



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:10 PM GMT

PDB ID : 1SHJ
Title : Caspase-7 in complex with DICA allosteric inhibitor
Authors : Hardy, J.A.; Lam, J.; Nguyen, J.T.; O'Brien, T.; Wells, J.A.
Deposited on : 2004-02-25
Resolution : 2.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

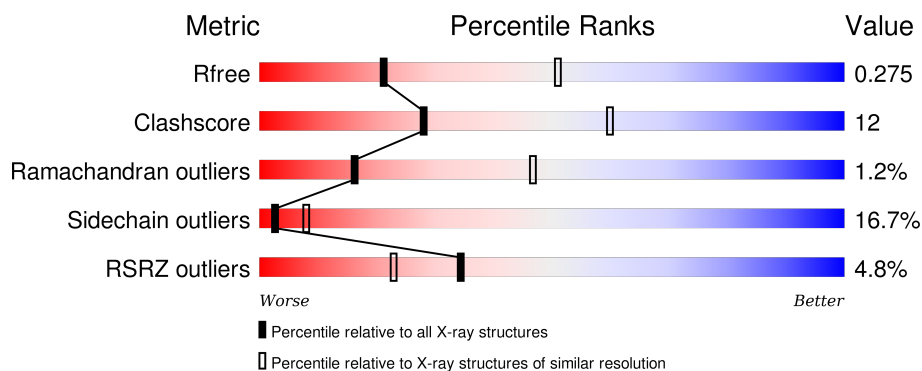
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	262	<div> <div>5%</div> <div> <div></div> <div>51%</div> <div>24%</div> <div>•</div> <div>21%</div> </div> </div>
1	B	262	<div> <div>3%</div> <div> <div></div> <div>51%</div> <div>25%</div> <div>•</div> <div>20%</div> </div> </div>

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	B	503	-	-	X	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3371 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	208	Total	C	N	O	S	4	0	0
			1662	1060	285	302	15			
1	B	209	Total	C	N	O	S	4	0	0
			1662	1062	282	303	15			

There are 18 discrepancies between the modelled and reference sequences:

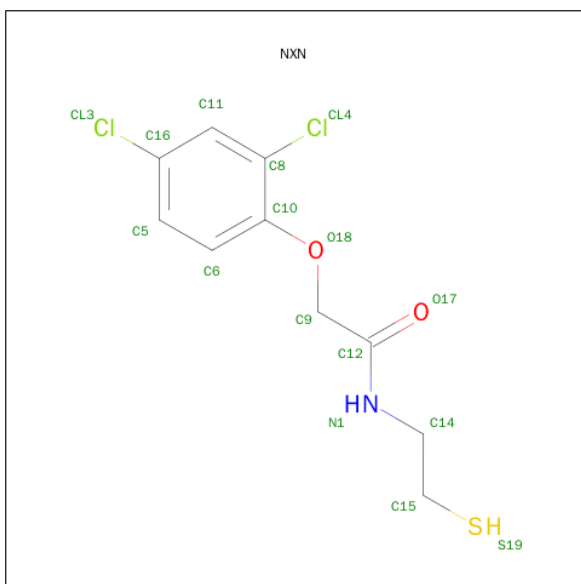
Chain	Residue	Modelled	Actual	Comment	Reference
A	169	ALA	ASP	ENGINEERED	UNP P55210
A	304	GLN	-	EXPRESSION TAG	UNP P55210
A	305	LEU	-	EXPRESSION TAG	UNP P55210
A	306	HIS	-	EXPRESSION TAG	UNP P55210
A	307	HIS	-	EXPRESSION TAG	UNP P55210
A	308	HIS	-	EXPRESSION TAG	UNP P55210
A	309	HIS	-	EXPRESSION TAG	UNP P55210
A	310	HIS	-	EXPRESSION TAG	UNP P55210
A	311	HIS	-	EXPRESSION TAG	UNP P55210
B	169	ALA	ASP	ENGINEERED	UNP P55210
B	304	GLN	-	EXPRESSION TAG	UNP P55210
B	305	LEU	-	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

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 3 is 2-(2,4-DICHLORO-PHENOXY)-N-(2-MERCAPTO-ETHYL)-ACETAMIDE (three-letter code: NXN) (formula: C₁₀H₁₁Cl₂NO₂S).

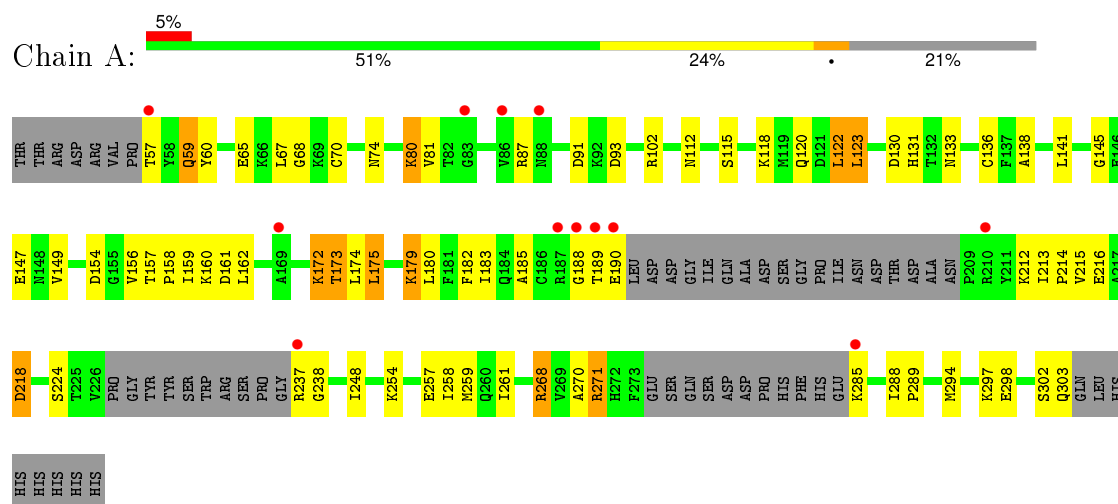


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	Cl	N	O	S	0	0
			16	10	2	1	2	1		
3	B	1	Total	C	Cl	N	O	S	0	0
			16	10	2	1	2	1		

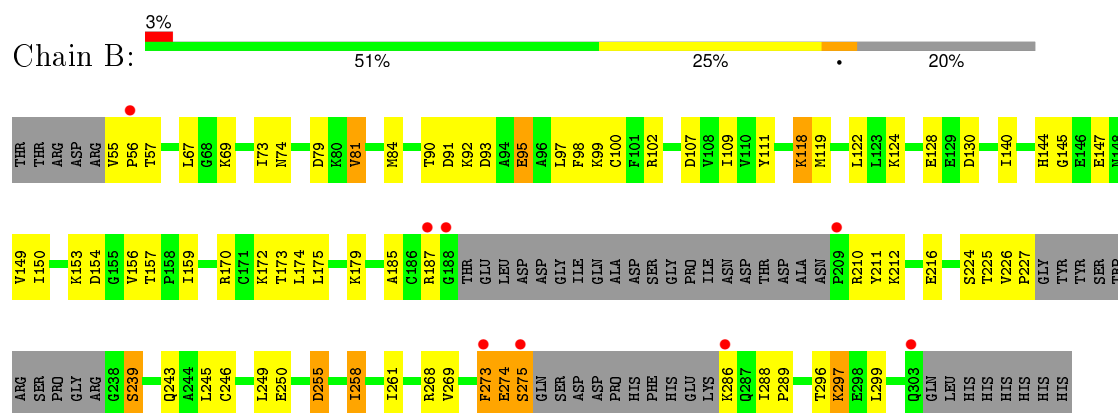
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Caspase-7



• Molecule 1: Caspase-7



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	91.10Å 91.10Å 184.47Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.80 19.98 – 2.80	Depositor EDS
% Data completeness (in resolution range)	97.3 (20.00-2.80) 97.3 (19.98-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.64 (at 2.79Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.244 , 0.287 0.231 , 0.275	Depositor DCC
R_{free} test set	1140 reflections (5.50%)	DCC
Wilson B-factor (Å ²)	64.5	Xtriage
Anisotropy	0.339	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 24.1	EDS
Estimated twinning fraction	0.021 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 22245 reflections (0.004%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3371	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.69% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NXN, 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	0.46	0/1691	0.80	7/2267 (0.3%)
1	B	0.45	0/1693	0.80	6/2274 (0.3%)
All	All	0.45	0/3384	0.80	13/4541 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	274	GLU	N-CA-C	-7.81	89.90	111.00
1	A	172	LYS	CA-CB-CG	-7.18	97.60	113.40
1	A	172	LYS	CB-CG-CD	-6.98	93.45	111.60
1	A	188	GLY	C-N-CA	-6.96	104.30	121.70
1	B	273	PHE	CB-CA-C	-6.90	96.59	110.40
1	B	130	ASP	CB-CG-OD2	6.27	123.94	118.30
1	A	218	ASP	CB-CG-OD2	5.86	123.57	118.30
1	A	91	ASP	CB-CG-OD2	5.82	123.53	118.30
1	A	154	ASP	CB-CG-OD2	5.59	123.33	118.30
1	B	107	ASP	CB-CG-OD2	5.43	123.19	118.30
1	B	255	ASP	CB-CG-OD2	5.30	123.07	118.30
1	B	154	ASP	CB-CG-OD2	5.23	123.00	118.30
1	A	130	ASP	CB-CG-OD2	5.20	122.98	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	274	GLU	Peptide

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	1662	0	1665	37	0
1	B	1662	0	1660	43	0
2	A	5	0	0	0	0
2	B	10	0	0	5	0
3	A	16	0	10	3	0
3	B	16	0	10	1	0
All	All	3371	0	3345	78	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 12.

All (78) 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:158:PRO:HG2	1:A:161:ASP:OD2	1.66	0.94
1:A:189:THR:HG22	1:A:190:GLU:H	1.33	0.93
1:B:111:TYR:CZ	1:B:122:LEU:HD11	2.08	0.89
1:B:91:ASP:HB2	2:B:503:SO4:O3	1.84	0.77
1:B:91:ASP:CB	2:B:503:SO4:O3	2.34	0.76
1:B:74:ASN:HD21	1:B:90:THR:HG23	1.50	0.75
1:A:141:LEU:HD12	1:A:183:ILE:HG12	1.70	0.73
1:B:91:ASP:N	2:B:503:SO4:O3	2.23	0.72
1:A:268:ARG:HG2	1:A:268:ARG:HH11	1.56	0.71
1:B:249:LEU:HD13	1:B:261:ILE:HG21	1.75	0.67
1:B:97:LEU:HD23	1:B:246:CYS:SG	2.36	0.66
1:B:149:VAL:HG11	1:B:156:VAL:HG13	1.78	0.65
1:B:275:SER:HB3	1:B:286:LYS:HZ1	1.62	0.65
1:B:97:LEU:HD13	1:B:140:ILE:HG21	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:THR:CG2	1:A:190:GLU:H	2.08	0.62
1:B:73:ILE:HD13	1:B:119:MET:HG2	1.83	0.61
1:A:145:GLY:HA3	1:A:185:ALA:HB1	1.84	0.59
1:A:93:ASP:OD1	1:A:238:GLY:HA3	2.03	0.59
1:A:271:ARG:HH21	1:B:55:VAL:HG11	1.68	0.58
1:A:268:ARG:HG2	1:A:268:ARG:NH1	2.18	0.57
1:A:189:THR:HG22	1:A:190:GLU:N	2.13	0.57
1:B:156:VAL:O	1:B:156:VAL:HG12	2.04	0.57
1:A:70:CYS:HA	1:A:138:ALA:O	2.04	0.57
1:A:149:VAL:CG2	1:A:156:VAL:HB	2.35	0.56
1:B:91:ASP:HB2	2:B:503:SO4:S	2.47	0.54
1:B:84:MET:HB3	1:B:144:HIS:CD2	2.42	0.54
1:B:269:VAL:CG2	1:B:289:PRO:HD3	2.37	0.54
1:B:93:ASP:OD2	1:B:239:SER:HB3	2.08	0.53
1:A:270:ALA:HB2	1:A:288:ILE:HD12	1.89	0.53
1:A:214:PRO:CD	3:A:401:NXX:CL3	2.94	0.52
1:A:215:VAL:HA	1:A:294:MET:HE3	1.91	0.52
1:B:269:VAL:HG21	1:B:289:PRO:HD3	1.91	0.51
1:A:288:ILE:HG13	1:A:289:PRO:HD2	1.92	0.51
1:B:145:GLY:HA3	1:B:185:ALA:HB1	1.92	0.51
1:B:149:VAL:CG1	1:B:156:VAL:HG13	2.40	0.51
1:B:124:LYS:HE3	1:B:128:GLU:OE2	2.11	0.51
1:B:159:ILE:HG22	3:B:401:NXX:CL3	2.48	0.50
1:B:273:PHE:HB3	1:B:286:LYS:HD3	1.93	0.50
1:A:120:GLN:NE2	1:A:162:LEU:HD23	2.27	0.50
1:B:79:ASP:HB3	1:B:81:VAL:HG23	1.94	0.48
1:A:180:LEU:HB3	1:A:182:PHE:HE1	1.79	0.48
1:A:65:GLU:HB2	1:A:133:ASN:HB3	1.95	0.48
1:B:55:VAL:O	1:B:57:THR:O	2.32	0.48
1:B:258:ILE:HG12	1:B:299:LEU:HD23	1.94	0.48
1:A:60:TYR:OH	1:A:218:ASP:OD1	2.23	0.48
1:B:118:LYS:O	1:B:122:LEU:HB2	2.14	0.47
1:A:271:ARG:NH2	1:B:55:VAL:HG11	2.29	0.47
1:B:275:SER:HB3	1:B:286:LYS:NZ	2.30	0.47
1:A:131:HIS:HB2	1:A:173:THR:HB	1.98	0.46
1:A:288:ILE:HG13	1:A:289:PRO:CD	2.46	0.46
1:B:174:LEU:O	1:B:179:LYS:NZ	2.49	0.46
1:B:156:VAL:O	1:B:156:VAL:CG1	2.64	0.45
1:B:245:LEU:O	1:B:249:LEU:HB2	2.17	0.45
1:B:97:LEU:CD1	1:B:140:ILE:HG21	2.44	0.45
1:A:180:LEU:HB3	1:A:182:PHE:CE1	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:LEU:HD12	1:A:122:LEU:HA	1.70	0.45
1:B:74:ASN:HD21	1:B:90:THR:CG2	2.24	0.45
1:B:55:VAL:O	1:B:57:THR:N	2.50	0.44
1:A:123:LEU:HD13	1:A:162:LEU:HB3	1.99	0.44
1:B:95:GLU:OE2	1:B:99:LYS:HE3	2.18	0.44
1:A:172:LYS:HA	1:A:175:LEU:HD12	2.01	0.43
1:A:214:PRO:HD2	3:A:401:NXN:CL3	2.56	0.43
1:B:111:TYR:OH	1:B:122:LEU:HD11	2.18	0.42
1:B:91:ASP:CG	2:B:503:SO4:O3	2.58	0.42
1:B:100:CYS:SG	1:B:249:LEU:HB3	2.59	0.42
1:B:288:ILE:HG12	1:B:289:PRO:HD2	2.01	0.42
1:A:268:ARG:HH11	1:A:268:ARG:CG	2.27	0.42
1:B:97:LEU:HD13	1:B:140:ILE:HD13	2.00	0.42
1:B:296:THR:C	1:B:297:LYS:HG2	2.39	0.42
1:A:257:GLU:OE1	1:A:259:MET:HB2	2.20	0.42
1:B:226:VAL:HA	1:B:227:PRO:HD3	1.83	0.42
1:A:57:THR:HG23	1:A:59:GLN:H	1.83	0.42
1:A:214:PRO:HD3	3:A:401:NXN:CL3	2.57	0.41
1:A:74:ASN:HB3	1:A:112:ASN:ND2	2.35	0.41
1:A:68:GLY:HA3	1:A:136:CYS:O	2.21	0.41
1:A:268:ARG:HD2	1:A:271:ARG:HH11	1.86	0.41
1:A:174:LEU:HB3	1:A:179:LYS:HE3	2.04	0.40
1:A:257:GLU:HG3	1:A:298:GLU:HB3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	200/262 (76%)	180 (90%)	18 (9%)	2 (1%)	19	52
1	B	201/262 (77%)	185 (92%)	13 (6%)	3 (2%)	13	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	401/524 (76%)	365 (91%)	31 (8%)	5 (1%)	16	47

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	147	GLU
1	A	80	LYS
1	B	187	ARG
1	A	81	VAL
1	B	56	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	182/230 (79%)	151 (83%)	31 (17%)	2	7
1	B	183/230 (80%)	153 (84%)	30 (16%)	3	8
All	All	365/460 (79%)	304 (83%)	61 (17%)	3	8

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	59	GLN
1	A	67	LEU
1	A	80	LYS
1	A	87	ARG
1	A	102	ARG
1	A	115	SER
1	A	118	LYS
1	A	122	LEU
1	A	123	LEU
1	A	147	GLU
1	A	157	THR
1	A	159	ILE
1	A	160	LYS

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Mol	Chain	Res	Type
1	A	173	THR
1	A	175	LEU
1	A	179	LYS
1	A	212	LYS
1	A	213	ILE
1	A	216	GLU
1	A	224	SER
1	A	237	ARG
1	A	248	ILE
1	A	254	LYS
1	A	258	ILE
1	A	261	ILE
1	A	268	ARG
1	A	271	ARG
1	A	285	LYS
1	A	297	LYS
1	A	302	SER
1	A	303	GLN
1	B	67	LEU
1	B	69	LYS
1	B	81	VAL
1	B	92	LYS
1	B	95	GLU
1	B	98	PHE
1	B	102	ARG
1	B	109	ILE
1	B	118	LYS
1	B	150	ILE
1	B	153	LYS
1	B	157	THR
1	B	170	ARG
1	B	172	LYS
1	B	173	THR
1	B	175	LEU
1	B	210	ARG
1	B	211	TYR
1	B	212	LYS
1	B	216	GLU
1	B	224	SER
1	B	225	THR
1	B	239	SER
1	B	243	GLN

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Mol	Chain	Res	Type
1	B	250	GLU
1	B	255	ASP
1	B	258	ILE
1	B	268	ARG
1	B	275	SER
1	B	297	LYS

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

Mol	Chain	Res	Type
1	A	74	ASN
1	A	112	ASN
1	A	120	GLN
1	A	243	GLN
1	B	74	ASN
1	B	112	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

5 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
3	NXN	A	401	1	16,16,16	0.71	1 (6%)	19,20,20	1.09	1 (5%)
2	SO4	A	502	-	4,4,4	0.12	0	6,6,6	0.18	0
3	NXN	B	401	1	16,16,16	0.98	2 (12%)	19,20,20	0.99	1 (5%)
2	SO4	B	501	-	4,4,4	0.07	0	6,6,6	0.19	0
2	SO4	B	503	-	4,4,4	0.20	0	6,6,6	0.26	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	NXN	A	401	1	-	0/9/9/9	0/1/1/1
2	SO4	A	502	-	-	0/0/0/0	0/0/0/0
3	NXN	B	401	1	-	0/9/9/9	0/1/1/1
2	SO4	B	501	-	-	0/0/0/0	0/0/0/0
2	SO4	B	503	-	-	0/0/0/0	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	401	NXN	C8-CL4	2.10	1.78	1.73
3	B	401	NXN	C8-CL4	2.24	1.79	1.73
3	B	401	NXN	C16-CL3	2.37	1.79	1.74

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	401	NXN	C9-O18-C10	3.49	125.55	117.58
3	A	401	NXN	C9-O18-C10	3.52	125.61	117.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	401	NXN	3	0
3	B	401	NXN	1	0
2	B	503	SO4	5	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	208/262 (79%)	-0.11	12 (5%) 26 16	36, 58, 98, 134	1 (0%)
1	B	209/262 (79%)	-0.22	8 (3%) 44 32	39, 57, 91, 118	2 (0%)
All	All	417/524 (79%)	-0.17	20 (4%) 34 23	36, 58, 95, 134	3 (0%)

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	189	THR	7.2
1	B	188	GLY	6.9
1	A	188	GLY	5.8
1	A	190	GLU	4.0
1	B	187	ARG	4.0
1	A	237	ARG	3.6
1	A	187	ARG	3.2
1	A	88	ASN	3.2
1	A	285	LYS	3.1
1	B	303	GLN	3.0
1	B	275	SER	2.9
1	A	210	ARG	2.3
1	A	169	ALA	2.3
1	B	273	PHE	2.3
1	B	56	PRO	2.2
1	B	209	PRO	2.1
1	A	86	VAL	2.1
1	A	57	THR	2.1
1	B	286	LYS	2.0
1	A	83	GLY	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	LLDF	B-factors(\AA^2)	Q<0.9
2	SO4	B	503	5/5	0.92	0.52	6.66	80,80,84,85	0
2	SO4	B	501	5/5	0.97	0.25	1.16	82,83,87,88	0
3	NXN	B	401	16/16	0.96	0.12	-0.76	51,55,59,62	0
2	SO4	A	502	5/5	0.97	0.11	-0.98	78,78,80,81	0
3	NXN	A	401	16/16	0.96	0.12	-1.30	48,54,60,64	0

6.5 Other polymers [i](#)

There are no such residues in this entry.