Full wwPDB X-ray Structure Validation Report (i)

Mar 6, 2026 – 07:00 PM UTC

PDB ID	:	8VQK / pdb_00008vqk
Title	:	YcjN from Escherichia coli
Authors	:	Trevino, M.A.; Fernandez, D.; Sharaf, N.G.
Deposited on	:	2024-01-18
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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

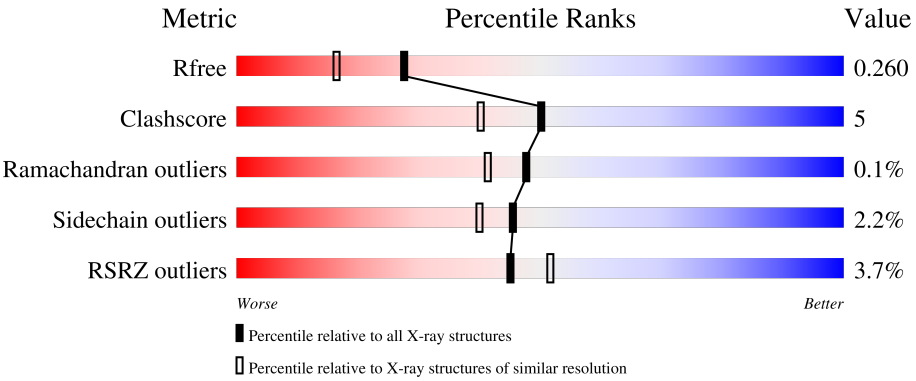
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

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 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}	180053	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (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 of 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	440	4% 79% 11% • 9%
1	B	440	3% 80% 11% 9%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 6501 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.

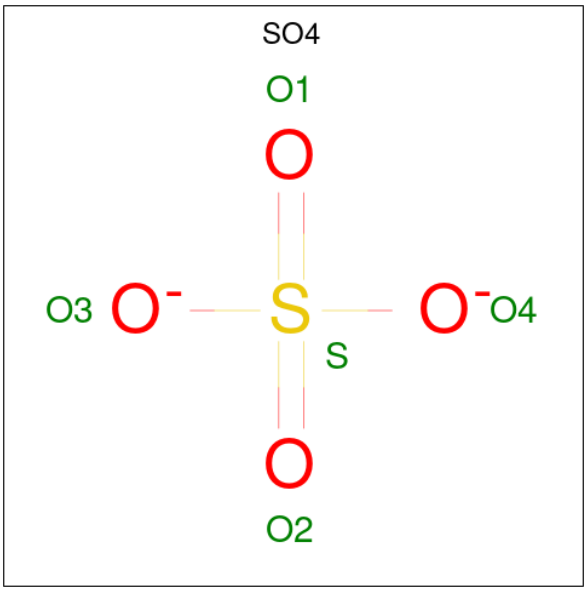
- Molecule 1 is a protein called Putative ABC transporter periplasmic-binding protein YcjN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	401	Total	C	N	O	S	0	0	0
			3065	1936	506	609	14			
1	B	402	Total	C	N	O	S	0	0	0
			3074	1941	507	612	14			

There are 20 discrepancies between the modelled and reference sequences:

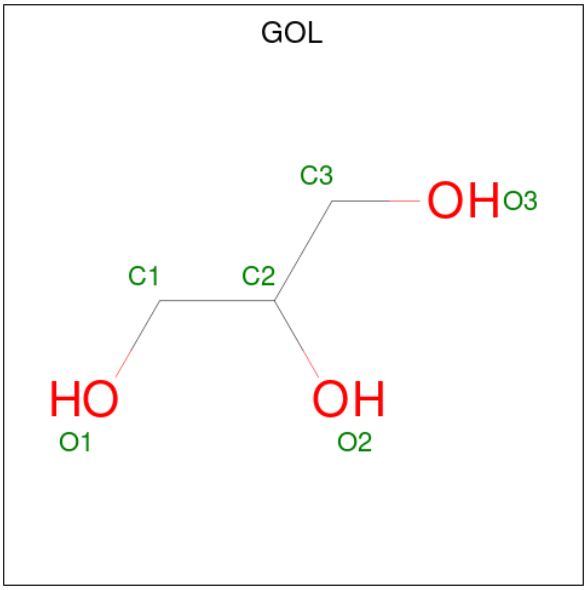
Chain	Residue	Modelled	Actual	Comment	Reference
A	431	HIS	-	expression tag	UNP P76042
A	432	HIS	-	expression tag	UNP P76042
A	433	HIS	-	expression tag	UNP P76042
A	434	HIS	-	expression tag	UNP P76042
A	435	HIS	-	expression tag	UNP P76042
A	436	HIS	-	expression tag	UNP P76042
A	437	HIS	-	expression tag	UNP P76042
A	438	HIS	-	expression tag	UNP P76042
A	439	HIS	-	expression tag	UNP P76042
A	440	HIS	-	expression tag	UNP P76042
B	431	HIS	-	expression tag	UNP P76042
B	432	HIS	-	expression tag	UNP P76042
B	433	HIS	-	expression tag	UNP P76042
B	434	HIS	-	expression tag	UNP P76042
B	435	HIS	-	expression tag	UNP P76042
B	436	HIS	-	expression tag	UNP P76042
B	437	HIS	-	expression tag	UNP P76042
B	438	HIS	-	expression tag	UNP P76042
B	439	HIS	-	expression tag	UNP P76042
B	440	HIS	-	expression tag	UNP P76042

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



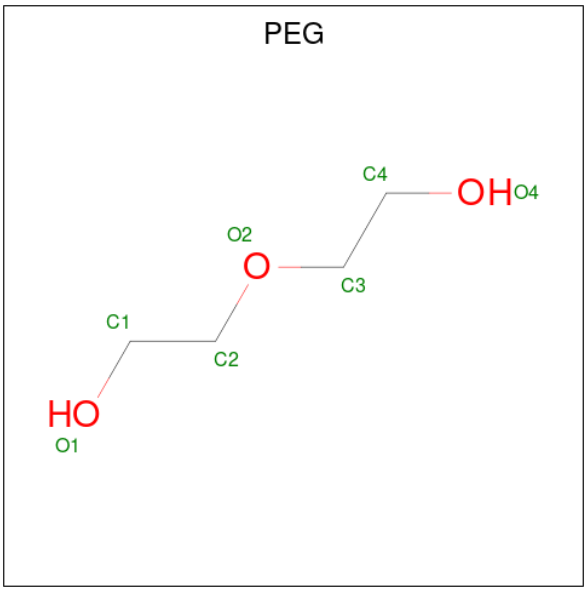
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 4 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



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

- Molecule 5 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	2	Total K 2 2	0	0
5	B	2	Total K 2 2	0	0

- Molecule 6 is CADMIUM ION (CCD ID: CD) (formula: Cd).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	2	Total Cd 2 2	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	155	Total O 155 155	0	0

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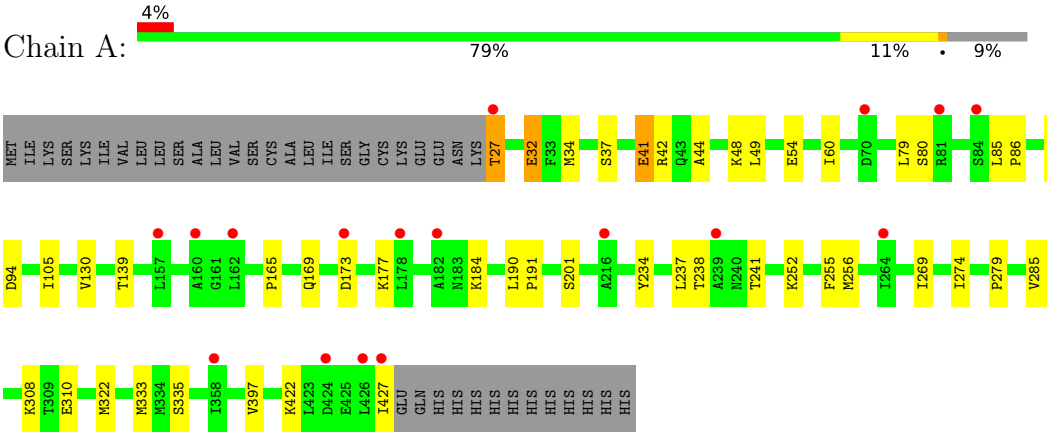
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	164	Total 164	O 164	0	0

3 Residue-property plots (i)

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

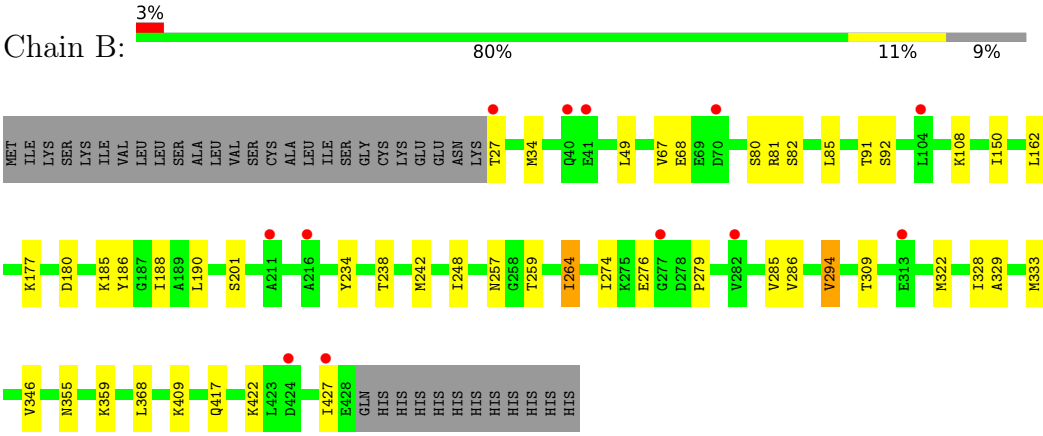
• Molecule 1: Putative ABC transporter periplasmic-binding protein YcjN

Chain A:



• Molecule 1: Putative ABC transporter periplasmic-binding protein YcjN

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	63.22Å 63.29Å 74.31Å 110.01° 91.09° 118.66°	Depositor
Resolution (Å)	35.65 – 1.95 35.65 – 1.95	Depositor EDS
% Data completeness (in resolution range)	91.2 (35.65-1.95) 91.3 (35.65-1.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.26 (at 1.95Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.215 , 0.264 0.211 , 0.260	Depositor DCC
R_{free} test set	3095 reflections (4.58%)	wwPDB-VP
Wilson B-factor (Å^2)	32.8	Xtriage
Anisotropy	0.360	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 40.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.000 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	6501	wwPDB-VP
Average B, all atoms (Å^2)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.61% 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, K, CD, PEG

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	0.30	0/3118	0.48	0/4237
1	B	0.29	0/3127	0.47	0/4249
All	All	0.30	0/6245	0.47	0/8486

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	3065	0	3062	36	0
1	B	3074	0	3068	29	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	A	6	0	8	3	0
4	A	7	0	10	2	0
4	B	14	0	20	5	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
6	B	2	0	0	0	0
7	A	155	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	164	0	0	5	0
All	All	6501	0	6168	66	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 5.

All (66) 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:422:LYS:HD2	3:A:502:GOL:H12	1.64	0.79
1:B:49:LEU:HD13	1:B:322:MET:HE1	1.69	0.75
1:A:92:SER:H	4:A:503:PEG:H22	1.50	0.75
1:B:92:SER:H	4:B:504:PEG:H31	1.55	0.70
1:A:190:LEU:HD11	1:A:237:LEU:HG	1.81	0.63
1:B:422:LYS:HD2	4:B:505:PEG:H31	1.81	0.61
1:A:308:LYS:NZ	7:A:602:HOH:O	2.32	0.61
1:A:256:MET:HA	1:A:256:MET:HE2	1.83	0.60
1:A:92:SER:HB2	1:A:297:MET:HE3	1.83	0.60
1:A:397:VAL:HG13	3:A:502:GOL:H11	1.86	0.57
1:B:190:LEU:HD23	1:B:264:ILE:HG13	1.85	0.57
1:A:41:GLU:H	1:A:41:GLU:CD	2.12	0.57
1:B:165:PRO:O	1:B:285:VAL:HG21	2.08	0.54
1:A:37:SER:HB3	1:A:42:ARG:HB3	1.90	0.53
1:A:94:ASP:HB2	1:A:297:MET:HE1	1.92	0.51
1:B:422:LYS:HZ2	4:B:505:PEG:H31	1.75	0.51
1:A:165:PRO:O	1:A:285:VAL:HG21	2.09	0.51
1:A:80:SER:HB3	1:A:85:LEU:HD13	1.92	0.51
1:B:180:ASP:HB3	1:B:185:LYS:HB2	1.93	0.51
1:A:333:MET:HA	1:A:333:MET:HE2	1.91	0.51
1:A:255:PHE:HD2	1:A:256:MET:HE3	1.76	0.51
1:A:234:TYR:O	1:A:238:THR:HG23	2.11	0.51
1:A:130:VAL:HG13	1:A:298:LEU:HD12	1.94	0.50
1:B:355:ASN:O	1:B:359:LYS:HD3	2.13	0.49
1:A:274:ILE:HD13	1:A:279:PRO:HG3	1.94	0.49
1:B:234:TYR:O	1:B:238:THR:HG23	2.13	0.49
1:A:27:THR:O	1:A:27:THR:OG1	2.28	0.48
1:B:80:SER:HB3	1:B:85:LEU:HG	1.95	0.48
1:B:286:VAL:HG13	1:B:294:VAL:HG23	1.96	0.48
1:A:42:ARG:NH2	1:A:335:SER:OG	2.42	0.48
1:A:238:THR:O	1:A:241:THR:HG22	2.13	0.48
1:A:285:VAL:HG22	1:A:286:VAL:H	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:HIS:CE1	1:A:297:MET:SD	3.07	0.47
1:B:409:LYS:NZ	7:B:614:HOH:O	2.48	0.47
1:B:329:ALA:O	1:B:333:MET:HG2	2.15	0.46
1:A:422:LYS:NZ	7:A:612:HOH:O	2.47	0.46
1:A:191:PRO:HG2	1:A:201:SER:OG	2.16	0.45
1:A:32:GLU:HB2	1:A:86:PRO:HB3	1.98	0.45
1:A:255:PHE:CD2	1:A:256:MET:HE3	2.51	0.45
1:B:108:LYS:NZ	7:B:618:HOH:O	2.50	0.45
1:A:310:GLU:OE1	1:A:310:GLU:N	2.49	0.45
4:A:503:PEG:H21	4:A:503:PEG:H41	1.68	0.44
1:B:336:PRO:HA	7:B:603:HOH:O	2.17	0.44
1:B:150:ILE:HG12	1:B:264:ILE:CD1	2.48	0.43
1:A:34:MET:HE2	1:A:89:ILE:HG23	1.99	0.43
1:A:49:LEU:HD13	1:A:322:MET:HE1	2.00	0.43
1:A:54:GLU:HG2	1:A:60:ILE:O	2.18	0.43
1:B:188:ILE:HD11	1:B:264:ILE:HD11	1.98	0.43
1:B:186:TYR:CD2	1:B:242:MET:HG3	2.53	0.43
1:B:34:MET:HE3	1:B:67:VAL:HG21	2.01	0.42
1:A:252:LYS:HD2	1:A:269:ILE:HD12	2.01	0.42
1:B:328:ILE:HG23	1:B:346:VAL:HG22	2.01	0.42
1:B:85:LEU:HD23	1:B:85:LEU:HA	1.92	0.42
1:B:91:THR:HA	4:B:504:PEG:H31	2.01	0.42
1:B:417:GLN:NE2	7:B:620:HOH:O	2.52	0.42
1:B:340:LEU:HD11	1:B:368:LEU:HB3	2.02	0.42
1:A:44:ALA:O	1:A:48:LYS:HG2	2.20	0.41
1:A:173:ASP:O	1:A:177:LYS:HD3	2.20	0.41
1:A:422:LYS:NZ	3:A:502:GOL:H31	2.35	0.41
1:B:274:ILE:HD13	1:B:279:PRO:HG3	2.03	0.41
1:B:162:LEU:HD21	1:B:177:LYS:HD2	2.03	0.41
1:A:105:ILE:HD13	1:A:139:THR:O	2.21	0.41
1:B:92:SER:H	4:B:504:PEG:C3	2.30	0.40
1:B:257:ASN:OD1	1:B:259:THR:HG23	2.21	0.40
1:A:79:LEU:HD13	1:A:86:PRO:HD3	2.02	0.40
1:B:81:ARG:NE	7:B:621:HOH:O	2.52	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	399/440 (91%)	390 (98%)	9 (2%)	0	100 100
1	B	400/440 (91%)	395 (99%)	4 (1%)	1 (0%)	36 28
All	All	799/880 (91%)	785 (98%)	13 (2%)	1 (0%)	48 41

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	427	ILE

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	336/372 (90%)	330 (98%)	6 (2%)	51 47
1	B	337/372 (91%)	328 (97%)	9 (3%)	39 32
All	All	673/744 (90%)	658 (98%)	15 (2%)	45 40

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	THR
1	A	32	GLU
1	A	41	GLU
1	A	169	GLN
1	A	184	LYS

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Mol	Chain	Res	Type
1	A	427	ILE
1	B	27	THR
1	B	68	GLU
1	B	82	SER
1	B	201	SER
1	B	248	ILE
1	B	264	ILE
1	B	276	GLU
1	B	294	VAL
1	B	309	THR

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

Mol	Chain	Res	Type
1	A	57	ASN
1	A	73	ASN
1	A	240	ASN
1	B	204	GLN
1	B	324	GLN
1	B	376	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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 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	$\#\|Z\| > 2$
3	GOL	A	502	-	5,5,5	1.01	0	5,5,5	1.05	0
4	PEG	A	503	-	6,6,6	0.16	0	5,5,5	0.11	0
4	PEG	B	504	-	6,6,6	0.20	0	5,5,5	0.08	0
2	SO4	B	501	-	4,4,4	0.36	0	6,6,6	0.16	0
4	PEG	B	505	-	6,6,6	0.17	0	5,5,5	0.07	0
2	SO4	A	501	-	4,4,4	0.25	0	6,6,6	0.28	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	502	-	-	4/4/4/4	-
4	PEG	B	505	-	-	4/4/4/4	-
4	PEG	A	503	-	-	2/4/4/4	-
4	PEG	B	504	-	-	3/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	502	GOL	C1-C2-C3-O3
4	A	503	PEG	O1-C1-C2-O2
4	B	505	PEG	O2-C3-C4-O4
4	B	504	PEG	C4-C3-O2-C2
3	A	502	GOL	O1-C1-C2-C3
3	A	502	GOL	O2-C2-C3-O3
4	B	504	PEG	O2-C3-C4-O4
4	B	505	PEG	O1-C1-C2-O2
4	A	503	PEG	C4-C3-O2-C2
3	A	502	GOL	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
4	B	505	PEG	C4-C3-O2-C2
4	B	505	PEG	C1-C2-O2-C3
4	B	504	PEG	O1-C1-C2-O2

There are no ring outliers.

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	502	GOL	3	0
4	A	503	PEG	2	0
4	B	504	PEG	3	0
4	B	505	PEG	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	401/440 (91%)	0.60	17 (4%)	40	47	25, 36, 58, 72	0
1	B	402/440 (91%)	0.63	13 (3%)	50	56	26, 37, 58, 74	0
All	All	803/880 (91%)	0.61	30 (3%)	45	52	25, 37, 58, 74	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	27	THR	4.1
1	B	27	THR	4.0
1	B	40	GLN	2.9
1	B	211	ALA	2.9
1	A	427	ILE	2.8
1	A	182	ALA	2.7
1	A	426	LEU	2.5
1	B	313	GLU	2.5
1	A	424	ASP	2.5
1	A	84	SER	2.4
1	B	104	LEU	2.4
1	B	424	ASP	2.4
1	A	216	ALA	2.4
1	B	282	VAL	2.4
1	B	277	GLY	2.3
1	A	157	LEU	2.3
1	A	162	LEU	2.2
1	A	70	ASP	2.2
1	A	173	ASP	2.2
1	B	427	ILE	2.1
1	B	41	GLU	2.1
1	A	239	ALA	2.1
1	B	216	ALA	2.1
1	A	358	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	70	ASP	2.1
1	B	173	ASP	2.1
1	A	81	ARG	2.1
1	A	264	ILE	2.0
1	A	178	LEU	2.0
1	A	160	ALA	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 oligosaccharides 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
5	K	B	506	1/1	0.82	0.12	70,70,70,70	0
4	PEG	A	503	7/7	0.84	0.12	35,38,46,54	0
3	GOL	A	502	6/6	0.85	0.14	40,41,46,47	0
4	PEG	B	504	7/7	0.89	0.11	31,38,47,51	0
4	PEG	B	505	7/7	0.93	0.09	40,47,52,59	0
2	SO4	A	501	5/5	0.96	0.07	37,39,43,44	0
5	K	B	507	1/1	0.96	0.14	35,35,35,35	0
2	SO4	B	501	5/5	0.97	0.07	35,36,41,46	0
5	K	A	504	1/1	0.98	0.15	35,35,35,35	0
5	K	A	505	1/1	0.98	0.04	38,38,38,38	0
6	CD	B	502	1/1	0.99	0.06	57,57,57,57	0
6	CD	B	503	1/1	0.99	0.02	31,31,31,31	0

6.5 Other polymers (i)

There are no such residues in this entry.