Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 08:16 pm BST

PDB ID	:	4AI8
Title	:	FACTOR INHIBITING HIF-1 ALPHA IN COMPLEX WITH DAMINOZIDE
Authors	:	King, O.N.F.; Chowdhury, R.; Rose, N.R.; McDonough, M.A.; Clifton, I.J.; Schofield, C.J.; Kawamura, A.
Deposited on	:	2012-02-08
Resolution	:	2.40 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 ①) were used in the production of this report:

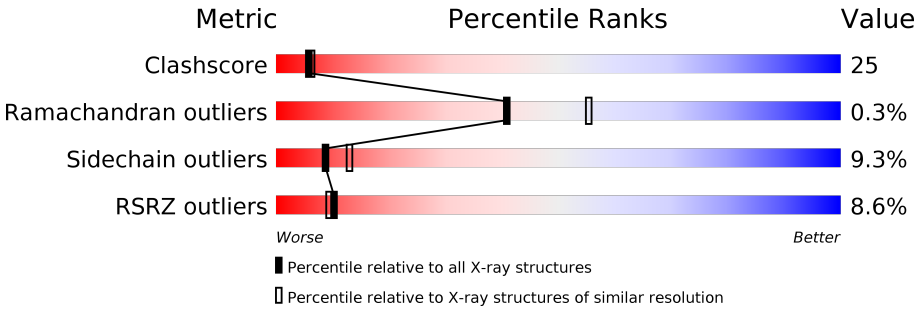
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.40 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	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 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	352	8%, 59%, 32%, 6%

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	A	1353	-	-	X	-
3	GOL	A	1355	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 2897 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.

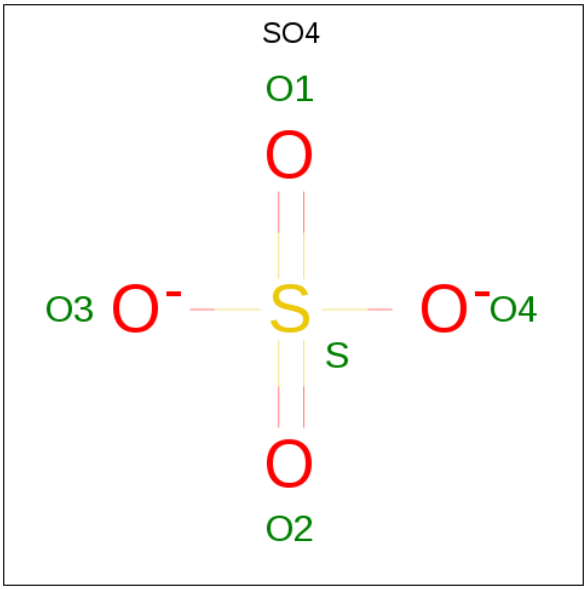
- Molecule 1 is a protein called HYPOXIA-INDUCIBLE FACTOR 1-ALPHA INHIBITOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	339	Total	C	N	O	S	0	0	0
			2707	1738	458	500	11			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q9NWT6
A	-1	SER	-	expression tag	UNP Q9NWT6
A	0	HIS	-	expression tag	UNP Q9NWT6

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

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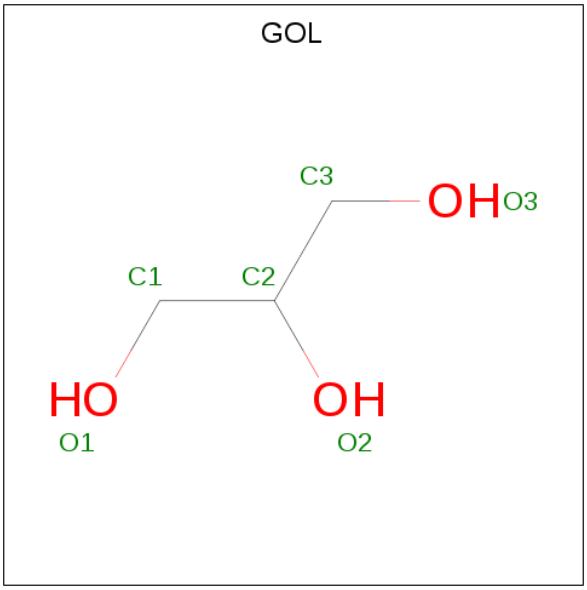
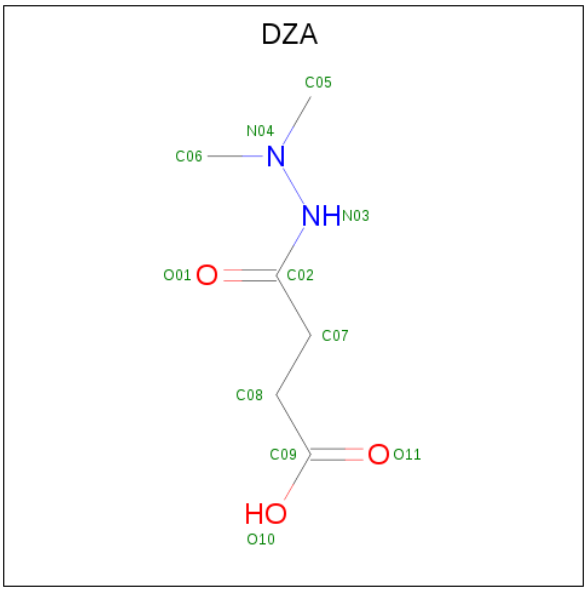
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 4 is DAMINOZIDE (three-letter code: DZA) (formula: $C_6H_{12}N_2O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O 11 6 2 3	0	0

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Zn 1 1	0	0

- Molecule 6 is water.

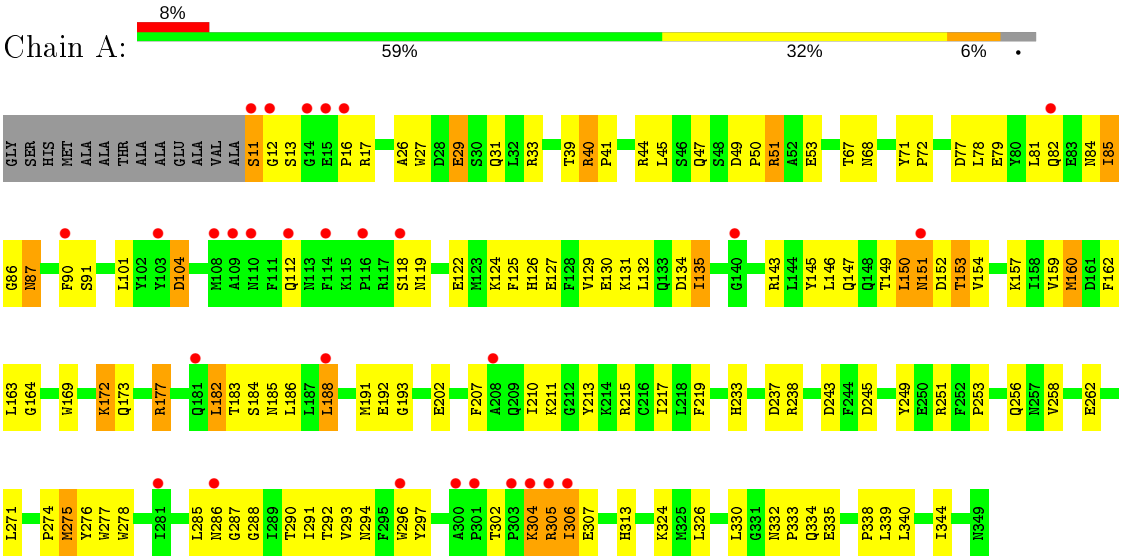
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	135	Total O 135 135	0	0

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 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: HYPOXIA-INDUCIBLE FACTOR 1-ALPHA INHIBITOR

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	86.76Å 86.76Å 145.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.37 – 2.40 28.36 – 2.40	Depositor EDS
% Data completeness (in resolution range)	97.8 (28.37-2.40) 83.9 (28.36-2.40)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.63 (at 2.39Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.231 , 0.248 0.241 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	48.5	Xtriage
Anisotropy	0.222	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 54.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	2897	wwPDB-VP
Average B, all atoms (Å^2)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.52% 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

Bond lengths and bond angles in the following residue types are not validated in this section: DZA, GOL, ZN, 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	0.43	0/2789	0.69	0/3797

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

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	2707	0	2534	135	1
2	A	25	0	0	3	0
3	A	18	0	24	0	0
4	A	11	0	11	0	0
5	A	1	0	0	0	0
6	A	135	0	0	5	0
All	All	2897	0	2569	135	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 25.

All (135) 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:332:ASN:HD21	1:A:334:GLN:HB2	1.13	1.14
1:A:125:PHE:O	1:A:129:VAL:HG23	1.61	1.01
1:A:160:MET:HA	1:A:160:MET:HE2	1.41	0.97
1:A:51:ARG:HH11	1:A:51:ARG:HG2	1.26	0.96
1:A:84:ASN:OD1	1:A:157:LYS:HD2	1.67	0.94
1:A:304:LYS:HG3	1:A:305:ARG:N	1.87	0.90
1:A:126:HIS:O	1:A:130:GLU:HG3	1.75	0.86
1:A:81:LEU:O	1:A:85:ILE:HG22	1.75	0.86
1:A:51:ARG:HH11	1:A:51:ARG:CG	1.90	0.85
1:A:182:LEU:HD12	1:A:182:LEU:C	1.97	0.84
1:A:51:ARG:NH1	1:A:51:ARG:HG2	1.91	0.82
1:A:304:LYS:HG3	1:A:305:ARG:H	1.42	0.82
1:A:151:ASN:ND2	1:A:153:THR:CG2	2.44	0.80
1:A:31:GLN:O	1:A:285:LEU:HD12	1.80	0.80
1:A:173:GLN:OE1	1:A:177:ARG:NH1	2.13	0.80
1:A:151:ASN:HD21	1:A:153:THR:CG2	1.95	0.78
1:A:160:MET:HE2	1:A:160:MET:CA	2.13	0.78
1:A:53:GLU:OE1	1:A:177:ARG:NH1	2.16	0.77
1:A:326:LEU:HD11	1:A:339:LEU:HD23	1.69	0.74
1:A:160:MET:HE2	1:A:163:LEU:HD12	1.69	0.74
1:A:332:ASN:HD21	1:A:334:GLN:CB	1.98	0.73
1:A:151:ASN:HD21	1:A:153:THR:HG21	1.53	0.73
1:A:183:THR:HB	1:A:296:TRP:CD1	2.24	0.72
1:A:183:THR:CG2	1:A:296:TRP:HE1	2.03	0.71
1:A:147:GLN:HG2	1:A:188:LEU:HD23	1.72	0.71
1:A:91:SER:HA	1:A:122:GLU:OE1	1.91	0.71
1:A:332:ASN:ND2	1:A:334:GLN:HB2	1.98	0.70
1:A:172:LYS:HB3	6:A:2063:HOH:O	1.93	0.68
1:A:29:GLU:OE1	1:A:29:GLU:N	2.26	0.68
1:A:124:LYS:HB2	1:A:127:GLU:HG3	1.75	0.67
1:A:215:ARG:NE	1:A:262:GLU:OE2	2.27	0.67
1:A:33:ARG:NH2	1:A:193:GLY:O	2.26	0.67
1:A:151:ASN:ND2	1:A:153:THR:HG22	2.10	0.66
1:A:160:MET:HA	1:A:160:MET:CE	2.23	0.66
1:A:71:TYR:HB3	1:A:72:PRO:HD3	1.78	0.65
1:A:183:THR:HG21	1:A:296:TRP:HE1	1.59	0.65
1:A:182:LEU:HD12	1:A:184:SER:N	2.13	0.64
1:A:202:GLU:O	1:A:275:MET:CE	2.45	0.63
1:A:160:MET:CE	1:A:163:LEU:HD12	2.28	0.63
1:A:39:THR:O	1:A:40:ARG:HD3	1.98	0.63
1:A:219:PHE:HB2	1:A:278:TRP:HB2	1.80	0.62
1:A:154:VAL:HG23	1:A:159:VAL:HG23	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:210:ILE:CD1	1:A:293:VAL:HG23	2.30	0.62
1:A:211:LYS:CD	1:A:291:ILE:HD12	2.29	0.62
1:A:192:GLU:HB3	1:A:288:GLY:O	2.01	0.61
1:A:192:GLU:OE1	1:A:286:ASN:C	2.39	0.60
1:A:11:SER:HB3	1:A:41:PRO:HD3	1.83	0.60
1:A:192:GLU:HG3	2:A:1353:SO4:O3	2.01	0.60
1:A:182:LEU:CD1	1:A:182:LEU:C	2.70	0.60
1:A:13:SER:HB2	1:A:27:TRP:CH2	2.37	0.60
1:A:182:LEU:HB2	1:A:297:TYR:CE1	2.37	0.59
1:A:324:LYS:CE	2:A:1352:SO4:O1	2.51	0.59
1:A:160:MET:CA	1:A:160:MET:CE	2.79	0.59
1:A:274:PRO:HB2	1:A:277:TRP:CD1	2.38	0.59
1:A:86:GLY:O	6:A:2040:HOH:O	2.16	0.59
1:A:151:ASN:CG	1:A:153:THR:HG22	2.24	0.58
1:A:330:LEU:HD13	1:A:335:GLU:HB3	1.85	0.58
1:A:85:ILE:HG13	1:A:85:ILE:O	2.04	0.57
1:A:249:TYR:CE1	1:A:256:GLN:HG3	2.39	0.57
1:A:85:ILE:HG12	1:A:90:PHE:HZ	1.69	0.57
1:A:211:LYS:HD3	1:A:291:ILE:HD12	1.87	0.57
1:A:26:ALA:HB1	1:A:213:TYR:CZ	2.40	0.56
1:A:182:LEU:CD1	1:A:184:SER:N	2.68	0.56
1:A:29:GLU:OE1	1:A:29:GLU:CA	2.55	0.55
1:A:101:LEU:O	1:A:118:SER:HB2	2.06	0.55
1:A:249:TYR:CD1	1:A:256:GLN:HG3	2.41	0.55
1:A:81:LEU:O	1:A:85:ILE:CG2	2.53	0.55
1:A:237:ASP:O	1:A:238:ARG:HB2	2.07	0.54
1:A:275:MET:O	1:A:276:TYR:HB2	2.07	0.54
1:A:82:GLN:HE21	1:A:126:HIS:HA	1.73	0.54
1:A:335:GLU:C	1:A:338:PRO:HD2	2.28	0.54
1:A:177:ARG:NH2	6:A:2066:HOH:O	2.41	0.53
1:A:134:ASP:OD1	1:A:134:ASP:C	2.45	0.53
1:A:211:LYS:HB3	1:A:291:ILE:HD12	1.91	0.53
1:A:12:GLY:HA2	1:A:262:GLU:HB3	1.92	0.52
1:A:143:ARG:NH1	2:A:1353:SO4:O1	2.42	0.51
1:A:87:ASN:O	1:A:87:ASN:ND2	2.44	0.51
1:A:233:HIS:CG	1:A:333:PRO:HB3	2.45	0.51
1:A:131:LYS:O	1:A:135:ILE:HD12	2.11	0.51
1:A:192:GLU:OE1	1:A:286:ASN:CA	2.58	0.51
1:A:182:LEU:HD11	1:A:184:SER:CA	2.43	0.49
1:A:243:ASP:OD1	1:A:245:ASP:N	2.41	0.49
1:A:67:THR:O	1:A:68:ASN:HB2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:132:LEU:HD11	1:A:191:MET:HG2	1.94	0.48
1:A:17:ARG:HE	1:A:44:ARG:NE	2.10	0.48
1:A:306:ILE:HG23	1:A:307:GLU:N	2.29	0.48
1:A:192:GLU:OE1	1:A:286:ASN:HA	2.14	0.48
1:A:243:ASP:OD1	1:A:243:ASP:C	2.52	0.48
1:A:31:GLN:C	1:A:285:LEU:HD12	2.33	0.48
1:A:340:LEU:O	1:A:344:ILE:HD12	2.14	0.47
1:A:77:ASP:C	1:A:77:ASP:OD1	2.53	0.47
1:A:154:VAL:HG23	1:A:159:VAL:CG2	2.43	0.47
1:A:202:GLU:O	1:A:275:MET:HE3	2.14	0.47
1:A:183:THR:HB	1:A:296:TRP:NE1	2.29	0.47
1:A:182:LEU:HD12	1:A:182:LEU:O	2.14	0.46
1:A:47:GLN:HG2	6:A:2021:HOH:O	2.15	0.46
1:A:104:ASP:C	1:A:104:ASP:OD1	2.53	0.46
1:A:77:ASP:OD1	1:A:79:GLU:N	2.48	0.46
1:A:85:ILE:HG12	1:A:90:PHE:CZ	2.49	0.46
1:A:251:ARG:C	1:A:253:PRO:HD2	2.36	0.45
1:A:251:ARG:O	1:A:253:PRO:HD2	2.16	0.45
1:A:335:GLU:O	1:A:338:PRO:HD2	2.15	0.45
1:A:17:ARG:HH21	1:A:44:ARG:HE	1.63	0.45
1:A:173:GLN:O	1:A:177:ARG:CG	2.65	0.45
1:A:87:ASN:C	1:A:87:ASN:ND2	2.69	0.45
1:A:149:THR:HG22	1:A:150:LEU:N	2.31	0.44
1:A:182:LEU:HD12	1:A:183:THR:C	2.38	0.44
1:A:192:GLU:OE1	1:A:287:GLY:N	2.51	0.44
1:A:13:SER:HB2	1:A:27:TRP:HH2	1.83	0.44
1:A:211:LYS:O	1:A:290:THR:HA	2.17	0.44
1:A:49:ASP:HA	1:A:50:PRO:HD2	1.88	0.44
1:A:146:LEU:C	1:A:146:LEU:HD23	2.38	0.43
1:A:210:ILE:HD11	1:A:293:VAL:HG23	2.00	0.43
1:A:45:LEU:HD22	1:A:49:ASP:OD2	2.18	0.43
1:A:185:ASN:HA	1:A:294:ASN:O	2.18	0.43
1:A:119:ASN:HA	6:A:2050:HOH:O	2.18	0.43
1:A:82:GLN:HE21	1:A:126:HIS:CB	2.32	0.43
1:A:211:LYS:CB	1:A:291:ILE:HD12	2.48	0.43
1:A:47:GLN:HG3	1:A:169:TRP:NE1	2.33	0.43
1:A:146:LEU:O	1:A:146:LEU:HD23	2.18	0.42
1:A:207:PHE:CZ	1:A:292:THR:HG21	2.54	0.42
1:A:112:GLN:CD	1:A:112:GLN:N	2.72	0.42
1:A:150:LEU:HD12	1:A:150:LEU:HA	1.37	0.42
1:A:182:LEU:HA	1:A:297:TYR:CD1	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:PHE:HB3	1:A:271:LEU:HB3	2.02	0.42
1:A:207:PHE:CE2	1:A:292:THR:HG21	2.56	0.41
1:A:72:PRO:HG2	1:A:164:GLY:HA3	2.02	0.41
1:A:78:LEU:HD23	1:A:78:LEU:HA	1.86	0.41
1:A:173:GLN:O	1:A:177:ARG:HG3	2.21	0.41
1:A:124:LYS:CB	1:A:127:GLU:HG3	2.46	0.41
1:A:182:LEU:HD12	1:A:183:THR:N	2.34	0.40
1:A:182:LEU:CD1	1:A:184:SER:CA	3.00	0.40
1:A:186:LEU:HD23	1:A:188:LEU:HD21	2.02	0.40
1:A:276:TYR:CD2	1:A:313:HIS:HB2	2.56	0.40
1:A:173:GLN:O	1:A:177:ARG:HG2	2.21	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:A:344:ILE:CD1	1:A:344:ILE:CD1[8_665]	2.02	0.18

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	337/352 (96%)	324 (96%)	12 (4%)	1 (0%)	41 55

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	152	ASP

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	281/306 (92%)	255 (91%)	26 (9%)	9 13

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	SER
1	A	16	PRO
1	A	29	GLU
1	A	40	ARG
1	A	51	ARG
1	A	85	ILE
1	A	87	ASN
1	A	104	ASP
1	A	135	ILE
1	A	145	TYR
1	A	150	LEU
1	A	151	ASN
1	A	153	THR
1	A	160	MET
1	A	162	PHE
1	A	172	LYS
1	A	177	ARG
1	A	182	LEU
1	A	188	LEU
1	A	217	ILE
1	A	258	VAL
1	A	275	MET
1	A	302	THR
1	A	304	LYS
1	A	305	ARG
1	A	306	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	82	GLN
1	A	126	HIS
1	A	151	ASN
1	A	332	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)

Of 10 ligands modelled in this entry, 1 is monoatomic - leaving 9 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	$\#\|Z\| > 2$
2	SO4	A	1351	-	4,4,4	0.27	0	6,6,6	0.05	0
3	GOL	A	1357	-	5,5,5	0.54	0	5,5,5	0.26	0
2	SO4	A	1352	-	4,4,4	0.19	0	6,6,6	0.33	0
4	DZA	A	1358	5	7,10,10	8.61	1 (14%)	9,12,12	4.45	6 (66%)
3	GOL	A	1355	-	5,5,5	0.48	0	5,5,5	0.22	0
2	SO4	A	1350	-	4,4,4	0.27	0	6,6,6	0.08	0
3	GOL	A	1356	-	5,5,5	0.27	0	5,5,5	0.28	0
2	SO4	A	1354	-	4,4,4	0.35	0	6,6,6	0.27	0
2	SO4	A	1353	-	4,4,4	0.24	0	6,6,6	0.09	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	GOL	A	1356	-	-	0/4/4/4	-
3	GOL	A	1355	-	-	0/4/4/4	-
4	DZA	A	1358	5	-	0/7/9/9	-
3	GOL	A	1357	-	-	0/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1358	DZA	N03-N04	-22.64	1.12	1.42

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	1358	DZA	C06-N04-N03	-8.17	101.56	109.06
4	A	1358	DZA	C02-N03-N04	-5.98	114.32	120.29
4	A	1358	DZA	C07-C08-C09	-5.44	103.55	112.67
4	A	1358	DZA	C05-N04-C06	4.35	117.01	110.98
4	A	1358	DZA	C05-N04-N03	-3.83	105.54	109.06
4	A	1358	DZA	C08-C07-C02	-3.27	105.20	112.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1352	SO4	1	0
2	A	1353	SO4	2	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, 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	339/352 (96%)	0.36	29 (8%)	10	9	31, 60, 91, 98	26 (7%)

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	304	LYS	3.9
1	A	301	PRO	3.7
1	A	305	ARG	3.7
1	A	14	GLY	3.5
1	A	103	TYR	3.5
1	A	110	ASN	3.3
1	A	140	GLY	3.1
1	A	109	ALA	3.1
1	A	118	SER	3.0
1	A	16	PRO	2.9
1	A	281	ILE	2.8
1	A	306	ILE	2.8
1	A	90	PHE	2.7
1	A	11	SER	2.7
1	A	151	ASN	2.7
1	A	12	GLY	2.7
1	A	303	PRO	2.6
1	A	188	LEU	2.5
1	A	208	ALA	2.4
1	A	116	PRO	2.3
1	A	112	GLN	2.2
1	A	286	ASN	2.2
1	A	296	TRP	2.2
1	A	300	ALA	2.2
1	A	108	MET	2.1
1	A	15	GLU	2.1
1	A	114	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	82	GLN	2.1
1	A	181	GLN	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, 95^{th} 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
3	GOL	A	1355	6/6	0.65	0.60	98,100,100,100	0
2	SO4	A	1352	5/5	0.81	0.20	100,100,100,100	5
3	GOL	A	1357	6/6	0.83	0.23	65,67,68,69	0
2	SO4	A	1354	5/5	0.87	0.26	100,100,100,100	5
2	SO4	A	1353	5/5	0.89	0.37	100,100,100,100	5
3	GOL	A	1356	6/6	0.92	0.30	80,81,81,83	0
2	SO4	A	1350	5/5	0.95	0.20	80,81,81,82	5
2	SO4	A	1351	5/5	0.95	0.16	91,91,91,92	5
4	DZA	A	1358	11/11	0.96	0.27	41,45,47,47	0
5	ZN	A	1359	1/1	0.98	0.14	42,42,42,42	0

6.5 Other polymers (i)

There are no such residues in this entry.