Full wwPDB X-ray Structure Validation Report (i)

Oct 17, 2021 – 07:22 AM EDT

PDB ID	:	1K88
Title	:	Crystal structure of procaspase-7
Authors	:	Chai, J.; Wu, Q.; Shiozaki, E.; Srinivasa, S.M.; Alnemri, E.S.; Shi, Y.
Deposited on	:	2001-10-23
Resolution	:	2.70 Å(reported)

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

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

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

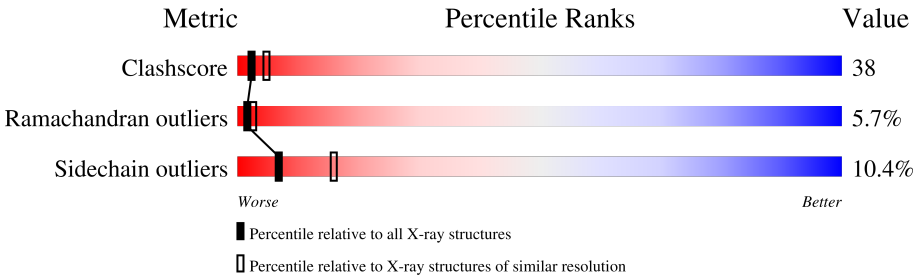
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

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 2.70 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))
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	253	42% 38% 9% • 10%
1	B	253	43% 39% 10% 8%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 3766 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 procaspase-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	227	Total	C	N	O	S	0	0	0
			1821	1161	313	333	14			
1	B	234	Total	C	N	O	S	0	0	0
			1871	1189	321	347	14			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	169	ALA	ASP	engineered mutation	UNP P55210
A	186	ALA	CYS	engineered mutation	UNP P55210
B	169	ALA	ASP	engineered mutation	UNP P55210
B	186	ALA	CYS	engineered mutation	UNP P55210

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	33	Total	O	0	0
			33	33		
2	B	41	Total	O	0	0
			41	41		

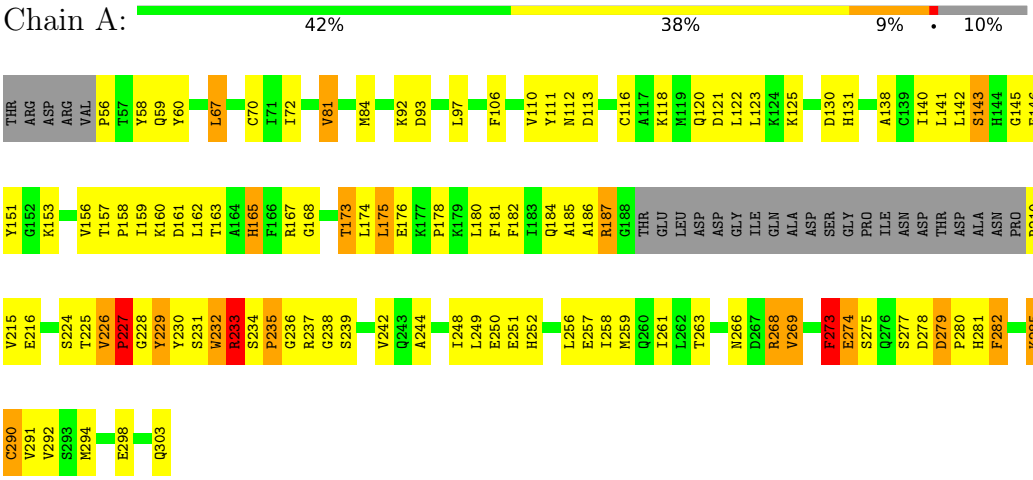
3 Residue-property plots (i)

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. 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. 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.

Note EDS was not executed.

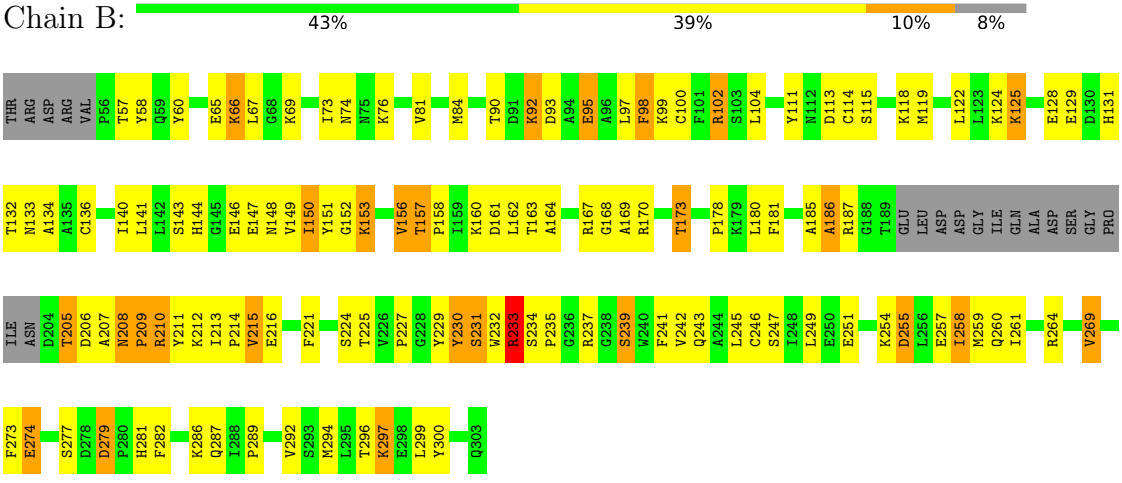
• Molecule 1: procaspase-7

Chain A:



• Molecule 1: procaspase-7

Chain B:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	91.20Å 91.20Å 185.20Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.70	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.70)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.227 , 0.253	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3766	wwPDB-VP
Average B, all atoms (Å^2)	71.0	wwPDB-VP

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	0.47	0/1862	0.77	4/2505 (0.2%)
1	B	0.47	0/1913	0.73	1/2577 (0.0%)
All	All	0.47	0/3775	0.75	5/5082 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	273	PHE	N-CA-C	7.43	131.05	111.00
1	B	152	GLY	N-CA-C	-6.65	96.47	113.10
1	A	279	ASP	N-CA-C	-5.82	95.30	111.00
1	A	275	SER	N-CA-C	5.50	125.86	111.00
1	A	277	SER	N-CA-C	-5.43	96.33	111.00

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	1821	0	1794	147	0
1	B	1871	0	1834	168	0
2	A	33	0	0	6	0
2	B	41	0	0	2	0
All	All	3766	0	3628	281	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 38.

All (281) 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:175:LEU:HD23	1:A:176:GLU:HG2	1.34	1.07
1:A:215:VAL:H	1:B:205:THR:HG21	1.06	1.06
1:B:210:ARG:CZ	1:B:292:VAL:HG13	1.85	1.06
1:A:215:VAL:N	1:B:205:THR:HG21	1.76	1.00
1:A:167:ARG:HG3	1:A:167:ARG:HH11	1.22	0.99
1:A:290:CYS:SG	1:B:210:ARG:HD2	2.04	0.95
1:B:212:LYS:O	1:B:213:ILE:HG13	1.66	0.95
1:A:273:PHE:CE1	1:A:286:LYS:HA	2.01	0.94
1:B:210:ARG:NH2	1:B:292:VAL:HA	1.83	0.92
1:A:150:ILE:HG23	1:A:159:ILE:HD11	1.54	0.88
1:B:277:SER:HG	1:B:282:PHE:HD2	1.21	0.88
1:A:158:PRO:HG2	1:A:161:ASP:OD2	1.76	0.85
1:B:232:TRP:O	1:B:233:ARG:HB3	1.77	0.84
1:A:226:VAL:HG21	1:B:215:VAL:HG11	1.60	0.83
1:B:124:LYS:HE3	1:B:128:GLU:OE2	1.79	0.82
1:B:296:THR:O	1:B:297:LYS:HD2	1.80	0.82
1:A:215:VAL:H	1:B:205:THR:CG2	1.89	0.81
1:B:160:LYS:HB2	1:B:212:LYS:HD3	1.61	0.81
1:B:167:ARG:HD2	1:B:170:ARG:CZ	2.12	0.80
1:A:233:ARG:HD3	1:A:233:ARG:N	1.96	0.80
1:B:149:VAL:HG11	1:B:156:VAL:HG13	1.63	0.80
1:A:213:ILE:CG2	1:B:209:PRO:HD3	2.11	0.80
1:A:213:ILE:HG21	1:B:209:PRO:HD3	1.65	0.78
1:A:291:VAL:O	1:B:210:ARG:NH2	2.13	0.78
1:B:148:ASN:HB3	1:B:212:LYS:HE3	1.64	0.77
1:A:165:HIS:H	1:A:165:HIS:CD2	2.02	0.77
1:A:93:ASP:OD1	1:A:238:GLY:HA3	1.85	0.76
1:A:145:GLY:HA3	1:A:185:ALA:HB1	1.65	0.76
1:B:111:TYR:CZ	1:B:122:LEU:HD11	2.21	0.75
1:A:292:VAL:HA	1:B:210:ARG:NH2	2.01	0.75
1:A:292:VAL:HA	1:B:210:ARG:HH21	1.52	0.74
1:B:269:VAL:HG21	1:B:289:PRO:HD3	1.69	0.74
1:B:111:TYR:CE2	1:B:122:LEU:HD11	2.23	0.74
1:B:210:ARG:NH1	1:B:292:VAL:HG13	2.04	0.73
1:B:73:ILE:HD13	1:B:119:MET:HG2	1.70	0.72
1:B:167:ARG:HD2	1:B:170:ARG:NH2	2.03	0.72
1:B:210:ARG:NE	1:B:292:VAL:HG13	2.03	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:149:VAL:HA	1:A:158:PRO:HA	1.73	0.71
1:A:150:ILE:HD11	1:A:162:LEU:HD11	1.72	0.70
1:A:291:VAL:C	1:B:210:ARG:HH22	1.94	0.69
1:B:93:ASP:HB3	1:B:242:VAL:HG11	1.74	0.69
1:A:148:ASN:OD1	1:B:209:PRO:HG2	1.93	0.69
1:B:164:ALA:O	1:B:167:ARG:HG2	1.93	0.69
1:A:167:ARG:HG3	1:A:167:ARG:NH1	2.01	0.69
1:B:224:SER:O	1:B:225:THR:HB	1.92	0.69
1:A:291:VAL:C	1:B:210:ARG:NH2	2.47	0.68
1:B:95:GLU:OE2	1:B:99:LYS:HE3	1.94	0.67
1:A:273:PHE:CZ	1:A:286:LYS:HA	2.30	0.67
1:A:268:ARG:HG2	1:A:268:ARG:HH11	1.60	0.66
1:A:231:SER:HA	1:A:287:GLN:OE1	1.96	0.66
1:B:92:LYS:HE3	1:B:235:PRO:HB3	1.77	0.66
1:A:160:LYS:HD3	1:A:210:ARG:HD3	1.78	0.65
1:A:269:VAL:HG11	1:A:289:PRO:HG2	1.77	0.65
1:A:244:ALA:O	1:A:248:ILE:HG12	1.96	0.65
1:B:118:LYS:O	1:B:122:LEU:HB2	1.97	0.65
1:A:120:GLN:HE21	1:A:157:THR:HG21	1.59	0.65
1:B:92:LYS:HE2	1:B:92:LYS:HA	1.79	0.65
1:A:233:ARG:HG2	1:A:234:SER:H	1.61	0.65
1:B:247:SER:O	1:B:251:GLU:HG3	1.96	0.65
1:A:233:ARG:HG2	1:A:234:SER:N	2.11	0.65
1:A:226:VAL:HG21	1:B:215:VAL:CG1	2.28	0.64
1:B:208:ASN:O	1:B:210:ARG:N	2.31	0.63
1:A:149:VAL:HG23	1:A:157:THR:C	2.19	0.63
1:B:160:LYS:HD2	1:B:211:TYR:O	2.00	0.62
1:B:230:TYR:O	1:B:231:SER:HB2	1.99	0.62
1:A:273:PHE:CD1	1:A:274:GLU:N	2.67	0.61
1:B:274:GLU:OE2	1:B:282:PHE:HB3	2.00	0.61
1:A:175:LEU:HD23	1:A:176:GLU:CG	2.19	0.61
1:A:149:VAL:HG23	1:A:157:THR:O	2.01	0.61
1:B:97:LEU:HD23	1:B:246:CYS:SG	2.40	0.60
1:A:268:ARG:HG2	1:A:268:ARG:NH1	2.16	0.60
1:B:115:SER:OG	1:B:118:LYS:HB2	2.02	0.60
1:B:69:LYS:HZ1	1:B:129:GLU:CD	2.04	0.60
1:B:213:ILE:HG23	1:B:221:PHE:CE2	2.35	0.60
1:B:148:ASN:HA	1:B:212:LYS:HG2	1.82	0.60
1:B:92:LYS:HE3	1:B:235:PRO:CB	2.32	0.60
1:B:149:VAL:HG12	1:B:150:ILE:N	2.17	0.60
1:A:167:ARG:HH21	1:A:214:PRO:HG2	1.66	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:213:ILE:HG12	1:B:221:PHE:CE1	2.36	0.59
1:B:149:VAL:HG11	1:B:156:VAL:CG1	2.32	0.59
1:A:292:VAL:CA	1:B:210:ARG:NH2	2.66	0.59
1:B:65:GLU:HB2	1:B:133:ASN:HB2	1.83	0.59
1:B:92:LYS:HA	1:B:92:LYS:CE	2.32	0.59
1:B:209:PRO:O	1:B:211:TYR:N	2.33	0.59
1:A:130:ASP:OD1	1:A:173:THR:HG21	2.02	0.58
1:A:145:GLY:O	1:A:186:ALA:O	2.20	0.58
1:A:224:SER:HB3	2:A:307:HOH:O	2.02	0.58
1:B:74:ASN:HD21	1:B:90:THR:HG23	1.68	0.58
1:B:132:THR:N	1:B:173:THR:HG22	2.19	0.58
1:B:210:ARG:NE	1:B:292:VAL:HG22	2.19	0.58
1:B:136:CYS:HB3	1:B:178:PRO:HG2	1.85	0.58
1:B:258:ILE:CG1	1:B:299:LEU:HB3	2.33	0.57
1:A:234:SER:HB2	1:A:237:ARG:HG3	1.87	0.57
1:A:60:TYR:CD1	1:A:178:PRO:HD3	2.38	0.57
1:A:149:VAL:CG2	1:A:156:VAL:HB	2.35	0.57
1:A:279:ASP:HB3	1:A:282:PHE:HB2	1.85	0.57
1:A:257:GLU:OE2	1:A:258:ILE:HG22	2.05	0.56
1:B:84:MET:HB3	1:B:144:HIS:CD2	2.39	0.56
1:B:205:THR:OG1	1:B:206:ASP:N	2.39	0.56
1:A:150:ILE:CG2	1:A:159:ILE:HD11	2.32	0.56
1:A:250:GLU:O	1:A:251:GLU:HG2	2.06	0.56
1:A:278:ASP:C	1:A:280:PRO:HD3	2.27	0.55
1:A:212:LYS:O	1:A:214:PRO:HD3	2.06	0.55
1:A:226:VAL:HG11	1:B:215:VAL:HG21	1.87	0.55
1:B:258:ILE:HG12	1:B:299:LEU:HD23	1.89	0.55
1:A:116:CYS:HB3	1:A:157:THR:OG1	2.07	0.55
1:A:225:THR:O	1:A:226:VAL:HG23	2.07	0.55
1:B:237:ARG:HG3	1:B:237:ARG:HH11	1.70	0.55
1:B:97:LEU:HD13	1:B:140:ILE:HG21	1.87	0.55
1:A:184:GLN:O	1:A:184:GLN:HG3	2.07	0.55
1:A:290:CYS:SG	1:B:210:ARG:CD	2.89	0.54
1:B:209:PRO:C	1:B:211:TYR:H	2.11	0.54
1:B:149:VAL:HG13	1:B:157:THR:O	2.07	0.54
1:B:167:ARG:HD2	1:B:170:ARG:NH1	2.23	0.54
1:B:58:TYR:HA	1:B:297:LYS:NZ	2.21	0.54
1:A:72:ILE:HB	1:A:110:VAL:HG22	1.90	0.53
1:A:141:LEU:HD13	1:A:150:ILE:HD13	1.91	0.53
1:A:84:MET:HG3	1:A:151:TYR:CE2	2.44	0.53
1:B:74:ASN:HD21	1:B:90:THR:CG2	2.22	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:180:LEU:HB3	1:A:182:PHE:CE1	2.43	0.53
1:B:210:ARG:NH2	1:B:292:VAL:HG22	2.24	0.52
1:B:227:PRO:HD3	1:B:287:GLN:OE1	2.08	0.52
1:B:158:PRO:HG2	1:B:161:ASP:OD2	2.10	0.52
1:B:124:LYS:HE2	1:B:125:LYS:NZ	2.25	0.52
1:B:150:ILE:HD12	1:B:157:THR:O	2.09	0.52
1:B:230:TYR:O	1:B:231:SER:CB	2.57	0.52
1:A:111:TYR:CG	1:A:122:LEU:HD21	2.45	0.52
1:A:142:LEU:O	1:A:143:SER:HB2	2.10	0.52
1:A:81:VAL:HG12	1:A:81:VAL:O	2.09	0.52
1:B:93:ASP:OD2	1:B:239:SER:HB3	2.10	0.52
1:B:273:PHE:O	1:B:274:GLU:C	2.48	0.52
1:A:288:ILE:CG2	1:B:215:VAL:HG12	2.40	0.52
1:A:167:ARG:NH2	1:A:214:PRO:HG2	2.25	0.51
1:B:98:PHE:CD1	1:B:98:PHE:C	2.83	0.51
1:A:279:ASP:C	1:A:281:HIS:H	2.13	0.51
1:B:210:ARG:CZ	1:B:292:VAL:CG1	2.75	0.51
1:A:292:VAL:HG22	1:B:210:ARG:HE	1.75	0.51
1:A:257:GLU:HG3	1:A:298:GLU:HB3	1.93	0.50
1:A:292:VAL:HG22	1:B:210:ARG:HH21	1.76	0.50
1:B:254:LYS:N	1:B:254:LYS:HD2	2.26	0.50
1:B:269:VAL:CG2	1:B:289:PRO:HD3	2.41	0.50
1:B:277:SER:OG	1:B:282:PHE:HD2	1.88	0.50
1:A:273:PHE:CG	1:A:274:GLU:N	2.79	0.50
1:B:167:ARG:HB2	1:B:216:GLU:OE2	2.10	0.50
1:B:249:LEU:HD13	1:B:261:ILE:HG21	1.92	0.50
1:B:210:ARG:HE	1:B:292:VAL:HG22	1.76	0.50
1:A:147:GLU:C	1:A:149:VAL:H	2.13	0.50
1:B:146:GLU:O	1:B:147:GLU:C	2.48	0.50
1:A:226:VAL:HG12	1:B:211:TYR:HE1	1.76	0.50
1:A:147:GLU:HG3	1:A:148:ASN:H	1.77	0.50
1:B:163:THR:HG22	1:B:181:PHE:CE2	2.47	0.49
1:A:213:ILE:HG13	1:B:208:ASN:ND2	2.26	0.49
1:A:278:ASP:O	1:A:280:PRO:HD3	2.13	0.49
1:B:149:VAL:CG1	1:B:156:VAL:HG22	2.41	0.49
1:A:84:MET:HE3	1:A:187:ARG:HG3	1.94	0.49
1:B:245:LEU:O	1:B:249:LEU:HB2	2.12	0.49
1:A:256:LEU:HB2	1:A:261:ILE:CD1	2.43	0.49
1:A:70:CYS:HA	1:A:138:ALA:O	2.12	0.49
1:A:225:THR:HB	1:A:229:TYR:HB3	1.95	0.49
1:B:163:THR:HG21	1:B:221:PHE:CE1	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:258:ILE:HG13	1:B:299:LEU:HB3	1.93	0.49
1:A:158:PRO:CG	1:A:161:ASP:OD2	2.57	0.48
1:A:213:ILE:HG23	1:B:208:ASN:H	1.78	0.48
1:A:113:ASP:O	1:A:153:LYS:HD3	2.13	0.48
1:A:215:VAL:HG13	1:A:294:MET:SD	2.53	0.48
1:A:131:HIS:CG	1:A:174:LEU:HG	2.48	0.48
1:A:158:PRO:HG3	1:A:210:ARG:HB2	1.94	0.48
1:A:239:SER:OG	1:A:242:VAL:HG23	2.13	0.48
1:B:124:LYS:O	1:B:128:GLU:HG3	2.12	0.48
1:B:73:ILE:HD12	1:B:141:LEU:CD2	2.43	0.48
1:A:56:PRO:C	1:A:58:TYR:H	2.17	0.48
1:B:150:ILE:HD12	1:B:150:ILE:O	2.14	0.48
1:A:118:LYS:O	1:A:122:LEU:HB2	2.14	0.48
1:B:258:ILE:HD12	1:B:259:MET:H	1.79	0.48
1:A:163:THR:HG22	1:A:181:PHE:CZ	2.49	0.47
1:A:111:TYR:CZ	1:A:122:LEU:HD11	2.48	0.47
1:B:210:ARG:HH21	1:B:292:VAL:HG22	1.79	0.47
1:A:112:ASN:HB3	2:A:328:HOH:O	2.13	0.47
1:B:60:TYR:CD1	1:B:178:PRO:HD3	2.48	0.47
1:B:98:PHE:O	1:B:102:ARG:HB2	2.14	0.47
1:B:215:VAL:HA	1:B:294:MET:CE	2.44	0.47
1:B:136:CYS:CB	1:B:178:PRO:HG2	2.44	0.47
1:B:143:SER:O	1:B:185:ALA:HA	2.15	0.47
1:A:233:ARG:CG	1:A:234:SER:H	2.18	0.47
1:B:185:ALA:O	1:B:186:ALA:HB2	2.14	0.47
1:A:263:THR:O	1:A:266:ASN:HB2	2.15	0.47
1:A:268:ARG:HH11	1:A:268:ARG:CG	2.28	0.47
1:B:149:VAL:HG12	1:B:156:VAL:HG22	1.96	0.47
1:A:174:LEU:HD23	1:A:174:LEU:HA	1.82	0.46
1:B:237:ARG:HG3	1:B:237:ARG:NH1	2.28	0.46
1:A:227:PRO:HG2	1:B:209:PRO:HA	1.97	0.46
1:A:227:PRO:O	1:B:211:TYR:CE1	2.69	0.46
1:A:184:GLN:HA	1:A:224:SER:CB	2.46	0.46
1:B:163:THR:OG1	1:B:214:PRO:HD3	2.16	0.46
1:B:210:ARG:CZ	1:B:292:VAL:HG22	2.46	0.46
1:B:205:THR:HA	2:B:327:HOH:O	2.16	0.46
1:A:279:ASP:C	1:A:281:HIS:N	2.68	0.45
1:B:132:THR:N	1:B:173:THR:CG2	2.79	0.45
1:A:257:GLU:OE1	1:A:259:MET:HB2	2.17	0.45
1:B:233:ARG:CZ	1:B:233:ARG:HB2	2.45	0.45
1:B:277:SER:HB3	1:B:282:PHE:HB2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:225:THR:OG1	1:A:226:VAL:N	2.49	0.45
1:B:69:LYS:NZ	1:B:129:GLU:OE2	2.49	0.45
1:B:93:ASP:CB	1:B:242:VAL:HG11	2.45	0.45
1:A:225:THR:CG2	1:A:230:TYR:O	2.65	0.45
1:A:273:PHE:HZ	1:A:285:LYS:O	1.98	0.45
1:B:131:HIS:N	1:B:173:THR:HG21	2.31	0.45
1:B:210:ARG:CD	1:B:292:VAL:HG13	2.46	0.45
1:A:226:VAL:HG12	1:B:211:TYR:CE1	2.52	0.45
1:A:233:ARG:HG3	1:A:237:ARG:O	2.16	0.45
1:A:249:LEU:C	1:A:251:GLU:H	2.20	0.45
1:B:97:LEU:HD21	1:B:242:VAL:HG13	1.99	0.45
1:B:114:CYS:HB3	1:B:118:LYS:HB3	1.98	0.45
1:B:224:SER:HB2	1:B:241:PHE:CD2	2.51	0.45
1:A:148:ASN:CG	1:B:209:PRO:HG2	2.37	0.45
1:B:147:GLU:H	1:B:187:ARG:HH12	1.64	0.45
1:A:149:VAL:HG21	1:A:156:VAL:HB	1.97	0.44
1:A:121:ASP:OD1	1:A:125:LYS:HE3	2.17	0.44
1:A:165:HIS:HB3	2:A:305:HOH:O	2.18	0.44
1:A:288:ILE:HG23	1:B:215:VAL:HG12	2.00	0.44
1:B:100:CYS:SG	1:B:249:LEU:HB3	2.58	0.44
1:A:256:LEU:HB2	1:A:261:ILE:HD11	1.99	0.44
1:B:113:ASP:O	1:B:153:LYS:HD2	2.18	0.43
1:B:146:GLU:OE2	1:B:151:TYR:OH	2.30	0.43
1:B:210:ARG:HH22	1:B:292:VAL:HA	1.77	0.43
1:A:225:THR:CG2	1:A:231:SER:HB2	2.48	0.43
1:A:167:ARG:NH1	1:A:167:ARG:CG	2.69	0.43
1:B:104:LEU:HD11	1:B:249:LEU:HG	2.00	0.43
1:B:208:ASN:H	1:B:209:PRO:CD	2.32	0.43
1:B:279:ASP:C	1:B:281:HIS:H	2.22	0.43
1:B:149:VAL:CG1	1:B:150:ILE:N	2.82	0.43
1:A:211:TYR:HB2	1:A:212:LYS:H	1.56	0.43
1:A:269:VAL:HG11	1:A:289:PRO:CG	2.48	0.43
1:B:215:VAL:HA	1:B:294:MET:HE2	2.00	0.43
1:A:288:ILE:HG23	1:A:288:ILE:O	2.19	0.43
1:A:97:LEU:HD13	1:A:140:ILE:HG21	2.01	0.43
1:B:150:ILE:HD11	1:B:162:LEU:HD11	2.01	0.43
1:B:257:GLU:O	1:B:260:GLN:HB2	2.19	0.43
1:A:113:ASP:HA	2:A:320:HOH:O	2.18	0.42
1:A:146:GLU:O	1:A:228:GLY:CA	2.67	0.42
1:A:67:LEU:HD13	1:A:106:PHE:CD1	2.55	0.42
1:A:227:PRO:HG2	1:B:209:PRO:CB	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:118:LYS:O	1:B:118:LYS:HD3	2.19	0.42
1:A:215:VAL:N	1:B:205:THR:CG2	2.60	0.42
1:B:213:ILE:HG12	1:B:221:PHE:CD1	2.54	0.42
1:B:125:LYS:HD3	2:B:338:HOH:O	2.20	0.42
1:B:148:ASN:CA	1:B:212:LYS:HG2	2.47	0.42
1:B:206:ASP:HB3	1:B:207:ALA:H	1.70	0.42
1:B:210:ARG:NE	1:B:292:VAL:CG1	2.78	0.42
1:A:147:GLU:HG3	1:A:148:ASN:OD1	2.20	0.41
1:A:92:LYS:HD2	1:A:236:GLY:O	2.19	0.41
1:A:145:GLY:H	1:A:186:ALA:H	1.69	0.41
1:A:239:SER:HB2	2:A:317:HOH:O	2.21	0.41
1:B:66:LYS:O	1:B:134:ALA:HA	2.20	0.41
1:B:255:ASP:O	1:B:300:TYR:HE1	2.03	0.41
1:A:279:ASP:O	1:A:281:HIS:N	2.54	0.41
1:B:210:ARG:O	1:B:213:ILE:HB	2.20	0.41
1:B:233:ARG:CZ	1:B:233:ARG:CB	2.99	0.41
1:A:233:ARG:HB2	1:A:238:GLY:O	2.21	0.41
1:A:111:TYR:CE2	1:A:122:LEU:HD11	2.56	0.41
1:A:251:GLU:HB3	2:A:314:HOH:O	2.20	0.41
1:A:290:CYS:HB2	1:B:210:ARG:HH11	1.85	0.41
1:A:215:VAL:HG12	1:A:215:VAL:O	2.21	0.41
1:A:292:VAL:N	1:B:210:ARG:NH2	2.69	0.41
1:B:92:LYS:HE2	1:B:92:LYS:CA	2.50	0.41
1:B:208:ASN:N	1:B:209:PRO:CD	2.84	0.41
1:A:252:HIS:HB3	1:A:256:LEU:HG	2.03	0.41
1:B:150:ILE:CD1	1:B:162:LEU:HD11	2.51	0.41
1:A:149:VAL:HG22	1:A:156:VAL:HB	2.03	0.40
1:A:234:SER:O	1:A:235:PRO:C	2.60	0.40
1:B:163:THR:HG21	1:B:221:PHE:HE1	1.86	0.40
1:A:227:PRO:HG2	1:B:209:PRO:HB3	2.03	0.40
1:A:292:VAL:CA	1:B:210:ARG:HH21	2.23	0.40
1:B:168:GLY:O	1:B:169:ALA:C	2.60	0.40
1:A:286:LYS:HE3	1:A:286:LYS:HB2	1.86	0.40
1:A:184:GLN:HA	1:A:224:SER:HB3	2.04	0.40
1:A:225:THR:O	1:A:226:VAL:CB	2.69	0.40
1:B:213:ILE:HG23	1:B:221:PHE:CZ	2.56	0.40
1:A:225:THR:HG22	1:A:230:TYR:O	2.21	0.40
1:A:232:TRP:C	1:A:233:ARG:HD3	2.42	0.40
1:B:76:LYS:HB2	1:B:90:THR:HG21	2.04	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	223/253 (88%)	179 (80%)	29 (13%)	15 (7%)	1	1
1	B	230/253 (91%)	199 (86%)	20 (9%)	11 (5%)	2	4
All	All	453/506 (90%)	378 (83%)	49 (11%)	26 (6%)	1	2

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	214	PRO
1	A	226	VAL
1	A	227	PRO
1	B	205	THR
1	B	210	ARG
1	B	229	TYR
1	B	231	SER
1	B	274	GLU
1	A	81	VAL
1	A	148	ASN
1	A	187	ARG
1	B	233	ARG
1	A	143	SER
1	A	233	ARG
1	A	274	GLU
1	A	282	PHE
1	A	285	LYS
1	B	186	ALA
1	B	209	PRO
1	A	211	TYR
1	A	212	LYS
1	B	234	SER
1	B	215	VAL
1	A	168	GLY
1	A	235	PRO

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Mol	Chain	Res	Type
1	B	208	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	198/220 (90%)	182 (92%)	16 (8%)	11 27
1	B	204/220 (93%)	178 (87%)	26 (13%)	4 10
All	All	402/440 (91%)	360 (90%)	42 (10%)	7 16

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	59	GLN
1	A	67	LEU
1	A	123	LEU
1	A	165	HIS
1	A	173	THR
1	A	175	LEU
1	A	216	GLU
1	A	227	PRO
1	A	229	TYR
1	A	232	TRP
1	A	233	ARG
1	A	268	ARG
1	A	269	VAL
1	A	273	PHE
1	A	290	CYS
1	A	303	GLN
1	B	57	THR
1	B	66	LYS
1	B	67	LEU
1	B	81	VAL
1	B	92	LYS
1	B	95	GLU

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Mol	Chain	Res	Type
1	B	98	PHE
1	B	102	ARG
1	B	125	LYS
1	B	150	ILE
1	B	153	LYS
1	B	156	VAL
1	B	157	THR
1	B	173	THR
1	B	180	LEU
1	B	230	TYR
1	B	233	ARG
1	B	239	SER
1	B	243	GLN
1	B	255	ASP
1	B	258	ILE
1	B	264	ARG
1	B	269	VAL
1	B	279	ASP
1	B	286	LYS
1	B	297	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	74	ASN
1	A	112	ASN
1	A	120	GLN
1	A	165	HIS
1	A	243	GLN
1	A	272	HIS
1	B	63	ASN
1	B	74	ASN
1	B	148	ASN
1	B	272	HIS
1	B	303	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 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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.