



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 25, 2017 – 01:09 PM EST

PDB ID : 5FKY
Title : Structure of a hydrolase bound with an inhibitor
Authors : Cekic, N.; Heinonen, J.E.; Stubbs, K.A.; Roth, C.; McEachern, E.J.; Davies, G.J.; Vocadlo, D.J.
Deposited on : 2015-10-20
Resolution : 1.80 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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20028442
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) : rb-20028442

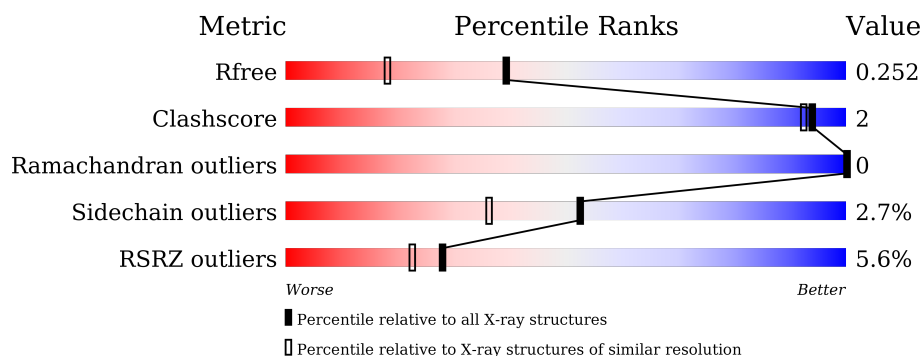
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	4533 (1.80-1.80)
Clashscore	102246	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (1.80-1.80)
RSRZ outliers	91569	4547 (1.80-1.80)

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	716	<div> <div>7%</div> <div> <div></div> <div>84%</div> <div>5%</div> <div>10%</div> </div> </div>
1	B	716	<div> <div>3%</div> <div> <div></div> <div>81%</div> <div>8%</div> <div>10%</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	GOL	A	1716	-	-	-	X

2 Entry composition [i](#)

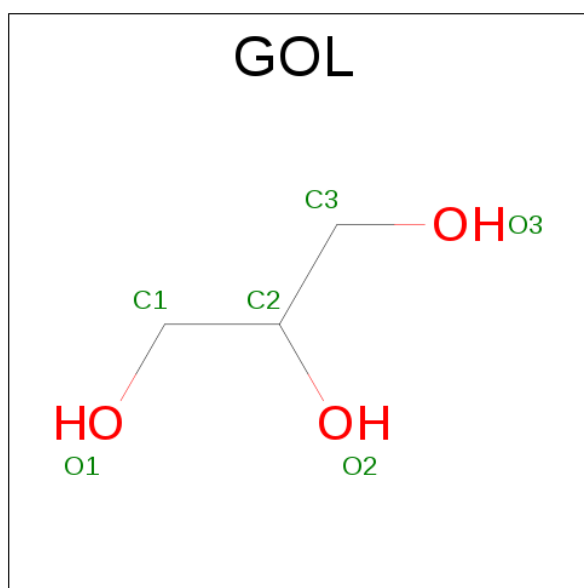
There are 4 unique types of molecules in this entry. The entry contains 11469 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 O-GLCNACASE BT_4395.

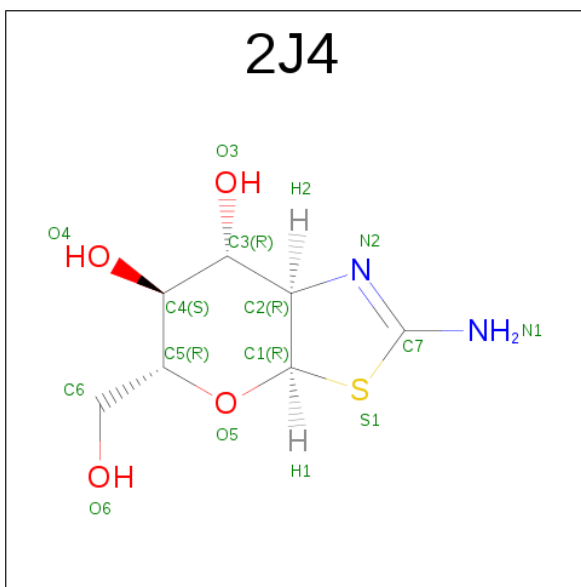
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	644	Total	C	N	O	S	0	6	0
			5263	3382	882	980	19			
1	B	645	Total	C	N	O	S	0	5	0
			5267	3379	889	980	19			

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 3 is (3AR,5R,6S,7R,7AR)-2-AMINO-5-(HYDROXYMETHYL)-5,6,7,7A-TETRAHYDRO-3AH-PYRANO[3,2-D][1,3]THIAZOLE-6,7-DIOL (three-letter code: 2J4) (formula: C₇H₁₂N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			14	7	2	4	1		
3	B	1	Total	C	N	O	S	0	0
			14	7	2	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	428	Total	O	0	0
			428	428		
4	B	477	Total	O	0	0
			477	477		

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	51.44Å 93.69Å 99.02Å 104.07° 94.18° 102.97°	Depositor
Resolution (Å)	95.17 – 1.80 33.83 – 1.80	Depositor EDS
% Data completeness (in resolution range)	95.8 (95.17-1.80) 87.0 (33.83-1.80)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.57 (at 1.81Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.211 , 0.249 0.217 , 0.252	Depositor DCC
R_{free} test set	7706 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	12.4	Xtriage
Anisotropy	0.392	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 50.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11469	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.87% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, 2J4

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	0.84	1/5413 (0.0%)	0.84	6/7334 (0.1%)
1	B	0.89	3/5413 (0.1%)	0.89	7/7332 (0.1%)
All	All	0.86	4/10826 (0.0%)	0.86	13/14666 (0.1%)

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	A	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	281	GLU	CD-OE2	6.25	1.32	1.25
1	A	378	GLU	CD-OE2	6.08	1.32	1.25
1	B	282	TYR	CE1-CZ	5.11	1.45	1.38
1	B	32	GLU	CG-CD	5.03	1.59	1.51

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	68	ARG	NE-CZ-NH1	7.63	124.11	120.30
1	A	408	ARG	NE-CZ-NH1	7.60	124.10	120.30
1	B	474	ARG	NE-CZ-NH1	7.24	123.92	120.30
1	B	408	ARG	NE-CZ-NH1	7.20	123.90	120.30
1	B	312	ASP	CB-CG-OD1	6.45	124.11	118.30
1	B	474	ARG	NE-CZ-NH2	-6.37	117.11	120.30
1	B	442	ASP	CB-CG-OD1	6.36	124.02	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	559	ARG	NE-CZ-NH1	6.07	123.34	120.30
1	A	442	ASP	CB-CG-OD1	5.55	123.29	118.30
1	A	168	ASP	CB-CG-OD2	-5.54	113.32	118.30
1	B	366	MET	CG-SD-CE	5.41	108.86	100.20
1	A	72	ARG	NE-CZ-NH1	5.39	122.99	120.30
1	A	615	LEU	CA-CB-CG	5.21	127.28	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	16	ASN	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	5263	0	5194	13	0
1	B	5267	0	5195	24	0
2	A	6	0	8	0	0
3	A	14	0	12	0	0
3	B	14	0	12	0	0
4	A	428	0	0	2	0
4	B	477	0	0	3	0
All	All	11469	0	10421	37	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 2.

All (37) 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:B:26:GLN:NE2	1:B:52:LYS:O	2.24	0.70
1:B:308:MET:HA	1:B:335:TYR:O	2.04	0.58
1:A:441[A]:MET:HG2	4:A:2336:HOH:O	2.02	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:454:PHE:HZ	1:B:572:VAL:HG12	1.70	0.56
1:B:19:ILE:HD12	1:B:20:ASP:O	2.06	0.55
1:B:557:ALA:HB1	1:B:561:ILE:HB	1.90	0.54
1:A:680:LEU:N	1:A:680:LEU:HD12	2.23	0.53
1:B:459:ASN:OD1	1:B:460:TYR:N	2.44	0.51
1:A:25:TYR:CE2	1:A:45:LEU:HD13	2.47	0.50
1:A:238:ALA:HA	1:A:276:VAL:O	2.11	0.49
1:B:396:LYS:HE2	4:B:2013:HOH:O	2.11	0.49
1:B:189:GLN:NE2	4:B:2190:HOH:O	2.38	0.49
1:B:454:PHE:CZ	1:B:572:VAL:HG12	2.48	0.49
1:B:56:LEU:HD23	1:B:89:GLU:OE1	2.14	0.46
1:A:41:LEU:HB2	1:A:104:LEU:HD11	1.97	0.46
1:B:17:LYS:HG2	1:B:118:GLU:OE1	2.15	0.46
1:A:442:ASP:HB2	4:A:2340:HOH:O	2.17	0.44
1:B:378:GLU:HG3	1:B:490:PRO:HB2	2.00	0.43
1:A:562:LYS:HB3	1:A:563:PRO:HD3	2.01	0.43
1:A:308:MET:HA	1:A:335:TYR:O	2.19	0.43
1:A:581:ASN:OD1	1:A:581:ASN:N	2.51	0.43
1:A:489:LYS:N	1:A:490:PRO:CD	2.83	0.42
1:B:173:ALA:HB2	4:B:2158:HOH:O	2.19	0.42
1:B:643:ASN:HD22	1:B:712:THR:HB	1.83	0.42
1:A:129:TYR:O	1:A:368:GLY:HA2	2.21	0.41
1:B:400:TRP:CH2	1:B:441[A]:MET:HE1	2.54	0.41
1:A:228:LYS:HD2	1:A:228:LYS:HA	1.90	0.41
1:B:170:TYR:HB2	1:B:180:TYR:CE2	2.56	0.41
1:B:176:TRP:CD1	1:B:208:PRO:HA	2.56	0.41
1:B:633:ILE:O	1:B:691:PHE:HA	2.21	0.41
1:B:222:LEU:HD13	1:B:257:LEU:HD21	2.02	0.41
1:B:74:ILE:HD11	1:B:93:ALA:HB1	2.03	0.40
1:A:73:GLN:HB3	1:A:82:TYR:CD1	2.57	0.40
1:B:532:LYS:HD2	1:B:532:LYS:HA	1.93	0.40
1:B:238:ALA:HA	1:B:276:VAL:O	2.21	0.40
1:B:310:THR:HA	1:B:337:TRP:O	2.22	0.40
1:B:451:LEU:HD22	1:B:564:LEU:HD12	2.04	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	638/716 (89%)	615 (96%)	23 (4%)	0	100	100
1	B	638/716 (89%)	620 (97%)	18 (3%)	0	100	100
All	All	1276/1432 (89%)	1235 (97%)	41 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	573/630 (91%)	555 (97%)	18 (3%)	47	30
1	B	572/630 (91%)	558 (98%)	14 (2%)	57	41
All	All	1145/1260 (91%)	1113 (97%)	32 (3%)	52	35

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	SER
1	A	52	LYS
1	A	88	LYS
1	A	112	LYS
1	A	119	VAL
1	A	165	PRO
1	A	264	LYS
1	A	371	THR

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Mol	Chain	Res	Type
1	A	408	ARG
1	A	441[A]	MET
1	A	441[B]	MET
1	A	462	LYS
1	A	581	ASN
1	A	615	LEU
1	A	642	GLU
1	A	643	ASN
1	A	680	LEU
1	A	685	GLN
1	B	6	GLN
1	B	46	SER
1	B	228	LYS
1	B	323	ILE
1	B	371	THR
1	B	408	ARG
1	B	448	GLU
1	B	451	LEU
1	B	469	GLN
1	B	595	MET
1	B	605	LEU
1	B	643	ASN
1	B	647	ASN
1	B	715	LYS

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	425	ASN
1	B	6	GLN
1	B	254	GLN
1	B	273	ASN
1	B	274	GLN
1	B	306	GLN
1	B	543	GLN
1	B	604	ASN
1	B	643	ASN

5.3.3 RNA ⓘ

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](#)

3 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	$\# Z > 2$
2	GOL	A	1716	-	5,5,5	0.36	0	5,5,5	0.47	0
3	2J4	A	1717	-	13,15,15	2.95	3 (23%)	12,22,22	2.79	3 (25%)
3	2J4	B	1716	-	13,15,15	2.84	2 (15%)	12,22,22	2.45	1 (8%)

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
2	GOL	A	1716	-	-	0/4/4/4	0/0/0/0
3	2J4	A	1717	-	-	0/2/30/30	0/2/2/2
3	2J4	B	1716	-	-	0/2/30/30	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1717	2J4	C7-S1	-2.53	1.72	1.77
3	B	1716	2J4	C7-N1	4.89	1.44	1.34
3	A	1717	2J4	C7-N1	5.47	1.45	1.34
3	A	1717	2J4	C7-N2	8.27	1.35	1.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1716	2J4	C7-N2	8.41	1.35	1.29

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1717	2J4	C1-O5-C5	2.28	117.12	112.73
3	A	1717	2J4	O3-C3-C2	2.42	115.03	108.99
3	B	1716	2J4	S1-C7-N1	7.81	127.17	118.69
3	A	1717	2J4	S1-C7-N1	8.58	128.00	118.69

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	A	644/716 (89%)	0.04	49 (7%)	17 13	8, 21, 65, 93	0
1	B	645/716 (90%)	-0.19	23 (3%)	46 40	7, 19, 55, 78	0
All	All	1289/1432 (90%)	-0.07	72 (5%)	28 22	7, 20, 61, 93	0

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	648	PHE	6.9
1	A	680	LEU	6.8
1	A	694	PHE	6.2
1	A	631	VAL	6.0
1	A	24	VAL	5.6
1	B	631	VAL	5.4
1	A	691	PHE	5.0
1	A	52	LYS	4.8
1	B	693	ARG	4.8
1	A	16	ASN	4.8
1	B	647	ASN	4.7
1	B	16	ASN	4.6
1	A	54	GLY	4.5
1	B	694	PHE	4.4
1	A	681	SER	4.3
1	B	680	LEU	4.3
1	B	618	PRO	4.3
1	A	709	PHE	4.2
1	A	53	LYS	4.1
1	A	23	ALA	4.1
1	A	682	ALA	4.0
1	A	638	ILE	4.0
1	B	646	ILE	3.9
1	A	51	SER	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	693	ARG	3.8
1	A	618	PRO	3.8
1	A	647	ASN	3.8
1	A	113	ASP	3.7
1	B	47	GLY	3.6
1	A	692	VAL	3.6
1	A	14	VAL	3.6
1	A	17	LYS	3.4
1	A	594	LYS	3.4
1	A	15	GLN	3.4
1	B	52	LYS	3.4
1	B	605	LEU	3.4
1	B	53	LYS	3.2
1	A	46	SER	3.2
1	A	21	LEU	3.1
1	A	646	ILE	2.9
1	A	710	VAL	2.8
1	B	113	ASP	2.7
1	A	715	LYS	2.7
1	B	604	ASN	2.7
1	B	581	ASN	2.6
1	A	711	LEU	2.6
1	B	452	LYS	2.6
1	B	617	SER	2.5
1	A	87	GLU	2.5
1	A	708	GLN	2.5
1	A	22	PRO	2.5
1	A	112	LYS	2.4
1	A	456	GLU	2.4
1	A	633	ILE	2.4
1	A	595	MET	2.3
1	A	581	ASN	2.3
1	B	292	ASN	2.3
1	A	50	SER	2.3
1	A	632	GLU	2.3
1	A	617	SER	2.3
1	A	583	HIS	2.3
1	A	645	GLN	2.2
1	A	685	GLN	2.2
1	A	118	GLU	2.1
1	A	18	THR	2.1
1	B	51	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	459	ASN	2.1
1	B	632	GLU	2.1
1	A	25	TYR	2.1
1	B	49	GLN	2.1
1	B	606	PRO	2.0
1	A	19	ILE	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	GOL	A	1716	6/6	0.90	0.14	13.65	30,35,36,40	0
3	2J4	B	1716	14/14	0.98	0.08	-0.44	8,9,10,11	0
3	2J4	A	1717	14/14	0.98	0.07	-0.99	8,10,11,12	0

6.5 Other polymers [i](#)

There are no such residues in this entry.