B:226:VAL:HG13	1.36	1.05
1:B:210:ARG:HH22	1:B:215:VAL:HA	1.25	1.00
1:A:226:VAL:CG1	1:B:210:ARG:HE	1.79	0.95
1:B:212:LYS:H	1:B:212:LYS:HD2	1.30	0.95
1:B:211:TYR:HB3	1:B:212:LYS:HE2	1.53	0.90
1:A:290:CYS:SG	1:B:294:MET:HE1	2.15	0.86
1:B:91:ASP:O	1:B:95:GLU:HG3	1.81	0.81
1:B:124:LYS:O	1:B:128:GLU:HG3	1.81	0.80
1:B:184:GLN:HA	1:B:224:SER:HB2	1.65	0.79
1:A:215:VAL:HG21	1:B:227:PRO:HD2	1.64	0.79
1:B:186:CYS:HB3	1:B:230:TYR:HE2	1.48	0.79
1:A:80:LYS:N	1:A:80:LYS:HD3	1.97	0.78
1:B:56:PRO:HD2	1:B:59:GLN:HE21	1.48	0.77
1:A:226:VAL:HG12	1:B:210:ARG:HE	1.50	0.77
1:A:226:VAL:HG11	1:B:210:ARG:HE	1.48	0.76
1:B:93:ASP:HB3	1:B:242:VAL:HG11	1.68	0.75
1:B:56:PRO:CD	1:B:59:GLN:HE21	1.99	0.75
1:B:226:VAL:HB	1:B:229:TYR:HB2	1.69	0.74
1:B:212:LYS:HD2	1:B:212:LYS:N	2.02	0.74
1:B:210:ARG:HA	1:B:213:ILE:HD13	1.69	0.72
1:B:56:PRO:HB2	1:B:58:TYR:HD1	1.54	0.72
1:B:167:ARG:NH2	1:B:170:ARG:HH21	1.87	0.72
1:B:184:GLN:HA	1:B:224:SER:CB	2.20	0.72
1:B:213:ILE:HG23	1:B:221:PHE:CE1	2.24	0.71
1:B:211:TYR:HB3	1:B:212:LYS:CE	2.21	0.70
1:A:215:VAL:CB	1:B:226:VAL:HG13	2.17	0.70
1:A:273:PHE:CZ	1:A:287:GLN:HB3	2.27	0.70
1:B:148:ASN:HA	1:B:212:LYS:HG2	1.74	0.70
1:A:273:PHE:CB	1:A:286:LYS:HD3	2.22	0.69
1:B:226:VAL:C	1:B:228:GLY:H	1.93	0.69
1:A:215:VAL:HG12	1:B:288:ILE:HG23	1.73	0.69
1:B:233:ARG:HA	1:B:239:SER:HA	1.74	0.69
1:B:148:ASN:HD21	1:B:211:TYR:HD2	1.41	0.68
1:B:148:ASN:ND2	1:B:212:LYS:HG3	2.08	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:187:ARG:HH11	1:A:187:ARG:HB2	1.59	0.68
1:A:273:PHE:HB3	1:A:286:LYS:HD3	1.75	0.68
1:A:273:PHE:HZ	1:A:287:GLN:HB3	1.56	0.67
1:A:187:ARG:NH1	1:A:187:ARG:HB2	2.09	0.67
1:B:210:ARG:NH2	1:B:215:VAL:HA	2.06	0.67
1:B:209:PRO:HD3	1:B:227:PRO:HG2	1.76	0.67
1:B:56:PRO:HD2	1:B:59:GLN:NE2	2.10	0.67
1:B:226:VAL:HG21	1:B:229:TYR:HD2	1.60	0.65
1:B:56:PRO:HB2	1:B:58:TYR:CD1	2.31	0.65
1:A:84:MET:HB3	1:A:144:HIS:CD2	2.32	0.64
1:B:163:THR:HG21	1:B:221:PHE:HE2	1.62	0.64
1:B:225:THR:HB	1:B:231:SER:CB	2.16	0.64
1:B:238:GLY:HA3	1:B:243:GLN:HE21	1.63	0.64
1:A:65:GLU:HB3	1:A:133:ASN:HB3	1.79	0.64
1:A:237:ARG:HG2	1:A:243:GLN:NE2	2.14	0.63
1:A:234:SER:HB3	1:A:237:ARG:HB3	1.80	0.63
1:A:244:ALA:O	1:A:248:ILE:HG12	1.98	0.63
1:B:257:GLU:OE2	1:B:258:ILE:HG22	1.99	0.63
1:B:56:PRO:C	1:B:58:TYR:H	2.02	0.63
1:A:187:ARG:HB3	1:A:227:PRO:O	1.99	0.62
1:B:71:ILE:HG21	1:B:122:LEU:HD21	1.80	0.62
1:A:147:GLU:HG3	1:B:211:TYR:HE1	1.64	0.62
1:A:273:PHE:CD2	1:A:286:LYS:HB3	2.35	0.61
1:B:54:ARG:O	1:B:56:PRO:HD3	2.00	0.61
1:A:234:SER:CB	1:A:237:ARG:HB3	2.30	0.61
1:A:78:PHE:HZ	1:A:143:SER:HB2	1.65	0.61
1:A:273:PHE:CE2	1:A:286:LYS:HB3	2.36	0.61
1:A:215:VAL:HB	1:B:226:VAL:CG1	2.23	0.61
1:A:78:PHE:CZ	1:A:143:SER:HB2	2.36	0.60
1:B:123:LEU:HD12	1:B:162:LEU:HD22	1.83	0.60
1:B:92:LYS:HD3	1:B:237:ARG:C	2.21	0.59
1:B:65:GLU:HB3	1:B:133:ASN:HB3	1.83	0.59
1:A:186:CYS:SG	1:A:231:SER:CB	2.80	0.59
1:B:97:LEU:HD13	1:B:140:ILE:HG21	1.85	0.59
1:A:81:VAL:O	1:A:81:VAL:HG23	2.02	0.59
1:A:80:LYS:H	1:A:80:LYS:CD	1.97	0.58
1:A:246:CYS:O	1:A:250:GLU:HB2	2.04	0.58
1:B:252:HIS:HB3	1:B:256:LEU:HG	1.85	0.58
1:B:168:GLY:HA2	1:B:175:LEU:HD13	1.85	0.58
1:A:273:PHE:CZ	1:A:287:GLN:N	2.72	0.58
1:A:130:ASP:OD2	1:A:173:THR:HG21	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:226:VAL:CG1	1:B:210:ARG:NE	2.60	0.57
1:A:233:ARG:CG	1:A:234:SER:H	2.15	0.57
1:A:229:TYR:CD2	1:B:215:VAL:HG11	2.39	0.57
1:A:92:LYS:NZ	1:A:237:ARG:HA	2.20	0.56
1:B:224:SER:HA	1:B:241:PHE:CD2	2.41	0.56
1:A:119:MET:HE3	1:A:157:THR:HG21	1.87	0.56
1:B:292:VAL:HG12	1:B:294:MET:HE3	1.88	0.55
1:A:233:ARG:HA	1:A:239:SER:HA	1.89	0.55
1:A:252:HIS:HB3	1:A:256:LEU:HG	1.88	0.54
1:A:263:THR:O	1:A:266:ASN:HB2	2.06	0.54
1:B:184:GLN:HG3	1:B:184:GLN:O	2.06	0.54
1:A:233:ARG:HG3	1:A:234:SER:H	1.72	0.54
1:A:170:ARG:H	1:A:170:ARG:HD2	1.71	0.54
1:A:234:SER:OG	1:A:237:ARG:HB3	2.07	0.54
1:B:186:CYS:HB3	1:B:230:TYR:CE2	2.37	0.54
1:B:84:MET:HB3	1:B:144:HIS:CD2	2.43	0.54
1:A:120:GLN:NE2	1:A:162:LEU:HD23	2.23	0.53
1:A:226:VAL:HG11	1:B:210:ARG:NE	2.22	0.53
1:B:226:VAL:C	1:B:228:GLY:N	2.61	0.53
1:B:226:VAL:HB	1:B:229:TYR:H	1.73	0.53
1:A:70:CYS:HA	1:A:138:ALA:O	2.08	0.53
1:B:158:PRO:HB2	1:B:161:ASP:OD2	2.08	0.53
1:B:111:TYR:CG	1:B:122:LEU:HD11	2.43	0.53
1:B:144:HIS:ND1	1:B:187:ARG:HD3	2.24	0.52
1:A:80:LYS:C	1:A:82:THR:H	2.13	0.52
1:A:147:GLU:HG3	1:B:211:TYR:CE1	2.44	0.52
1:A:225:THR:CG2	1:A:231:SER:HB2	2.41	0.51
1:A:233:ARG:HG3	1:A:234:SER:N	2.25	0.51
1:A:273:PHE:CG	1:A:286:LYS:HD3	2.45	0.51
1:A:115:SER:HB2	1:A:154:ASP:OD2	2.11	0.51
1:A:97:LEU:HD12	1:A:142:LEU:HD11	1.93	0.51
1:A:123:LEU:HD12	1:A:166:PHE:HE1	1.76	0.51
1:B:131:HIS:N	1:B:173:THR:OG1	2.44	0.51
1:B:238:GLY:HA3	1:B:243:GLN:NE2	2.26	0.51
1:A:62:MET:HG3	1:A:300:TYR:O	2.11	0.50
1:A:215:VAL:HG12	1:B:288:ILE:CG2	2.41	0.50
1:B:209:PRO:HG2	1:B:212:LYS:HE3	1.93	0.50
1:B:175:LEU:O	1:B:176:GLU:HB2	2.09	0.50
1:B:136:CYS:HB3	1:B:178:PRO:HG2	1.93	0.50
1:A:57:THR:O	1:A:297:LYS:HE3	2.11	0.50
1:B:145:GLY:HA3	1:B:185:ALA:HB1	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:76:LYS:HB2	1:B:90:THR:HG21	1.93	0.50
1:A:136:CYS:HB3	1:A:178:PRO:HG2	1.94	0.50
1:A:168:GLY:H	1:A:216:GLU:HG2	1.75	0.50
1:A:80:LYS:N	1:A:80:LYS:CD	2.68	0.49
1:B:111:TYR:CD1	1:B:122:LEU:HD11	2.47	0.49
1:B:226:VAL:HG11	1:B:229:TYR:CD2	2.47	0.49
1:B:168:GLY:CA	1:B:175:LEU:HD13	2.41	0.49
1:B:212:LYS:C	1:B:213:ILE:HD12	2.33	0.49
1:B:246:CYS:O	1:B:250:GLU:HG3	2.12	0.49
1:A:172:LYS:O	1:A:175:LEU:HB2	2.13	0.49
1:A:257:GLU:HG3	1:A:298:GLU:HB3	1.95	0.49
1:B:260:GLN:O	1:B:264:ARG:HG3	2.12	0.49
1:B:153:LYS:NZ	1:B:153:LYS:HB2	2.28	0.49
1:B:53:ASP:C	1:B:54:ARG:HG2	2.33	0.49
1:A:80:LYS:O	1:A:82:THR:N	2.45	0.48
1:A:93:ASP:O	1:A:96:ALA:HB3	2.14	0.48
1:A:84:MET:HG3	1:A:151:TYR:CE2	2.49	0.48
1:A:225:THR:HG22	1:A:231:SER:HB2	1.95	0.47
1:A:84:MET:CE	1:A:144:HIS:HB3	2.45	0.47
1:A:123:LEU:HD12	1:A:166:PHE:CE1	2.50	0.47
1:A:184:GLN:HG3	1:A:184:GLN:O	2.13	0.47
1:A:92:LYS:HE2	1:A:92:LYS:HB3	1.72	0.47
1:B:226:VAL:O	1:B:228:GLY:N	2.48	0.47
1:B:209:PRO:HD3	1:B:227:PRO:CG	2.44	0.47
1:A:150:ILE:HG22	1:A:157:THR:HG23	1.98	0.47
1:A:233:ARG:HD3	1:A:239:SER:N	2.30	0.47
1:A:233:ARG:O	1:A:234:SER:HB2	2.15	0.47
1:B:66:LYS:O	1:B:134:ALA:HA	2.15	0.47
1:B:212:LYS:CD	1:B:212:LYS:N	2.73	0.46
1:B:187:ARG:N	1:B:230:TYR:CD2	2.79	0.46
1:A:78:PHE:N	1:A:78:PHE:CD1	2.83	0.46
1:A:167:ARG:HB2	1:A:170:ARG:HD3	1.98	0.46
1:B:258:ILE:HG23	1:B:259:MET:N	2.31	0.46
1:A:170:ARG:HD2	1:A:170:ARG:N	2.31	0.46
1:A:172:LYS:HA	1:A:175:LEU:HD12	1.98	0.46
1:B:112:ASN:O	1:B:113:ASP:C	2.54	0.46
1:B:54:ARG:O	1:B:56:PRO:CD	2.63	0.46
1:B:257:GLU:O	1:B:260:GLN:HB2	2.15	0.45
1:A:113:ASP:O	1:A:153:LYS:HD2	2.16	0.45
1:B:93:ASP:CB	1:B:242:VAL:HG11	2.43	0.45
1:B:69:LYS:NZ	1:B:129:GLU:OE2	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:256:LEU:HD11	1:A:264:ARG:CZ	2.47	0.45
1:B:230:TYR:CE2	1:B:231:SER:O	2.70	0.45
1:B:52:ARG:O	1:B:53:ASP:HB3	2.17	0.45
1:B:60:TYR:O	1:B:62:MET:HE2	2.17	0.45
1:B:146:GLU:O	1:B:147:GLU:C	2.55	0.45
1:B:261:ILE:O	1:B:265:VAL:HG23	2.17	0.44
1:A:233:ARG:CG	1:A:234:SER:N	2.81	0.44
1:A:97:LEU:CD1	1:A:142:LEU:HD11	2.47	0.44
1:B:54:ARG:C	1:B:56:PRO:HD3	2.38	0.44
1:A:158:PRO:HB2	1:A:161:ASP:OD2	2.18	0.44
1:B:168:GLY:H	1:B:216:GLU:HG3	1.81	0.44
1:B:231:SER:HA	1:B:287:GLN:OE1	2.17	0.44
1:A:116:CYS:HB3	1:A:157:THR:HB	2.00	0.44
1:B:60:TYR:CD1	1:B:178:PRO:HD3	2.53	0.44
1:A:71:ILE:HG23	1:A:111:TYR:CE2	2.53	0.43
1:A:224:SER:O	1:A:225:THR:HB	2.18	0.43
1:A:226:VAL:CG1	1:B:210:ARG:HH21	2.31	0.43
1:A:257:GLU:OE2	1:A:258:ILE:HG22	2.19	0.43
1:B:148:ASN:HA	1:B:212:LYS:CG	2.45	0.43
1:B:65:GLU:CB	1:B:133:ASN:HB3	2.48	0.43
1:B:220:LEU:HD11	1:B:291:VAL:CG1	2.49	0.43
1:B:69:LYS:HD2	1:B:109:ILE:CD1	2.49	0.43
1:B:98:PHE:C	1:B:98:PHE:CD1	2.91	0.43
1:A:125:LYS:HE3	1:A:125:LYS:HA	1.99	0.43
1:A:97:LEU:HD13	1:A:140:ILE:HG21	2.01	0.43
1:A:60:TYR:CD1	1:A:178:PRO:HD3	2.54	0.43
1:A:186:CYS:HB3	1:A:230:TYR:CD2	2.53	0.43
1:A:184:GLN:HA	1:A:224:SER:HB2	2.01	0.42
1:B:148:ASN:CG	1:B:212:LYS:HG3	2.39	0.42
1:B:56:PRO:C	1:B:58:TYR:N	2.70	0.42
1:B:167:ARG:HH21	1:B:170:ARG:HE	1.68	0.42
1:B:251:GLU:HG3	1:B:252:HIS:CD2	2.54	0.42
1:B:61:ASN:ND2	1:B:64:PHE:CE1	2.87	0.42
1:A:75:ASN:HB2	1:A:143:SER:HB3	2.01	0.42
1:A:226:VAL:HG11	1:B:210:ARG:HH21	1.85	0.42
1:A:142:LEU:HD23	1:A:184:GLN:HB3	2.01	0.42
1:B:244:ALA:HB1	1:B:268:ARG:HG2	2.02	0.42
1:B:157:THR:HA	1:B:158:PRO:HD3	1.91	0.42
1:A:147:GLU:OE1	1:A:147:GLU:HA	2.19	0.42
1:B:96:ALA:O	1:B:100:CYS:HB2	2.20	0.41
1:B:226:VAL:HB	1:B:229:TYR:CB	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:215:VAL:HA	1:A:294:MET:CE	2.51	0.41
1:B:124:LYS:HB2	1:B:165:HIS:CE1	2.55	0.41
1:B:185:ALA:O	1:B:186:CYS:O	2.39	0.41
1:B:76:LYS:HB2	1:B:90:THR:CG2	2.50	0.41
1:A:136:CYS:CB	1:A:178:PRO:HG2	2.50	0.41
1:A:131:HIS:O	1:A:134:ALA:HB3	2.20	0.41
1:A:288:ILE:HG23	1:A:288:ILE:O	2.20	0.41
1:B:98:PHE:O	1:B:102:ARG:HB2	2.21	0.41
1:A:175:LEU:O	1:A:176:GLU:HB2	2.21	0.41
1:A:260:GLN:O	1:A:264:ARG:HG3	2.20	0.41
1:B:184:GLN:HA	1:B:224:SER:HB3	1.97	0.41
1:A:294:MET:SD	1:B:290:CYS:HB2	2.61	0.41
1:B:56:PRO:HG2	1:B:59:GLN:HG3	2.03	0.41
1:A:157:THR:HA	1:A:158:PRO:HD3	1.85	0.40
1:A:120:GLN:HE22	1:A:161:ASP:C	2.24	0.40
1:A:92:LYS:HZ3	1:A:237:ARG:HA	1.84	0.40
1:B:69:LYS:HD2	1:B:109:ILE:HD11	2.03	0.40
1:A:71:ILE:HD11	1:A:126:ALA:HB2	2.03	0.40
1:B:143:SER:OG	1:B:144:HIS:N	2.54	0.40
1:B:210:ARG:NH1	1:B:213:ILE:HG22	2.36	0.40
1:B:66:LYS:HB3	1:B:66:LYS:NZ	2.36	0.40
1:A:215:VAL:HA	1:A:294:MET:HE2	2.03	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	204/272 (75%)	178 (87%)	19 (9%)	7 (3%)	4	22
1	B	211/272 (78%)	186 (88%)	17 (8%)	8 (4%)	3	20
All	All	415/544 (76%)	364 (88%)	36 (9%)	15 (4%)	4	21

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	81	VAL
1	A	234	SER
1	B	56	PRO
1	B	186	CYS
1	A	147	GLU
1	A	215	VAL
1	A	225	THR
1	B	211	TYR
1	B	215	VAL
1	B	53	ASP
1	A	143	SER
1	B	55	VAL
1	A	235	PRO
1	B	210	ARG
1	B	227	PRO

### 5.3.2 Protein sidechains ⓘ

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	184/239 (77%)	170 (92%)	14 (8%)	14	46
1	B	191/239 (80%)	181 (95%)	10 (5%)	25	63
All	All	375/478 (78%)	351 (94%)	24 (6%)	19	55

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	THR
1	A	80	LYS
1	A	91	ASP
1	A	122	LEU
1	A	125	LYS
1	A	128	GLU
1	A	147	GLU
1	A	173	THR

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Mol	Chain	Res	Type
1	A	175	LEU
1	A	187	ARG
1	A	220	LEU
1	A	229	TYR
1	A	230	TYR
1	A	272	HIS
1	B	66	LYS
1	B	98	PHE
1	B	153	LYS
1	B	156	VAL
1	B	173	THR
1	B	212	LYS
1	B	235	PRO
1	B	268	ARG
1	B	290	CYS
1	B	294	MET

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

Mol	Chain	Res	Type
1	A	59	GLN
1	A	88	ASN
1	A	120	GLN
1	A	243	GLN
1	A	272	HIS
1	A	287	GLN
1	B	59	GLN
1	B	243	GLN

### 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 carbohydrates 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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	210/272 (77%)	0.29	3 (1%) 75 49	43, 69, 96, 101	0
1	B	217/272 (79%)	0.34	7 (3%) 47 20	40, 58, 96, 101	0
All	All	427/544 (78%)	0.32	10 (2%) 60 31	40, 62, 96, 101	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	227	PRO	4.6
1	B	287	GLN	4.1
1	B	228	GLY	3.8
1	B	226	VAL	3.6
1	A	229	TYR	3.5
1	B	229	TYR	3.2
1	B	210	ARG	2.7
1	A	215	VAL	2.4
1	B	233	ARG	2.2
1	A	235	PRO	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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.