Full wwPDB X-ray Structure Validation Report (i)

May 25, 2020 – 07:28 am BST

PDB ID	:	2CW8
Title	:	Crystal structure of intein homing endonuclease II
Authors	:	Matsumura, H.; Takahashi, H.; Inoue, T.; Hashimoto, H.; Nishioka, M.; Fujiwara, S.; Takagi, M.; Imanaka, T.; Kai, Y.
Deposited on	:	2005-06-17
Resolution	:	2.50 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 (1)) were used in the production of this report:

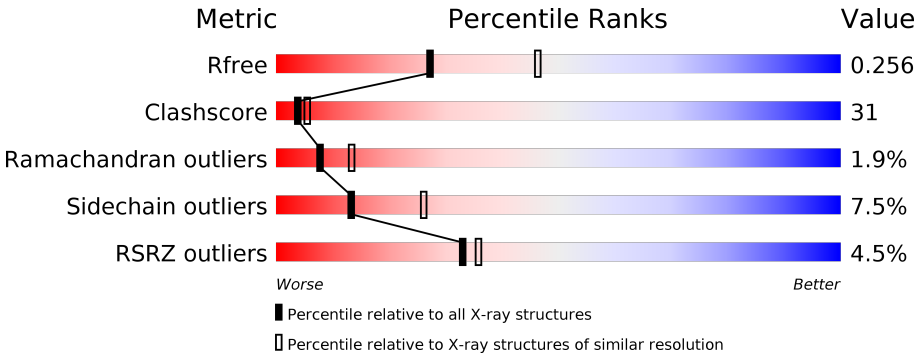
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA,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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	537	4% 53% 42%

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
3	GOL	A	2006	-	-	X	-

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4735 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.

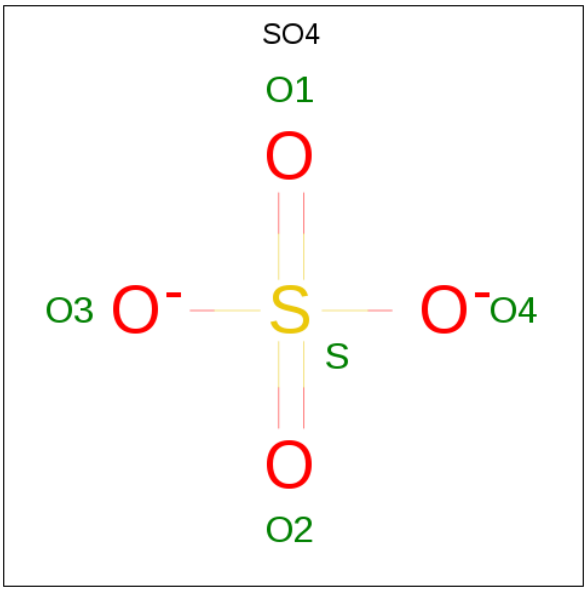
- Molecule 1 is a protein called Endonuclease PI-PkoII.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	537	4392	2809	772	801	1	9	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

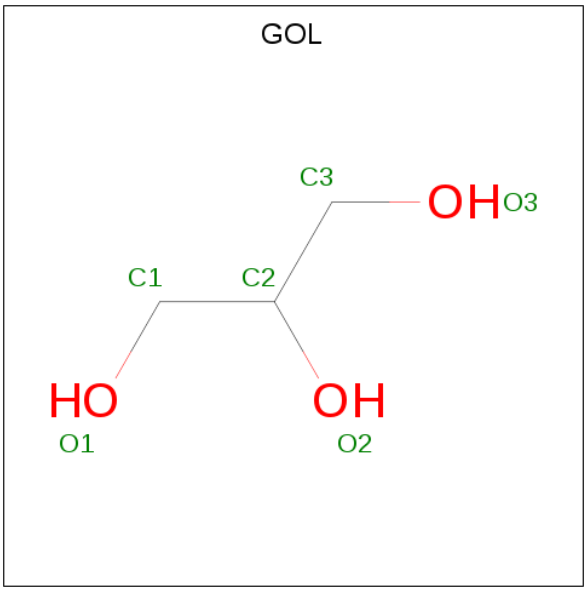
Chain	Residue	Modelled	Actual	Comment	Reference
A	28	MSE	MET	MODIFIED RESIDUE	UNP P77933
A	29	MSE	MET	MODIFIED RESIDUE	UNP P77933
A	60	ASN	LYS	SEE REMARK 999	UNP P77933
A	154	MSE	MET	MODIFIED RESIDUE	UNP P77933
A	168	MSE	MET	MODIFIED RESIDUE	UNP P77933
A	250	MSE	MET	MODIFIED RESIDUE	UNP P77933
A	268	MSE	MET	MODIFIED RESIDUE	UNP P77933
A	269	ARG	SER	SEE REMARK 999	UNP P77933
A	270	LYS	PRO	SEE REMARK 999	UNP P77933
A	318	MSE	MET	MODIFIED RESIDUE	UNP P77933
A	350	MSE	MET	MODIFIED RESIDUE	UNP P77933
A	476	MSE	MET	MODIFIED RESIDUE	UNP P77933

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



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
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
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
3	A	1	Total C O 6 3 3	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	279	Total O 279 279	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: Endonuclease PI-PkoII

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	103.97Å 150.54Å 145.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.39 – 2.50 38.39 – 2.49	Depositor EDS
% Data completeness (in resolution range)	88.6 (38.39-2.50) 93.8 (38.39-2.49)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.39 (at 2.48Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.217 , 0.252 0.222 , 0.256	Depositor DCC
R_{free} test set	3253 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å^2)	46.9	Xtriage
Anisotropy	0.235	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 41.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	4735	wwPDB-VP
Average B, all atoms (Å^2)	55.0	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: GOL, 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	0.41	0/4469	0.68	4/6004 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	301	TRP	N-CA-C	7.22	130.51	111.00
1	A	83	ARG	NE-CZ-NH1	-6.94	116.83	120.30
1	A	300	GLY	N-CA-C	5.77	127.52	113.10
1	A	302	SER	N-CA-C	-5.06	97.33	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	4392	0	4470	275	0
2	A	40	0	0	3	0
3	A	24	0	32	5	0
4	A	279	0	0	40	0
All	All	4735	0	4502	276	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 31.

All (276) 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:296:ASN:HB3	1:A:297:PRO:HD2	1.38	1.05
1:A:168:MSE:HE2	1:A:172:LEU:HG	1.43	0.99
1:A:270:LYS:CE	1:A:270:LYS:H	1.80	0.92
1:A:268:MSE:HE1	1:A:272:ILE:HD11	1.54	0.89
1:A:296:ASN:HD22	1:A:302:SER:HB3	1.35	0.89
1:A:227:VAL:HG22	1:A:238:VAL:HG22	1.58	0.86
1:A:235:GLU:HG2	4:A:2118:HOH:O	1.74	0.86
1:A:230:ASN:HB3	4:A:2118:HOH:O	1.77	0.84
1:A:154:MSE:HE1	1:A:250:MSE:HE1	1.60	0.83
1:A:190:ARG:HG2	1:A:200:LEU:HD11	1.61	0.83
1:A:189:LEU:HB3	1:A:200:LEU:HD21	1.62	0.81
1:A:7:TRP:HE1	1:A:20:ARG:NH1	1.80	0.80
1:A:259:LYS:HB3	1:A:267:ARG:HG2	1.64	0.79
1:A:517:ASP:HB2	4:A:2232:HOH:O	1.83	0.79
1:A:154:MSE:HE1	1:A:250:MSE:CE	2.13	0.77
1:A:204:GLY:HA2	4:A:2214:HOH:O	1.83	0.77
1:A:270:LYS:H	1:A:270:LYS:HE3	1.50	0.76
1:A:270:LYS:HE3	1:A:270:LYS:N	2.00	0.75
1:A:450:VAL:HG13	1:A:467:ASN:HB3	1.68	0.75
1:A:99:PHE:HB3	1:A:106:LEU:HD22	1.69	0.74
1:A:145:PRO:HA	3:A:2006:GOL:H12	1.71	0.73
1:A:296:ASN:CB	1:A:297:PRO:HD2	2.17	0.72
1:A:296:ASN:HB3	1:A:297:PRO:CD	2.17	0.72
1:A:168:MSE:HE3	1:A:171:THR:HB	1.72	0.71
1:A:203:ILE:HD13	1:A:204:GLY:N	2.06	0.71
1:A:452:PRO:HB2	1:A:455:VAL:HG23	1.73	0.69
1:A:537:ASN:C	1:A:537:ASN:HD22	1.96	0.68
1:A:270:LYS:CE	1:A:270:LYS:N	2.56	0.67
1:A:128:LEU:HD11	1:A:407:LEU:HD21	1.76	0.67
1:A:155:THR:HG22	1:A:237:LEU:HD12	1.74	0.67
1:A:361:PRO:HG2	1:A:364:VAL:HG23	1.77	0.67
1:A:218:ARG:NH2	1:A:249:ILE:HD11	2.10	0.67
1:A:17:HIS:HE1	1:A:362:GLU:OE2	1.78	0.66
1:A:7:TRP:HE1	1:A:20:ARG:HH12	1.43	0.66
1:A:293:LYS:HE2	1:A:303:TYR:HE2	1.60	0.66
1:A:168:MSE:HE3	1:A:168:MSE:O	1.97	0.65
1:A:481:ARG:HD3	4:A:2155:HOH:O	1.94	0.65
1:A:472:THR:O	1:A:476:MSE:HG3	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:ARG:HG3	1:A:270:LYS:NZ	2.11	0.65
1:A:301:TRP:CE3	1:A:301:TRP:N	2.64	0.65
1:A:190:ARG:HG2	1:A:200:LEU:CD1	2.27	0.64
1:A:228:ARG:HH21	1:A:237:LEU:CD2	2.09	0.64
1:A:80:TYR:HE1	1:A:94:SER:HB3	1.62	0.64
1:A:381:ILE:HG12	1:A:386:VAL:HG21	1.80	0.64
1:A:361:PRO:HG2	1:A:364:VAL:CG2	2.28	0.64
1:A:125:ARG:NH1	4:A:2140:HOH:O	2.29	0.63
1:A:187:ARG:O	1:A:187:ARG:HG2	1.98	0.63
1:A:7:TRP:HZ3	1:A:400:LEU:HD23	1.63	0.62
1:A:217:ARG:HD3	1:A:221:GLU:OE2	1.99	0.62
1:A:27:ARG:O	1:A:31:GLU:HG3	2.00	0.62
1:A:3:LEU:HB3	1:A:5:GLU:OE1	1.99	0.62
1:A:268:MSE:CE	1:A:272:ILE:HD11	2.28	0.61
1:A:337:GLU:HG2	1:A:339:PRO:HG3	1.82	0.61
1:A:7:TRP:NE1	1:A:20:ARG:NH1	2.48	0.61
1:A:231:GLY:HA2	4:A:2190:HOH:O	2.00	0.61
1:A:399:GLU:HB3	1:A:426:TYR:CZ	2.35	0.61
1:A:5:GLU:CD	1:A:5:GLU:H	2.04	0.61
1:A:66:ARG:HD2	4:A:2274:HOH:O	2.00	0.61
1:A:296:ASN:HD22	1:A:302:SER:CB	2.12	0.61
1:A:25:ILE:O	1:A:29:MSE:HG3	2.01	0.60
1:A:300:GLY:O	1:A:301:TRP:HB2	2.02	0.60
1:A:250:MSE:HE3	1:A:255:LEU:HD23	1.83	0.60
1:A:458:GLU:HG2	4:A:2189:HOH:O	2.01	0.60
1:A:184:THR:HG22	1:A:187:ARG:HB3	1.84	0.60
1:A:440:ASP:OD1	1:A:442:LYS:HD3	2.01	0.60
1:A:295:ARG:HB3	1:A:300:GLY:N	2.17	0.59
1:A:466:LYS:HA	4:A:2261:HOH:O	2.02	0.59
1:A:145:PRO:HA	3:A:2006:GOL:C1	2.31	0.59
1:A:396:THR:HG22	1:A:398:SER:H	1.68	0.59
1:A:467:ASN:HB2	4:A:2248:HOH:O	2.02	0.59
1:A:25:ILE:HD12	1:A:516:TYR:HB3	1.83	0.59
1:A:537:ASN:C	1:A:537:ASN:ND2	2.55	0.59
1:A:227:VAL:HG22	1:A:238:VAL:CG2	2.32	0.59
1:A:83:ARG:NH1	1:A:507:ASP:OD2	2.32	0.58
1:A:258:TRP:O	1:A:270:LYS:CE	2.51	0.58
1:A:29:MSE:HE1	1:A:43:GLU:O	2.02	0.58
1:A:454:GLU:OE2	1:A:502:ARG:NH2	2.37	0.58
1:A:203:ILE:HD13	1:A:204:GLY:H	1.69	0.57
1:A:154:MSE:CE	1:A:250:MSE:HE1	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:308:TYR:O	1:A:309:ASN:HB2	2.05	0.57
1:A:207:VAL:HG13	1:A:213:LEU:HD12	1.86	0.57
1:A:421:HIS:HA	1:A:425:VAL:O	2.05	0.57
1:A:158:VAL:HG12	4:A:2115:HOH:O	2.05	0.57
1:A:181:ARG:HH11	1:A:181:ARG:HG2	1.70	0.56
1:A:172:LEU:HD13	1:A:217:ARG:HA	1.87	0.56
1:A:455:VAL:O	1:A:459:VAL:HG23	2.06	0.56
1:A:17:HIS:CE1	1:A:362:GLU:OE2	2.57	0.56
1:A:317:ASP:OD1	1:A:320:ARG:NH1	2.36	0.56
1:A:173:ARG:HH21	1:A:178:GLU:HB3	1.69	0.56
1:A:258:TRP:O	1:A:270:LYS:HE2	2.05	0.56
1:A:308:TYR:CD2	1:A:335:TYR:HB3	2.41	0.56
1:A:300:GLY:O	1:A:301:TRP:CB	2.52	0.56
1:A:309:ASN:ND2	1:A:314:VAL:HG11	2.21	0.56
1:A:11:LEU:HD22	1:A:64:LEU:HD13	1.87	0.56
1:A:401:LEU:HD22	1:A:405:LEU:HG	1.88	0.56
1:A:190:ARG:HB2	4:A:2215:HOH:O	2.06	0.56
1:A:468:VAL:HG13	1:A:472:THR:HB	1.88	0.56
1:A:161:LYS:O	1:A:236:TYR:HE1	1.90	0.55
1:A:1:SER:H2	1:A:96:HIS:HB2	1.70	0.55
1:A:346:LEU:HD23	1:A:346:LEU:C	2.27	0.55
1:A:28:MSE:HE2	1:A:28:MSE:HA	1.89	0.55
1:A:201:LYS:HG2	1:A:204:GLY:C	2.27	0.55
1:A:238:VAL:HG11	1:A:243:ILE:HD13	1.89	0.55
1:A:450:VAL:CG1	1:A:467:ASN:HB3	2.36	0.55
1:A:174:TRP:CH2	1:A:205:TYR:HE2	2.25	0.54
1:A:255:LEU:O	1:A:270:LYS:HD3	2.06	0.54
1:A:441:LYS:HG3	1:A:442:LYS:HD2	1.90	0.54
1:A:147:GLU:O	1:A:147:GLU:HG2	2.07	0.54
1:A:531:GLY:O	1:A:532:LEU:HB2	2.07	0.54
1:A:162:LYS:H	1:A:162:LYS:HD2	1.71	0.54
1:A:255:LEU:HD22	1:A:270:LYS:HG2	1.90	0.54
1:A:186:ARG:NH1	4:A:2214:HOH:O	2.41	0.54
1:A:481:ARG:CD	4:A:2155:HOH:O	2.54	0.54
1:A:165:PHE:CE1	1:A:227:VAL:HG11	2.43	0.54
1:A:296:ASN:ND2	1:A:302:SER:HB3	2.13	0.54
1:A:295:ARG:HA	1:A:301:TRP:H	1.74	0.53
1:A:319:GLU:HG2	4:A:2171:HOH:O	2.09	0.53
1:A:146:GLU:HG2	1:A:244:ARG:CD	2.39	0.53
1:A:479:ASP:OD1	1:A:481:ARG:HG3	2.08	0.53
1:A:301:TRP:HE3	1:A:301:TRP:HA	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:VAL:HG13	1:A:123:PRO:HD2	1.91	0.52
1:A:164:PHE:HZ	1:A:191:HIS:HD1	1.57	0.52
1:A:301:TRP:CE3	1:A:301:TRP:HA	2.44	0.52
1:A:80:TYR:CE1	1:A:94:SER:HB3	2.42	0.52
1:A:296:ASN:CB	1:A:297:PRO:CD	2.84	0.52
1:A:470:PRO:HD2	2:A:1006:SO4:O2	2.09	0.52
1:A:256:LYS:O	1:A:270:LYS:NZ	2.36	0.52
1:A:301:TRP:CE3	1:A:301:TRP:CA	2.92	0.52
1:A:11:LEU:HA	1:A:15:GLU:O	2.09	0.52
1:A:130:GLU:HB2	4:A:2050:HOH:O	2.08	0.52
1:A:416:ALA:HB2	1:A:449:HIS:CD2	2.44	0.52
1:A:198:VAL:HG12	1:A:199:ARG:N	2.25	0.51
1:A:476:MSE:HB3	1:A:482:LEU:HG	1.92	0.51
1:A:526:PHE:HE1	1:A:537:ASN:HA	1.75	0.51
1:A:270:LYS:H	1:A:270:LYS:HE2	1.70	0.51
1:A:301:TRP:HE3	1:A:301:TRP:N	2.07	0.51
1:A:189:LEU:HB3	1:A:200:LEU:CD2	2.39	0.51
1:A:293:LYS:HE2	1:A:303:TYR:CE2	2.43	0.51
1:A:269:ARG:HG2	4:A:2163:HOH:O	2.11	0.51
1:A:346:LEU:HD23	1:A:350:MSE:HG3	1.93	0.51
1:A:88:ARG:CZ	1:A:122:VAL:HG11	2.40	0.51
1:A:11:LEU:HG	1:A:16:VAL:HG22	1.93	0.51
1:A:258:TRP:O	1:A:259:LYS:HD2	2.11	0.51
1:A:383:ASP:HB3	1:A:385:ASP:OD2	2.11	0.51
1:A:391:ARG:NH1	4:A:2252:HOH:O	2.43	0.51
1:A:471:GLN:HA	4:A:2262:HOH:O	2.10	0.50
1:A:471:GLN:HG3	4:A:2262:HOH:O	2.11	0.50
1:A:494:ILE:HG22	1:A:495:GLU:OE2	2.11	0.50
1:A:369:LYS:N	4:A:2278:HOH:O	2.44	0.50
1:A:155:THR:HG21	1:A:267:ARG:NH1	2.26	0.49
1:A:227:VAL:HA	1:A:237:LEU:O	2.11	0.49
1:A:168:MSE:HE2	1:A:172:LEU:CG	2.27	0.49
1:A:234:ARG:HA	4:A:2190:HOH:O	2.12	0.49
1:A:181:ARG:CZ	1:A:185:ALA:HB3	2.43	0.49
1:A:75:TYR:HB2	1:A:515:VAL:HG22	1.93	0.49
1:A:201:LYS:CG	1:A:204:GLY:H	2.25	0.49
1:A:269:ARG:HG3	1:A:270:LYS:HZ2	1.78	0.49
1:A:201:LYS:HG3	1:A:204:GLY:H	1.77	0.49
1:A:266:PHE:CE2	1:A:268:MSE:HG2	2.47	0.49
1:A:400:LEU:HD22	1:A:404:GLN:HG3	1.95	0.48
1:A:55:PHE:H	1:A:525:ASN:HD21	1.60	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:436:PHE:CD1	1:A:437:VAL:HG23	2.48	0.48
1:A:141:LEU:CD2	1:A:345:LEU:HD13	2.43	0.48
1:A:193:GLU:HA	1:A:198:VAL:O	2.13	0.48
1:A:393:ARG:HG3	1:A:429:TYR:CE2	2.49	0.48
1:A:401:LEU:CD2	1:A:405:LEU:HG	2.44	0.48
1:A:394:LEU:O	1:A:427:ARG:HA	2.14	0.47
1:A:468:VAL:HG12	1:A:469:SER:O	2.14	0.47
1:A:124:ARG:HB2	1:A:499:VAL:HG13	1.95	0.47
1:A:146:GLU:H	3:A:2006:GOL:H32	1.79	0.47
1:A:269:ARG:HB2	4:A:2242:HOH:O	2.14	0.47
1:A:335:TYR:C	1:A:335:TYR:CD1	2.88	0.47
1:A:59:THR:O	1:A:60:ASN:HB2	2.15	0.47
1:A:155:THR:HG22	1:A:237:LEU:CD1	2.44	0.47
1:A:168:MSE:CE	1:A:171:THR:HB	2.43	0.47
1:A:13:GLU:HA	1:A:13:GLU:OE1	2.14	0.47
1:A:47:VAL:HG12	4:A:2200:HOH:O	2.15	0.47
1:A:516:TYR:CD1	1:A:516:TYR:N	2.82	0.47
1:A:230:ASN:OD1	1:A:232:ASN:HB2	2.14	0.47
1:A:402:ALA:O	1:A:406:VAL:HG23	2.15	0.47
1:A:300:GLY:O	1:A:301:TRP:CG	2.68	0.46
1:A:181:ARG:NH1	1:A:181:ARG:HG2	2.30	0.46
3:A:2006:GOL:H2	4:A:2208:HOH:O	2.14	0.46
1:A:89:ARG:NH1	4:A:2126:HOH:O	2.49	0.46
1:A:20:ARG:HD2	1:A:23:GLU:OE1	2.15	0.46
1:A:263:LEU:O	1:A:267:ARG:NH2	2.49	0.46
1:A:385:ASP:HB3	1:A:392:LEU:HD22	1.98	0.46
1:A:296:ASN:ND2	1:A:302:SER:CB	2.76	0.46
1:A:54:SER:HB2	1:A:525:ASN:ND2	2.31	0.46
1:A:297:PRO:O	1:A:299:ASN:N	2.49	0.46
1:A:349:ASN:HD22	1:A:349:ASN:N	2.11	0.45
1:A:168:MSE:CE	1:A:168:MSE:O	2.64	0.45
1:A:235:GLU:N	4:A:2118:HOH:O	2.42	0.45
1:A:391:ARG:HD2	4:A:2253:HOH:O	2.15	0.45
1:A:346:LEU:CD2	1:A:350:MSE:HG3	2.47	0.45
1:A:186:ARG:O	1:A:190:ARG:HG3	2.16	0.45
1:A:442:LYS:HD2	1:A:442:LYS:H	1.82	0.45
1:A:291:ALA:HB1	1:A:344:TYR:CE1	2.51	0.45
1:A:311:ASP:CB	4:A:2221:HOH:O	2.63	0.44
1:A:462:LYS:HB2	1:A:464:PHE:CE1	2.52	0.44
1:A:183:ARG:H	1:A:183:ARG:HD2	1.82	0.44
1:A:443:LYS:HE3	1:A:444:ASN:ND2	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:476:MSE:CB	1:A:482:LEU:HG	2.48	0.44
1:A:62:ALA:HB3	1:A:127:GLU:HG2	1.99	0.44
1:A:514:TYR:HB2	4:A:2111:HOH:O	2.17	0.44
1:A:98:LEU:HD12	1:A:114:LEU:HD11	1.99	0.44
1:A:228:ARG:HG2	4:A:2282:HOH:O	2.17	0.44
1:A:207:VAL:HG21	1:A:210:TRP:CH2	2.52	0.44
1:A:100:SER:O	1:A:106:LEU:HD23	2.18	0.44
1:A:141:LEU:HD21	1:A:345:LEU:HD13	2.00	0.44
1:A:159:LYS:HE2	4:A:2115:HOH:O	2.18	0.43
1:A:265:GLY:HA3	2:A:1005:SO4:O4	2.18	0.43
1:A:313:GLU:HB2	4:A:2221:HOH:O	2.18	0.43
1:A:363:PHE:C	1:A:363:PHE:CD1	2.91	0.43
1:A:329:VAL:CG1	1:A:330:ARG:N	2.81	0.43
1:A:472:THR:O	1:A:472:THR:HG22	2.18	0.43
1:A:89:ARG:HD3	2:A:1008:SO4:O1	2.18	0.43
1:A:173:ARG:HB3	1:A:173:ARG:HE	1.44	0.43
1:A:306:LYS:HD3	1:A:308:TYR:HE2	1.83	0.43
1:A:124:ARG:O	1:A:415:SER:HB3	2.19	0.43
1:A:190:ARG:HA	1:A:200:LEU:HD11	2.01	0.43
1:A:266:PHE:HB2	1:A:340:LYS:HD3	2.01	0.43
1:A:453:LYS:HB3	1:A:467:ASN:ND2	2.33	0.43
1:A:518:LEU:O	1:A:537:ASN:HB2	2.18	0.43
1:A:269:ARG:CG	1:A:270:LYS:HZ2	2.31	0.43
1:A:203:ILE:CD1	1:A:204:GLY:N	2.79	0.43
1:A:476:MSE:HB3	1:A:481:ARG:HB2	1.99	0.43
1:A:171:THR:O	1:A:175:ILE:HG13	2.19	0.43
1:A:250:MSE:HE3	1:A:255:LEU:CD2	2.47	0.42
1:A:295:ARG:HB3	1:A:299:ASN:C	2.39	0.42
1:A:468:VAL:CG1	1:A:472:THR:HB	2.49	0.42
1:A:190:ARG:CG	1:A:200:LEU:HD11	2.42	0.42
1:A:116:PRO:HA	1:A:503:VAL:HG12	2.00	0.42
1:A:124:ARG:HD2	4:A:2235:HOH:O	2.19	0.42
1:A:146:GLU:HG3	3:A:2006:GOL:H32	2.01	0.42
1:A:255:LEU:HD22	1:A:270:LYS:CG	2.49	0.42
1:A:1:SER:N	1:A:96:HIS:HD2	2.18	0.42
1:A:223:LEU:O	1:A:227:VAL:HG23	2.19	0.42
1:A:68:LYS:HE3	1:A:521:GLU:HA	2.01	0.42
1:A:296:ASN:O	1:A:297:PRO:C	2.57	0.42
1:A:282:LEU:HD13	1:A:361:PRO:HG3	2.02	0.42
1:A:201:LYS:HE3	1:A:201:LYS:HB2	1.78	0.42
1:A:269:ARG:HG2	1:A:270:LYS:HE3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:228:ARG:HH21	1:A:237:LEU:HD23	1.83	0.41
1:A:295:ARG:HG2	1:A:300:GLY:HA2	2.02	0.41
1:A:280:LYS:HD2	4:A:2220:HOH:O	2.20	0.41
1:A:442:LYS:HD2	1:A:442:LYS:N	2.34	0.41
1:A:293:LYS:HG2	1:A:303:TYR:CD2	2.55	0.41
1:A:96:HIS:CE1	1:A:536:HIS:O	2.74	0.41
1:A:230:ASN:O	1:A:231:GLY:C	2.59	0.41
1:A:162:LYS:CD	1:A:162:LYS:H	2.34	0.41
1:A:164:PHE:HZ	1:A:191:HIS:ND1	2.18	0.41
1:A:207:VAL:CG1	1:A:213:LEU:HD12	2.49	0.41
1:A:266:PHE:CE2	1:A:268:MSE:CG	3.03	0.41
1:A:376:LEU:HG	1:A:408:LEU:HD13	2.01	0.41
1:A:453:LYS:HD2	4:A:2261:HOH:O	2.20	0.41
1:A:156:ILE:CG2	1:A:236:TYR:HB2	2.51	0.41
1:A:268:MSE:HE1	1:A:272:ILE:CD1	2.36	0.41
1:A:64:LEU:HD11	1:A:129:PRO:HD3	2.03	0.41
1:A:100:SER:HA	1:A:119:LEU:O	2.20	0.41
1:A:324:ARG:NH2	4:A:2271:HOH:O	2.53	0.41
1:A:260:ILE:HG23	1:A:342:ILE:CD1	2.50	0.41
1:A:225:GLU:HB2	4:A:2240:HOH:O	2.21	0.41
1:A:399:GLU:HB3	1:A:426:TYR:CE1	2.56	0.41
1:A:241:ASN:HA	1:A:244:ARG:HD2	2.03	0.41
1:A:80:TYR:CD2	1:A:508:VAL:HG22	2.55	0.41
1:A:84:LEU:HD12	1:A:88:ARG:HB2	2.02	0.41
1:A:1:SER:H2	1:A:96:HIS:CD2	2.39	0.41
1:A:20:ARG:HD2	1:A:23:GLU:CD	2.42	0.40
1:A:88:ARG:HD3	1:A:532:LEU:O	2.21	0.40
1:A:201:LYS:O	1:A:202:LYS:C	2.60	0.40
1:A:260:ILE:O	1:A:342:ILE:HD13	2.21	0.40
1:A:303:TYR:CZ	1:A:341:LYS:HE3	2.56	0.40
1:A:396:THR:HG23	4:A:2120:HOH:O	2.20	0.40
1:A:75:TYR:HB2	1:A:515:VAL:CG2	2.52	0.40
1:A:88:ARG:HD2	1:A:122:VAL: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	535/537 (100%)	489 (91%)	36 (7%)	10 (2%)	8 13

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	159	LYS
1	A	297	PRO
1	A	299	ASN
1	A	301	TRP
1	A	300	GLY
1	A	309	ASN
1	A	202	LYS
1	A	296	ASN
1	A	246	ALA
1	A	390	LYS

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	479/470 (102%)	443 (92%)	36 (8%)	13 26

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	GLU

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Mol	Chain	Res	Type
1	A	10	VAL
1	A	13	GLU
1	A	61	LYS
1	A	113	GLU
1	A	115	LYS
1	A	122	VAL
1	A	162	LYS
1	A	183	ARG
1	A	184	THR
1	A	194	ASP
1	A	202	LYS
1	A	203	ILE
1	A	217	ARG
1	A	219	LEU
1	A	255	LEU
1	A	270	LYS
1	A	278	LEU
1	A	281	LEU
1	A	297	PRO
1	A	301	TRP
1	A	302	SER
1	A	328	LYS
1	A	391	ARG
1	A	393	ARG
1	A	396	THR
1	A	400	LEU
1	A	401	LEU
1	A	408	LEU
1	A	439	LEU
1	A	478	GLU
1	A	512	ASP
1	A	517	ASP
1	A	525	ASN
1	A	528	VAL
1	A	537	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	17	HIS
1	A	96	HIS
1	A	296	ASN

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Mol	Chain	Res	Type
1	A	349	ASN
1	A	357	ASN
1	A	421	HIS
1	A	444	ASN
1	A	467	ASN
1	A	525	ASN

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

12 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	GOL	A	2006	-	5,5,5	0.89	0	5,5,5	0.33	0
2	SO4	A	1002	-	4,4,4	0.28	0	6,6,6	0.08	0
2	SO4	A	1005	-	4,4,4	0.29	0	6,6,6	0.11	0
3	GOL	A	2002	-	5,5,5	0.90	0	5,5,5	0.38	0
2	SO4	A	1007	-	4,4,4	0.29	0	6,6,6	0.07	0
3	GOL	A	2001	-	5,5,5	0.94	0	5,5,5	0.33	0
2	SO4	A	1003	-	4,4,4	0.30	0	6,6,6	0.11	0
2	SO4	A	1004	-	4,4,4	0.29	0	6,6,6	0.10	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	SO4	A	1001	-	4,4,4	0.28	0	6,6,6	0.09	0
3	GOL	A	2003	-	5,5,5	0.93	0	5,5,5	0.40	0
2	SO4	A	1008	-	4,4,4	0.25	0	6,6,6	0.09	0
2	SO4	A	1006	-	4,4,4	0.25	0	6,6,6	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
3	GOL	A	2006	-	-	0/4/4/4	-
3	GOL	A	2003	-	-	0/4/4/4	-
3	GOL	A	2001	-	-	0/4/4/4	-
3	GOL	A	2002	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	2002	GOL	O1-C1-C2-C3
3	A	2002	GOL	C1-C2-C3-O3
3	A	2002	GOL	O1-C1-C2-O2
3	A	2002	GOL	O2-C2-C3-O3

There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	2006	GOL	5	0
2	A	1005	SO4	1	0
2	A	1008	SO4	1	0
2	A	1006	SO4	1	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, 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	528/537 (98%)	0.21	24 (4%) 33 36	32, 52, 80, 103	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	296	ASN	6.6
1	A	300	GLY	5.9
1	A	299	ASN	5.8
1	A	203	ILE	4.8
1	A	297	PRO	3.5
1	A	389	ASN	3.4
1	A	463	VAL	3.2
1	A	387	HIS	3.2
1	A	232	ASN	3.1
1	A	465	GLN	3.0
1	A	200	LEU	3.0
1	A	39	GLU	2.7
1	A	301	TRP	2.7
1	A	298	LYS	2.5
1	A	439	LEU	2.5
1	A	464	PHE	2.5
1	A	468	VAL	2.4
1	A	234	ARG	2.2
1	A	444	ASN	2.2
1	A	438	LYS	2.2
1	A	204	GLY	2.2
1	A	233	LYS	2.2
1	A	269	ARG	2.0
1	A	40	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. 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
2	SO4	A	1007	5/5	0.89	0.29	115,115,116,117	0
3	GOL	A	2002	6/6	0.90	0.27	64,66,67,67	0
2	SO4	A	1008	5/5	0.91	0.18	111,111,112,112	0
2	SO4	A	1004	5/5	0.92	0.24	97,97,98,98	0
3	GOL	A	2006	6/6	0.92	0.34	80,80,80,81	0
2	SO4	A	1002	5/5	0.95	0.08	95,95,96,96	0
3	GOL	A	2001	6/6	0.95	0.23	63,65,67,67	0
3	GOL	A	2003	6/6	0.96	0.17	57,58,58,59	0
2	SO4	A	1006	5/5	0.96	0.17	100,100,101,101	0
2	SO4	A	1005	5/5	0.97	0.10	70,72,72,73	0
2	SO4	A	1003	5/5	0.97	0.24	100,100,101,102	0
2	SO4	A	1001	5/5	0.98	0.11	64,66,66,67	0

6.5 Other polymers (i)

There are no such residues in this entry.