Full wwPDB X-ray Structure Validation Report (i)

Nov 24, 2021 – 06:14 pm GMT

PDB ID	:	6FOK
Title	:	Copper transporter OprC
Authors	:	Bhamidimarri, S.P.; van den Berg, B.
Deposited on	:	2018-02-07
Resolution	:	1.97 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 (i)) were used in the production of this report:

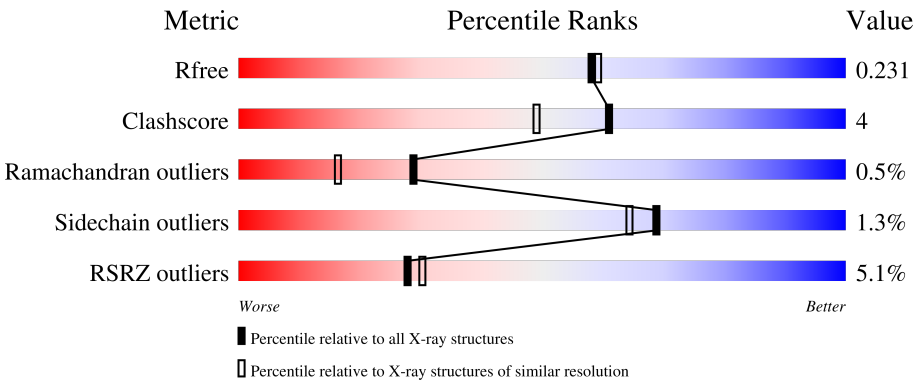
MolProbity	:	4.02b-467
Mogul	:	1.8.4 (270009), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

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 1.97 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	11647 (2.00-1.96)
Clashscore	141614	1014 (1.98-1.98)
Ramachandran outliers	138981	1006 (1.98-1.98)
Sidechain outliers	138945	1006 (1.98-1.98)
RSRZ outliers	127900	11410 (2.00-1.96)

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	723	6% 80% 9% • 10%
1	B	723	3% 82% 5% 12%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 10757 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.

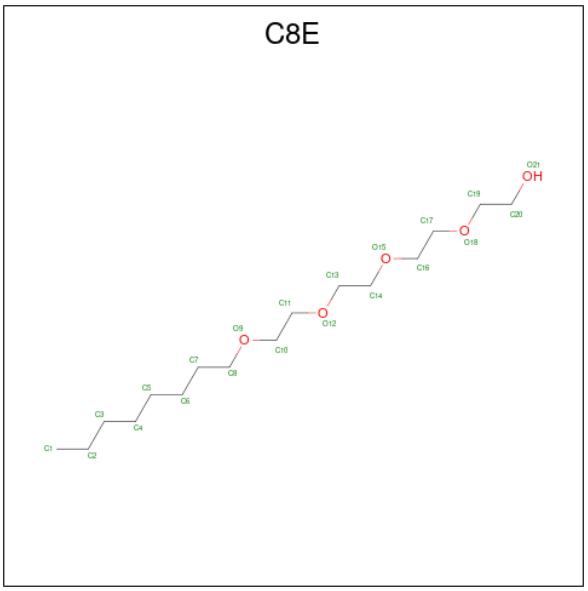
- Molecule 1 is a protein called Putative copper transport outer membrane porin OprC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	651	5086	3200	895	974	17	0	5	0
1	B	637	4964	3117	874	953	20	0	2	0

- Molecule 2 is COPPER (II) ION (three-letter code: CU) (formula: Cu) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cu		
2	A	1	1	1	0	0
2	B	1	1	1	0	0

- Molecule 3 is (HYDROXYETHYLOXY)TRI(ETHYLOXY)OCTANE (three-letter code: C8E) (formula: $C_{16}H_{34}O_5$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 13 10 3	0	0
3	A	1	Total C O 19 14 5	0	0
3	A	1	Total C O 17 13 4	0	0
3	A	1	Total C O 6 4 2	0	0
3	B	1	Total C 8 8	0	0
3	B	1	Total C O 12 8 4	0	0
3	B	1	Total C O 10 9 1	0	0
3	B	1	Total C O 11 10 1	0	0
3	B	1	Total C O 15 12 3	0	0
3	B	1	Total C O 14 10 4	0	0
3	B	1	Total C O 8 7 1	0	0
3	B	1	Total C O 16 13 3	0	0

- Molecule 4 is water.

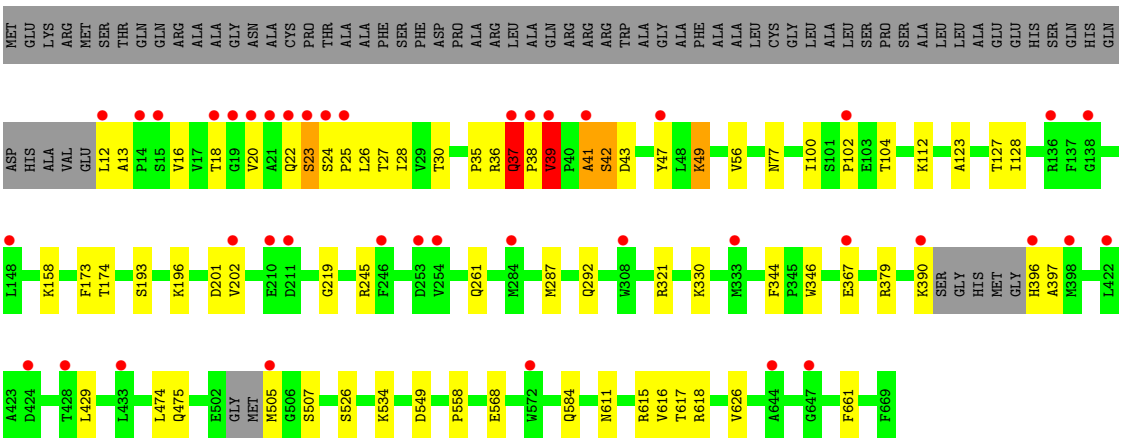
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	298	Total O 298 298	0	0
4	B	258	Total O 258 258	0	0

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.

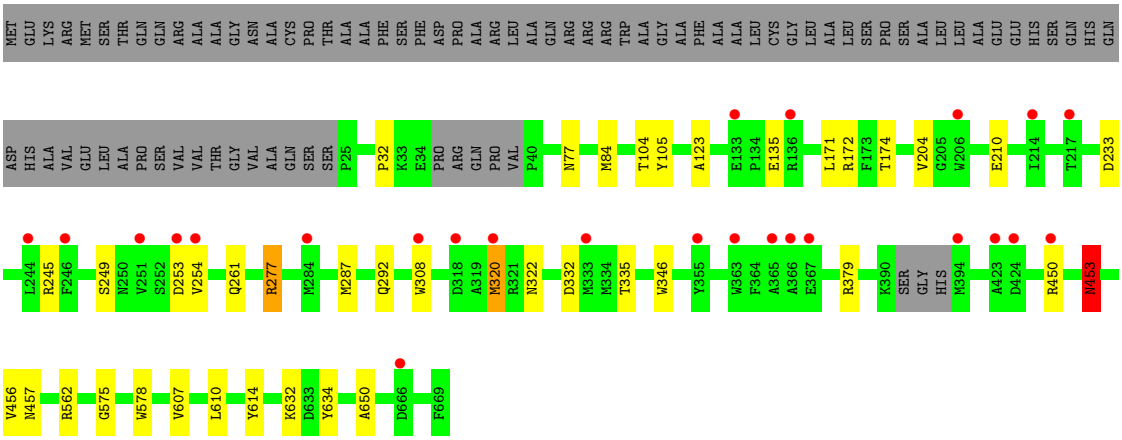
• Molecule 1: Putative copper transport outer membrane porin OprC

Chain A:



• Molecule 1: Putative copper transport outer membrane porin OprC

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	156.37Å 196.72Å 166.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	84.67 – 1.97 84.67 – 1.97	Depositor EDS
% Data completeness (in resolution range)	99.5 (84.67-1.97) 99.5 (84.67-1.97)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.51 (at 1.97Å)	Xtriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, R_{free}	0.210 , 0.232 0.209 , 0.231	Depositor DCC
R_{free} test set	8970 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	40.3	Xtriage
Anisotropy	0.292	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	10757	wwPDB-VP
Average B, all atoms (Å^2)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.88% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: C8E, CU

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	0/5224	0.63	0/7083
1	B	0.39	0/5092	0.60	0/6892
All	All	0.41	0/10316	0.62	0/13975

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	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	23	SER	Peptide
1	A	37	GLN	Peptide

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	A	5086	0	4874	57	0
1	B	4964	0	4743	31	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	55	0	76	2	0
3	B	94	0	145	6	0
4	A	298	0	0	3	0
4	B	258	0	0	4	0
All	All	10757	0	9838	90	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 4.

All (90) 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:37:GLN:HG3	1:A:611:ASN:HB3	1.46	0.95
1:A:22:GLN:HB3	1:A:25:PRO:HA	1.49	0.93
1:A:18:THR:HA	1:A:38:PRO:HD3	1.56	0.87
1:A:526:SER:HB2	1:A:534:LYS:HZ1	1.43	0.81
1:A:37:GLN:HG3	1:A:611:ASN:CB	2.17	0.75
1:A:526:SER:HB2	1:A:534:LYS:NZ	2.02	0.73
1:A:18:THR:HG22	1:A:37:GLN:HB3	1.73	0.71
1:A:37:GLN:CG	1:A:611:ASN:HB3	2.22	0.69
1:B:450:ARG:HH21	1:B:456:VAL:HA	1.58	0.67
1:A:28:ILE:HD11	1:A:112:LYS:HE3	1.78	0.66
1:B:578:TRP:HE1	3:B:709:C8E:H82	1.60	0.65
1:A:41:ALA:O	1:A:42:SER:HB3	1.97	0.65
1:B:632:LYS:NZ	4:B:802:HOH:O	2.29	0.65
1:B:450:ARG:NH2	1:B:456:VAL:HA	2.12	0.64
1:A:18:THR:HA	1:A:38:PRO:CD	2.30	0.62
1:A:549:ASP:OD2	4:A:801:HOH:O	2.16	0.62
1:B:233:ASP:OD2	1:B:277:ARG:HD2	2.01	0.61
1:A:24:SER:O	1:A:27:THR:N	2.28	0.61
1:A:20:VAL:HG11	1:A:30:THR:CG2	2.31	0.60
1:B:453:ASN:O	1:B:453:ASN:ND2	2.33	0.59
1:B:578:TRP:HD1	3:B:709:C8E:H132	1.67	0.59
1:A:36:ARG:NH2	1:A:47:TYR:HB3	2.18	0.58
1:A:77:ASN:HB2	1:A:123:ALA:HB2	1.86	0.57
1:B:320[A]:MET:SD	1:B:322:ASN:ND2	2.78	0.57
1:A:245:ARG:HG3	1:A:261:GLN:HB3	1.87	0.57
1:B:104:THR:HB	1:B:174:THR:HG21	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:77:ASN:HB2	1:B:123:ALA:HB2	1.85	0.57
1:B:578:TRP:CD1	3:B:709:C8E:H132	2.40	0.56
1:A:16:VAL:CG1	1:A:37:GLN:HB2	2.36	0.55
1:A:22:GLN:CB	1:A:25:PRO:HA	2.30	0.55
1:A:47:TYR:CE1	1:A:102:PRO:HD2	2.43	0.54
1:B:245:ARG:HG3	1:B:261:GLN:HB3	1.88	0.54
1:B:562:ARG:NH1	4:B:807:HOH:O	2.41	0.53
1:B:332:ASP:OD2	1:B:335:THR:HG22	2.07	0.53
1:B:84:MET:SD	1:B:320[B]:MET:HE1	2.48	0.53
1:A:100:ILE:HG22	1:A:102:PRO:HG3	1.90	0.53
1:B:104:THR:HB	1:B:174:THR:CG2	2.39	0.53
1:A:379:ARG:NH1	3:A:703:C8E:H171	2.24	0.52
1:A:38:PRO:C	1:A:39:VAL:HG23	2.28	0.52
1:A:16:VAL:HG12	1:A:37:GLN:HB2	1.92	0.51
1:A:36:ARG:NH2	1:A:47:TYR:HD2	2.08	0.51
1:A:367:GLU:OE1	1:A:367:GLU:N	2.29	0.51
1:B:32:PRO:HG2	1:B:105:TYR:O	2.11	0.51
1:A:36:ARG:HH21	1:A:47:TYR:HD2	1.59	0.51
1:A:615:ARG:NH1	4:A:811:HOH:O	2.44	0.51
1:A:201:ASP:OD2	1:A:219:GLY:HA3	2.11	0.50
1:A:100:ILE:C	1:A:102:PRO:HD3	2.31	0.50
1:A:292:GLN:HG2	1:A:346:TRP:CH2	2.48	0.49
1:A:49:LYS:HG3	1:A:56:VAL:HG23	1.95	0.49
1:A:396:HIS:CG	1:A:397:ALA:H	2.30	0.49
3:B:705:C8E:H72	3:B:705:C8E:H101	1.50	0.48
1:B:171:LEU:HD12	1:B:204:VAL:HG22	1.96	0.48
1:A:20:VAL:HG11	1:A:30:THR:HG22	1.94	0.48
1:B:614:TYR:CE2	3:B:706:C8E:H81	2.50	0.47
1:A:626:VAL:HG22	1:A:661:PHE:CD2	2.49	0.47
1:B:253:ASP:OD1	1:B:253:ASP:N	2.41	0.47
1:B:210:GLU:N	1:B:210:GLU:OE2	2.48	0.46
1:B:292:GLN:HG2	1:B:346:TRP:CH2	2.51	0.46
1:B:457:ASN:HB2	4:B:838:HOH:O	2.15	0.46
1:A:558:PRO:HB3	1:A:584:GLN:HB2	1.97	0.46
1:A:616:VAL:HG12	1:A:617:THR:HG23	1.99	0.45
1:A:100:ILE:O	1:A:102:PRO:HD3	2.16	0.45
1:A:104:THR:HB	1:A:174:THR:HG21	1.99	0.45
1:B:320[B]:MET:HB2	1:B:320[B]:MET:HE2	1.59	0.45
1:A:24:SER:HA	1:A:475:GLN:OE1	2.16	0.45
1:B:379:ARG:HB2	3:B:703:C8E:H191	1.99	0.45
1:A:22:GLN:N	1:A:22:GLN:OE1	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:36:ARG:HH21	1:A:47:TYR:HB3	1.81	0.44
1:A:367:GLU:H	1:A:367:GLU:CD	2.14	0.44
1:A:12:LEU:HD12	1:A:13:ALA:O	2.17	0.43
1:A:13:ALA:HB3	1:A:568:GLU:HB2	2.00	0.43
1:A:330:LYS:HD2	1:A:344:PHE:CZ	2.53	0.43
1:B:332:ASP:HB3	1:B:335:THR:HG22	2.01	0.43
1:A:321:ARG:NH1	4:A:815:HOH:O	2.47	0.43
1:B:575:GLY:O	1:B:610:LEU:HD12	2.19	0.43
1:A:390:LYS:HE2	1:A:396:HIS:CD2	2.53	0.43
1:A:429:LEU:HD23	1:A:474:LEU:HB2	2.01	0.43
1:A:24:SER:O	1:A:26:LEU:N	2.52	0.42
1:A:16:VAL:HG13	1:A:35:PRO:HB2	2.01	0.42
1:A:127:THR:C	1:A:128:ILE:HD12	2.40	0.42
1:A:128:ILE:HD12	1:A:128:ILE:N	2.35	0.42
1:A:28:ILE:CD1	1:A:112:LYS:HE3	2.48	0.41
1:A:173:PHE:HD2	1:A:202[B]:VAL:HG22	1.86	0.41
3:A:703:C8E:H141	3:A:703:C8E:H112	1.78	0.41
1:A:196:LYS:HB3	1:A:196:LYS:HE2	1.93	0.41
1:B:135:GLU:OE2	1:B:172:ARG:HD2	2.21	0.41
1:B:607:VAL:HG11	1:B:634:TYR:CZ	2.56	0.41
1:B:254:VAL:HG12	1:B:308:TRP:HB3	2.03	0.40
1:A:43:ASP:O	1:A:47:TYR:HD1	2.04	0.40
1:B:457:ASN:HA	4:B:938:HOH:O	2.21	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	650/723 (90%)	625 (96%)	20 (3%)	5 (1%)	19 9
1	B	633/723 (88%)	610 (96%)	21 (3%)	2 (0%)	41 29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1283/1446 (89%)	1235 (96%)	41 (3%)	7 (0%)	29 16

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	41	ALA
1	B	650	ALA
1	A	42	SER
1	B	453	ASN
1	A	193	SER
1	A	39	VAL
1	A	37	GLN

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	526/573 (92%)	518 (98%)	8 (2%)	65 59
1	B	511/573 (89%)	505 (99%)	6 (1%)	71 67
All	All	1037/1146 (90%)	1023 (99%)	14 (1%)	69 62

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	SER
1	A	39	VAL
1	A	49	LYS
1	A	158	LYS
1	A	287	MET
1	A	505	MET
1	A	507	SER
1	A	618	ARG
1	B	249	SER
1	B	277	ARG
1	B	287	MET

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Mol	Chain	Res	Type
1	B	320[A]	MET
1	B	320[B]	MET
1	B	453	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 14 ligands modelled in this entry, 2 are monoatomic - leaving 12 for Mogul analysis.

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.

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 (i)

6.1 Protein, DNA and RNA chains (i)

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	651/723 (90%)	0.63	41 (6%)	20	22	30, 43, 77, 123	0
1	B	637/723 (88%)	0.57	25 (3%)	39	42	33, 46, 76, 106	0
All	All	1288/1446 (89%)	0.60	66 (5%)	28	30	30, 45, 77, 123	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	21	ALA	6.4
1	A	12	LEU	5.5
1	A	22	GLN	5.5
1	A	333	MET	5.3
1	A	20	VAL	4.6
1	B	253	ASP	4.4
1	B	394	MET	4.3
1	A	38	PRO	4.1
1	A	138	GLY	3.9
1	B	365	ALA	3.8
1	A	18	THR	3.7
1	A	396	HIS	3.7
1	A	47	TYR	3.6
1	A	367	GLU	3.3
1	B	206	TRP	3.3
1	A	572[A]	TRP	3.2
1	A	253	ASP	3.2
1	B	308	TRP	3.2
1	B	666	ASP	3.1
1	A	284	MET	3.0
1	B	217	THR	2.9
1	A	19	GLY	2.8
1	A	254	VAL	2.8
1	B	367	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	254	VAL	2.8
1	A	246	PHE	2.7
1	A	424	ASP	2.7
1	A	102	PRO	2.7
1	A	23	SER	2.7
1	A	308	TRP	2.7
1	B	366	ALA	2.6
1	B	284	MET	2.6
1	B	333	MET	2.6
1	A	14	PRO	2.6
1	A	647	GLY	2.6
1	A	39	VAL	2.6
1	A	210	GLU	2.6
1	A	202[A]	VAL	2.5
1	B	423	ALA	2.5
1	A	505	MET	2.4
1	B	355	TYR	2.4
1	B	424	ASP	2.4
1	B	246	PHE	2.4
1	B	133	GLU	2.4
1	A	211	ASP	2.4
1	A	136	ARG	2.4
1	B	450	ARG	2.4
1	A	422	LEU	2.3
1	B	244	LEU	2.3
1	B	320[A]	MET	2.3
1	B	136	ARG	2.3
1	B	214	ILE	2.2
1	A	148	LEU	2.2
1	B	251	VAL	2.2
1	A	24	SER	2.1
1	A	37	GLN	2.1
1	A	25	PRO	2.1
1	A	398	MET	2.1
1	B	318	ASP	2.1
1	A	428	THR	2.0
1	A	433	LEU	2.0
1	A	15	SER	2.0
1	A	390	LYS	2.0
1	A	41	ALA	2.0
1	A	644	ALA	2.0
1	B	363	TRP	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 monosaccharides in this entry.

6.4 Ligands (i)

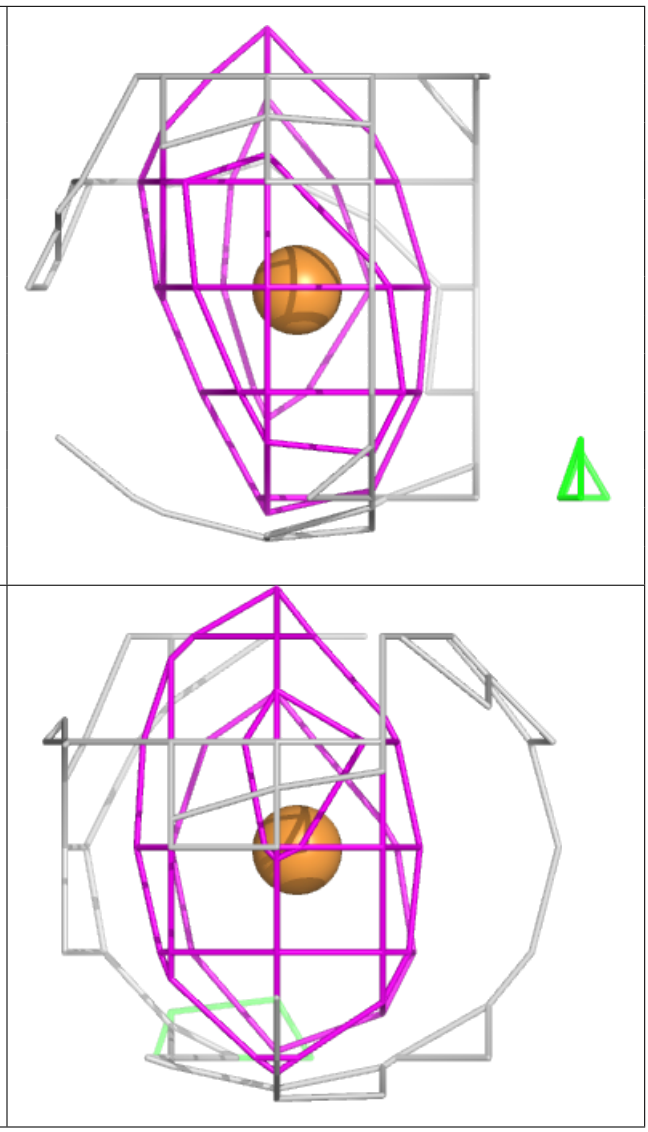
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	C8E	A	705	6/21	0.75	0.40	52,58,68,74	0
3	C8E	A	704	17/21	0.77	0.37	53,65,81,82	0
3	C8E	B	705	11/21	0.77	0.34	58,68,87,88	0
3	C8E	B	707	14/21	0.77	0.24	56,65,72,76	0
3	C8E	B	706	15/21	0.79	0.20	50,59,79,82	0
3	C8E	B	702	8/21	0.81	0.33	51,57,58,60	0
3	C8E	B	708	8/21	0.82	0.18	53,57,62,62	0
3	C8E	B	704	10/21	0.83	0.13	54,57,61,62	0
3	C8E	B	709	16/21	0.83	0.15	49,55,65,65	0
3	C8E	A	703	19/21	0.84	0.19	52,62,80,82	0
3	C8E	A	702	13/21	0.86	0.24	53,59,65,66	0
3	C8E	B	703	12/21	0.89	0.21	53,58,73,80	0
2	CU	B	701	1/1	0.99	0.06	43,43,43,43	0
2	CU	A	701	1/1	1.00	0.07	37,37,37,37	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

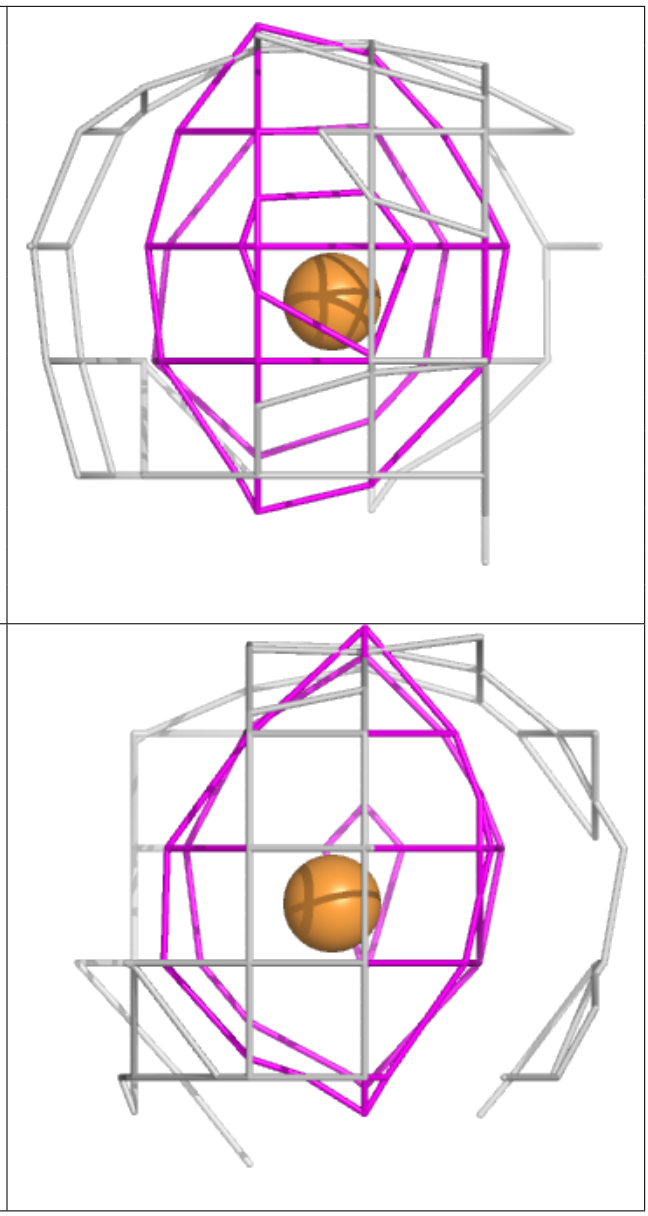
Electron density around CU B 701:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around CU A 701:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers (i)

There are no such residues in this entry.