



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2018 – 01:21 am GMT

PDB ID : 4JRP
Title : Structure of E. coli Exonuclease I in complex with a 5cy-dT13 oligonucleotide
Authors : Bell, C.E.
Deposited on : 2013-03-21
Resolution : 1.95 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.3 (157068), CSD as539be (2018)
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

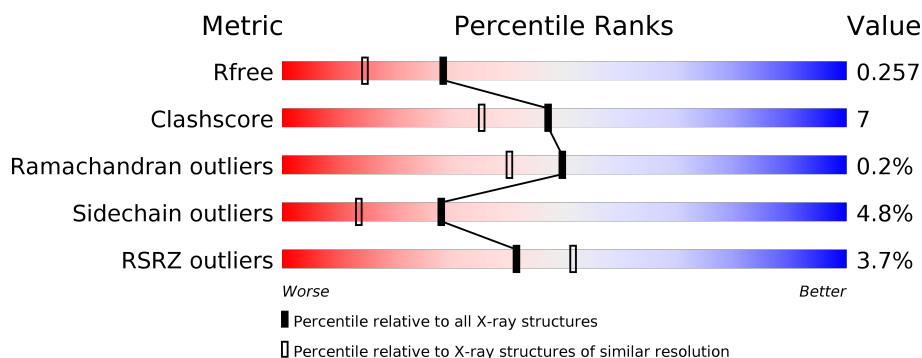
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	2220 (1.96-1.96)
Clashscore	122126	2333 (1.96-1.96)
Ramachandran outliers	120053	2314 (1.96-1.96)
Sidechain outliers	120020	2314 (1.96-1.96)
RSRZ outliers	108989	2174 (1.96-1.96)

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	C	14	
1	D	14	
2	A	478	
2	B	478	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 8474 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 DNA chain called 5cy-dT13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	14	Total	C	N	O	P	0	0	0
			295	161	28	93	13			
1	D	14	Total	C	N	O	P	0	0	0
			295	161	28	93	13			

- Molecule 2 is a protein called Exodeoxyribonuclease I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	460	Total	C	N	O	S	0	0	0
			3684	2350	647	673	14			
2	B	465	Total	C	N	O	S	0	0	0
			3708	2369	644	681	14			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	EXPRESSION TAG	UNP P04995
A	-1	SER	-	EXPRESSION TAG	UNP P04995
A	0	HIS	-	EXPRESSION TAG	UNP P04995
B	-2	GLY	-	EXPRESSION TAG	UNP P04995
B	-1	SER	-	EXPRESSION TAG	UNP P04995
B	0	HIS	-	EXPRESSION TAG	UNP P04995

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	1	Total	Mg	0	0
			1	1		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



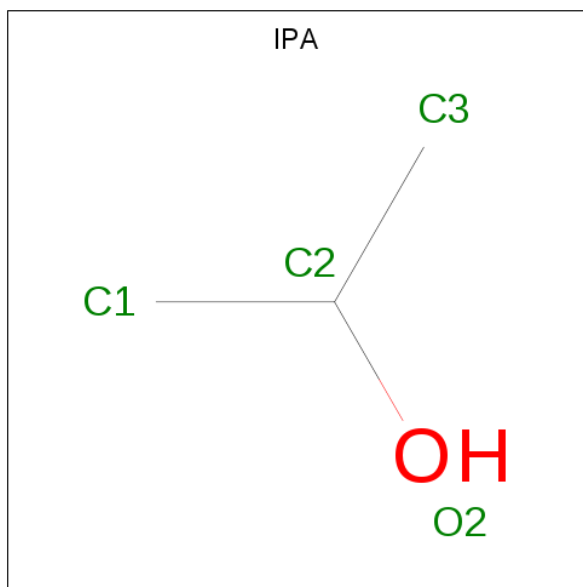
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total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

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is ISOPROPYL ALCOHOL (three-letter code: IPA) (formula: C_3H_8O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			4	3	1		

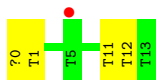
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	C	15	Total 15	O 15	0	0
7	D	19	Total 19	O 19	0	0
7	A	207	Total 207	O 207	0	0
7	B	164	Total 164	O 164	0	0

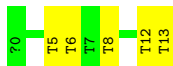
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

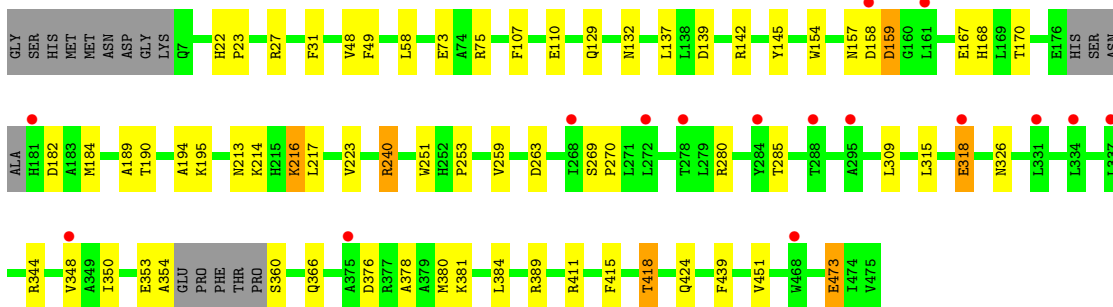
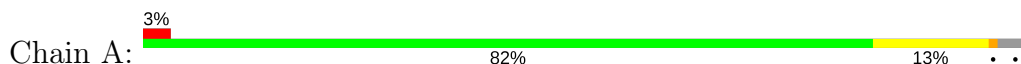
- Molecule 1: 5cy-dT13



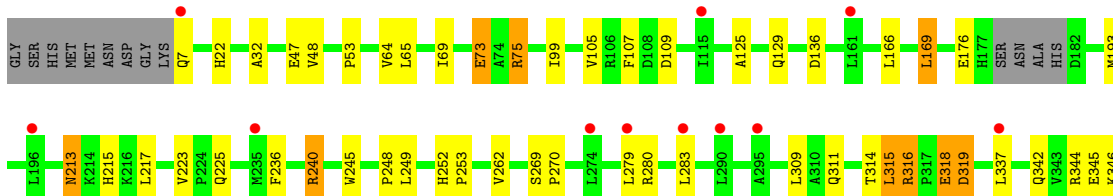
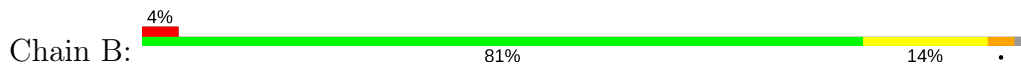
- Molecule 1: 5cy-dT13

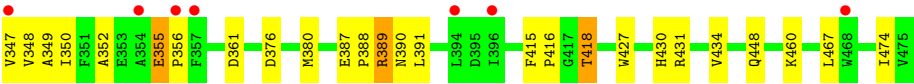


- Molecule 2: Exodeoxyribonuclease I



- Molecule 2: Exodeoxyribonuclease I





4 Data and refinement statistics

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α , β , γ	91.30Å 91.30Å 159.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.58 – 1.95 36.58 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.1 (36.58-1.95) 99.1 (36.58-1.95)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.213 , 0.259 0.214 , 0.257	Depositor DCC
R_{free} test set	4738 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	27.7	Xtriage
Anisotropy	0.143	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 31.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.216 for h,-k,-l	Xtriage
Reported twinning fraction	0.768 for H, K, L 0.232 for K, H, -L	Depositor
Outliers	0 of 94045 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8474	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.80% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, MG, IPA, SO4, 5CY

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	C	0.39	0/285	0.77	0/438
1	D	0.35	0/285	0.71	0/438
2	A	0.42	0/3778	0.61	0/5145
2	B	0.40	0/3805	0.61	0/5189
All	All	0.41	0/8153	0.62	0/11210

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	295	0	196	6	0
1	D	295	0	195	4	0
2	A	3684	0	3543	46	0
2	B	3708	0	3556	53	0
3	C	1	0	0	0	0
4	A	25	0	0	0	0
4	B	45	0	0	1	0
5	A	12	0	16	0	0
6	B	4	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	207	0	0	4	0
7	B	164	0	0	3	0
7	C	15	0	0	0	0
7	D	19	0	0	0	0
All	All	8474	0	7514	104	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 7.

All (104) 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)
2:A:411:ARG:HH21	2:A:418:THR:CG2	1.81	0.93
2:A:411:ARG:HH21	2:A:418:THR:HG23	1.38	0.89
2:A:48:VAL:HG23	2:A:184:MET:CE	2.10	0.82
2:A:418:THR:HG21	7:A:660:HOH:O	1.80	0.80
2:A:213:ASN:HB3	2:A:216:LYS:HB2	1.68	0.76
2:B:22:HIS:HB3	4:B:503:SO4:O3	1.85	0.75
2:A:48:VAL:HG23	2:A:184:MET:HE3	1.67	0.74
2:B:107:PHE:HB3	7:B:650:HOH:O	1.86	0.74
2:A:195:LYS:NZ	7:A:647:HOH:O	2.23	0.70
2:B:213:ASN:ND2	2:B:215:HIS:H	1.89	0.70
2:B:213:ASN:HD22	2:B:215:HIS:H	1.40	0.69
2:B:262:VAL:HG11	2:B:337:LEU:HD11	1.76	0.67
2:A:253:PRO:HB3	2:B:348:VAL:HG11	1.77	0.66
2:A:344:ARG:O	2:A:348:VAL:HG23	1.97	0.65
2:B:418:THR:HG23	7:B:663:HOH:O	1.97	0.64
2:B:342:GLN:HA	2:B:345:GLU:OE1	2.00	0.62
2:A:217:LEU:HD22	2:A:309:LEU:HD12	1.82	0.62
2:A:48:VAL:CG2	2:A:184:MET:CE	2.78	0.61
2:B:427:TRP:NE1	2:B:431:ARG:HD2	2.16	0.61
2:B:213:ASN:HD22	2:B:215:HIS:N	1.99	0.60
1:C:11:DT:H4'	1:C:12:DT:OP1	2.02	0.60
2:A:48:VAL:CG2	2:A:184:MET:HE2	2.32	0.59
2:B:415:PHE:O	2:B:418:THR:HB	2.02	0.58
2:B:280:ARG:HG3	2:B:350:ILE:HG23	1.85	0.58
2:A:170:THR:HG21	2:A:189:ALA:HB1	1.86	0.57
2:A:360:SER:O	2:A:366:GLN:NE2	2.37	0.57
1:D:5:DT:H2'	1:D:6:DT:C6	2.40	0.56
2:A:280:ARG:HH11	2:A:350:ILE:HA	1.70	0.56
2:A:73:GLU:OE1	7:A:712:HOH:O	2.18	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:415:PHE:O	2:A:418:THR:HB	2.05	0.56
1:D:8:DT:C4	2:B:356:PRO:HG3	2.41	0.55
2:B:64:VAL:HG21	2:B:467:LEU:HD21	1.88	0.55
2:A:353:GLU:O	2:A:354:ALA:HB2	2.07	0.54
2:B:311:GLN:O	2:B:314:THR:OG1	2.14	0.53
2:B:69:ILE:HG23	2:B:73:GLU:HG2	1.91	0.53
2:A:137:LEU:HD12	2:A:190:THR:CG2	2.39	0.52
2:B:213:ASN:HD21	2:B:215:HIS:CD2	2.27	0.52
1:C:0:5CY:H38	1:C:1:DT:H5'	1.91	0.52
2:B:418:THR:CG2	7:B:663:HOH:O	2.56	0.52
2:A:251:TRP:CZ3	2:A:259:VAL:HB	2.45	0.52
2:B:315:LEU:CD2	2:B:319:ASP:HB2	2.40	0.52
2:A:48:VAL:HG23	2:A:184:MET:HE2	1.88	0.51
2:A:353:GLU:O	2:A:354:ALA:CB	2.59	0.51
1:C:0:5CY:C27	1:C:0:5CY:H24	2.40	0.51
2:A:157:ASN:C	2:A:159:ASP:H	2.13	0.51
2:A:240:ARG:NH2	2:A:263:ASP:OD2	2.40	0.51
2:B:99:ILE:HD12	2:B:99:ILE:N	2.25	0.51
2:A:411:ARG:HH21	2:A:418:THR:HG22	1.72	0.50
2:B:236:PHE:HB3	2:B:240:ARG:HD2	1.94	0.49
2:B:75:ARG:CG	2:B:75:ARG:HH11	2.25	0.49
2:A:137:LEU:HD11	2:A:194:ALA:HB2	1.93	0.49
2:A:139:ASP:OD1	2:A:142:ARG:HD2	2.13	0.48
2:B:32:ALA:HA	2:B:47:GLU:O	2.13	0.48
1:D:13:DT:H5'	2:B:107:PHE:CE2	2.49	0.48
2:A:48:VAL:CG2	2:A:184:MET:HE3	2.39	0.47
2:B:315:LEU:HD23	2:B:319:ASP:HB2	1.97	0.47
2:B:344:ARG:O	2:B:348:VAL:HG22	2.15	0.47
2:B:416:PRO:C	2:B:418:THR:H	2.18	0.47
2:A:137:LEU:HD12	2:A:190:THR:HG22	1.96	0.47
2:B:316:ARG:HB3	2:B:318:GLU:HG2	1.95	0.47
2:B:387:GLU:HB3	2:B:390:ASN:HD22	1.78	0.47
2:B:355:GLU:HG3	2:B:356:PRO:HD2	1.97	0.46
2:A:27:ARG:NE	7:A:664:HOH:O	2.43	0.46
1:C:1:DT:OP1	2:A:214:LYS:NZ	2.43	0.46
2:A:344:ARG:HG2	2:B:352:ALA:HB1	1.97	0.46
2:B:125:ALA:HB1	2:B:129:GLN:HE21	1.81	0.45
2:A:411:ARG:NH2	2:A:418:THR:HG23	2.19	0.45
2:A:145:TYR:HD1	2:A:154:TRP:CG	2.35	0.45
2:A:269:SER:N	2:A:270:PRO:HD2	2.32	0.45
2:B:252:HIS:HA	2:B:253:PRO:HD3	1.84	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:388:PRO:HA	2:B:391:LEU:HD12	1.99	0.44
2:A:107:PHE:O	2:A:110:GLU:HB2	2.17	0.44
2:B:316:ARG:HE	2:B:316:ARG:HB2	1.40	0.44
2:B:346:LYS:O	2:B:349:ALA:HB3	2.17	0.44
1:D:12:DT:H2'	1:D:12:DT:O2	2.17	0.44
2:B:387:GLU:HG3	2:B:389:ARG:HG2	2.00	0.44
2:A:22:HIS:HA	2:A:23:PRO:HD3	1.82	0.43
2:B:347:VAL:HA	2:B:350:ILE:HD12	2.00	0.43
2:B:223:VAL:HG22	2:B:248:PRO:HB2	2.00	0.43
2:B:169:LEU:HB3	2:B:193:MET:SD	2.58	0.43
2:B:65:LEU:HD22	2:B:460:LYS:HG2	1.99	0.43
2:B:105:VAL:HA	2:B:109:ASP:OD2	2.19	0.43
2:B:105:VAL:HG23	2:B:136:ASP:HB2	2.00	0.43
2:A:159:ASP:OD2	2:A:159:ASP:N	2.51	0.43
2:A:223:VAL:O	2:A:344:ARG:NH2	2.51	0.43
2:B:213:ASN:HD21	2:B:215:HIS:HD2	1.67	0.43
2:B:53:PRO:HD2	2:B:75:ARG:HD3	2.01	0.43
2:B:279:LEU:HD23	2:B:350:ILE:HD11	2.01	0.42
2:A:75:ARG:HH22	2:A:473:GLU:CD	2.22	0.42
2:A:376:ASP:O	2:A:380:MET:HG3	2.19	0.42
2:A:58:LEU:HD12	2:A:439:PHE:HE2	1.84	0.42
2:B:269:SER:N	2:B:270:PRO:HD2	2.34	0.42
2:B:431:ARG:NH2	2:B:474:ILE:O	2.53	0.42
2:B:430:HIS:O	2:B:434:VAL:HG23	2.20	0.41
1:C:11:DT:H2''	1:C:12:DT:O5'	2.19	0.41
2:A:378:ALA:O	2:A:381:LYS:HB3	2.21	0.41
2:B:217:LEU:HD22	2:B:309:LEU:HD12	2.03	0.41
2:B:75:ARG:HG2	2:B:75:ARG:NH1	2.36	0.41
2:A:129:GLN:O	2:A:132:ASN:HB2	2.20	0.41
2:A:31:PHE:CD2	2:A:49:PHE:CZ	3.09	0.41
1:C:0:5CY:H10	1:C:0:5CY:H40	2.02	0.40
2:B:75:ARG:CG	2:B:75:ARG:NH1	2.84	0.40
2:B:376:ASP:O	2:B:380:MET:HG3	2.21	0.40
2:A:318:GLU:H	2:A:318:GLU:CD	2.24	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	
2	A	454/478 (95%)	438 (96%)	15 (3%)	1 (0%)	49	40
2	B	461/478 (96%)	450 (98%)	10 (2%)	1 (0%)	49	40
All	All	915/956 (96%)	888 (97%)	25 (3%)	2 (0%)	49	40

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	176	GLU
2	A	182	ASP

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	
2	A	380/409 (93%)	364 (96%)	16 (4%)	32	18
2	B	383/409 (94%)	362 (94%)	21 (6%)	24	11
All	All	763/818 (93%)	726 (95%)	37 (5%)	28	13

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	158	ASP
2	A	159	ASP
2	A	167	GLU
2	A	168	HIS

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Mol	Chain	Res	Type
2	A	216	LYS
2	A	240	ARG
2	A	285	THR
2	A	315	LEU
2	A	318	GLU
2	A	326	ASN
2	A	384	LEU
2	A	389	ARG
2	A	418	THR
2	A	424	GLN
2	A	451	VAL
2	A	473	GLU
2	B	7	GLN
2	B	48	VAL
2	B	73	GLU
2	B	75	ARG
2	B	166	LEU
2	B	169	LEU
2	B	213	ASN
2	B	225	GLN
2	B	240	ARG
2	B	245	TRP
2	B	249	LEU
2	B	283	LEU
2	B	315	LEU
2	B	316	ARG
2	B	318	GLU
2	B	319	ASP
2	B	355	GLU
2	B	361	ASP
2	B	389	ARG
2	B	418	THR
2	B	448	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	225	GLN
2	A	326	ASN
2	A	328	GLN
2	A	340	ASN
2	A	369	ASN

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Mol	Chain	Res	Type
2	A	424	GLN
2	B	60	GLN
2	B	103	ASN
2	B	129	GLN
2	B	213	ASN
2	B	242	ASN
2	B	369	ASN
2	B	390	ASN
2	B	448	GLN
2	B	452	GLN
2	B	453	GLN

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](#)

Of 18 ligands modelled in this entry, 1 is monoatomic - leaving 17 for Mogul analysis.

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	$\# Z > 2$
4	SO4	A	501	-	4,4,4	0.42	0	6,6,6	0.33	0
4	SO4	A	502	-	4,4,4	0.39	0	6,6,6	0.21	0
4	SO4	A	503	-	4,4,4	0.40	0	6,6,6	0.17	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	SO4	A	504	-	4,4,4	0.41	0	6,6,6	0.12	0
4	SO4	A	505	-	4,4,4	0.41	0	6,6,6	0.19	0
5	GOL	A	506	-	5,5,5	0.23	0	5,5,5	0.34	0
5	GOL	A	507	-	5,5,5	0.29	0	5,5,5	0.60	0
4	SO4	B	501	-	4,4,4	0.46	0	6,6,6	0.14	0
4	SO4	B	502	-	4,4,4	0.42	0	6,6,6	0.14	0
4	SO4	B	503	-	4,4,4	0.41	0	6,6,6	0.23	0
4	SO4	B	504	-	4,4,4	0.41	0	6,6,6	0.19	0
4	SO4	B	505	-	4,4,4	0.42	0	6,6,6	0.08	0
4	SO4	B	506	-	4,4,4	0.41	0	6,6,6	0.10	0
4	SO4	B	507	-	4,4,4	0.42	0	6,6,6	0.07	0
4	SO4	B	508	-	4,4,4	0.42	0	6,6,6	0.06	0
4	SO4	B	509	-	4,4,4	0.43	0	6,6,6	0.09	0
6	IPA	B	510	-	3,3,3	0.57	0	3,3,3	0.13	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
4	SO4	A	501	-	-	0/0/0/0	0/0/0/0
4	SO4	A	502	-	-	0/0/0/0	0/0/0/0
4	SO4	A	503	-	-	0/0/0/0	0/0/0/0
4	SO4	A	504	-	-	0/0/0/0	0/0/0/0
4	SO4	A	505	-	-	0/0/0/0	0/0/0/0
5	GOL	A	506	-	-	0/4/4/4	0/0/0/0
5	GOL	A	507	-	-	0/4/4/4	0/0/0/0
4	SO4	B	501	-	-	0/0/0/0	0/0/0/0
4	SO4	B	502	-	-	0/0/0/0	0/0/0/0
4	SO4	B	503	-	-	0/0/0/0	0/0/0/0
4	SO4	B	504	-	-	0/0/0/0	0/0/0/0
4	SO4	B	505	-	-	0/0/0/0	0/0/0/0
4	SO4	B	506	-	-	0/0/0/0	0/0/0/0
4	SO4	B	507	-	-	0/0/0/0	0/0/0/0
4	SO4	B	508	-	-	0/0/0/0	0/0/0/0
4	SO4	B	509	-	-	0/0/0/0	0/0/0/0
6	IPA	B	510	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	503	SO4	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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	C	13/14 (92%)	0.17	1 (7%) 13 21	37, 54, 98, 109	0
1	D	13/14 (92%)	-0.04	0 100 100	33, 45, 70, 89	0
2	A	460/478 (96%)	0.38	16 (3%) 44 54	24, 39, 71, 91	0
2	B	465/478 (97%)	0.38	18 (3%) 39 49	26, 40, 68, 86	0
All	All	951/984 (96%)	0.37	35 (3%) 41 51	24, 40, 71, 109	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	357	PHE	5.4
2	A	284	TYR	4.7
2	B	290	LEU	4.2
2	B	356	PRO	4.0
2	B	396	ILE	3.2
2	B	283	LEU	3.2
2	A	337	LEU	3.1
2	B	279	LEU	3.0
2	A	268	ILE	2.9
2	A	295	ALA	2.9
2	A	468	TRP	2.8
2	A	272	LEU	2.7
2	A	375	ALA	2.7
2	B	468	TRP	2.7
2	B	354	ALA	2.7
2	A	161	LEU	2.7
2	B	295	ALA	2.6
2	B	7	GLN	2.6
2	A	158	ASP	2.6
2	A	288	THR	2.6
2	B	115	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
2	A	181	HIS	2.4
2	B	161	LEU	2.3
2	A	348	VAL	2.3
2	A	278	THR	2.3
2	B	274	LEU	2.2
2	B	337	LEU	2.1
2	A	318	GLU	2.1
2	A	334	LEU	2.1
2	B	394	LEU	2.1
1	C	5	DT	2.1
2	A	331	LEU	2.1
2	B	347	VAL	2.0
2	B	196	LEU	2.0
2	B	235	MET	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. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	SO4	B	507	5/5	0.67	0.20	136,137,139,140	0
4	SO4	B	505	5/5	0.82	0.25	111,115,116,117	0
4	SO4	B	508	5/5	0.83	0.16	114,115,116,117	0
4	SO4	A	505	5/5	0.84	0.23	86,90,92,93	0
4	SO4	A	503	5/5	0.89	0.14	68,77,80,82	0
6	IPA	B	510	4/4	0.89	0.22	43,44,47,48	0
4	SO4	B	509	5/5	0.93	0.09	74,76,79,80	0
4	SO4	A	504	5/5	0.93	0.10	92,94,97,97	0
4	SO4	B	504	5/5	0.94	0.13	56,61,65,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	SO4	B	506	5/5	0.94	0.20	115,115,118,119	0
5	GOL	A	506	6/6	0.95	0.08	51,58,60,62	0
4	SO4	A	502	5/5	0.96	0.10	74,75,76,76	0
4	SO4	B	501	5/5	0.97	0.08	47,49,53,54	0
5	GOL	A	507	6/6	0.97	0.08	36,39,41,43	0
4	SO4	B	503	5/5	0.97	0.14	63,65,66,67	0
4	SO4	B	502	5/5	0.98	0.09	54,56,56,59	0
3	MG	C	101	1/1	0.99	0.06	42,42,42,42	0
4	SO4	A	501	5/5	0.99	0.10	37,38,39,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.