



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 4, 2023 – 05:50 pm GMT

PDB ID : 2WBK
Title : Structure of the Michaelis complex of beta-mannosidase, Man2A, provides insight into the conformational itinerary of mannoside hydrolysis
Authors : Offen, W.A.; Zechel, D.L.; Withers, S.G.; Gilbert, H.J.; Davies, G.J.
Deposited on : 2009-03-02
Resolution : 2.10 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
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) : 2.36

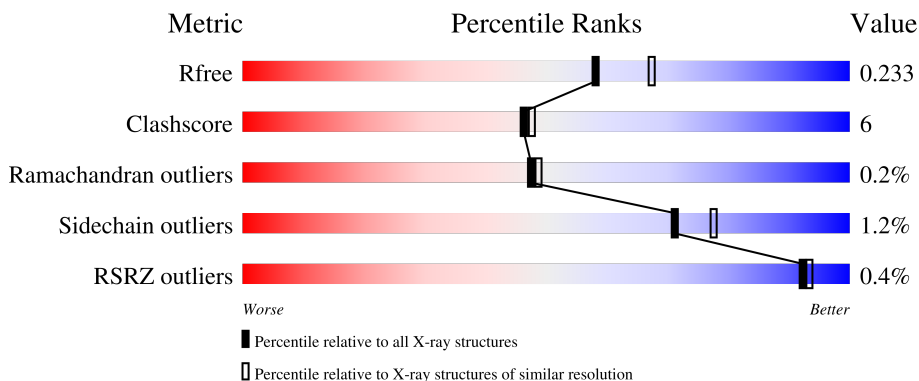
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 $\leq 5\%$. 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	847	 87% 11% .
1	B	847	 % 87% 12% ..

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	EDO	B	1871	-	-	X	-
2	EDO	B	1877	-	-	X	-
3	CL	B	1886	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 14932 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 BETA-MANNOSIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	837	6767	4351	1122	1261	33	3	13	0
1	B	840	6797	4372	1119	1273	33	4	14	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	555	GLN	GLU	engineered mutation	UNP Q8AAK6
B	555	GLN	GLU	engineered mutation	UNP Q8AAK6

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



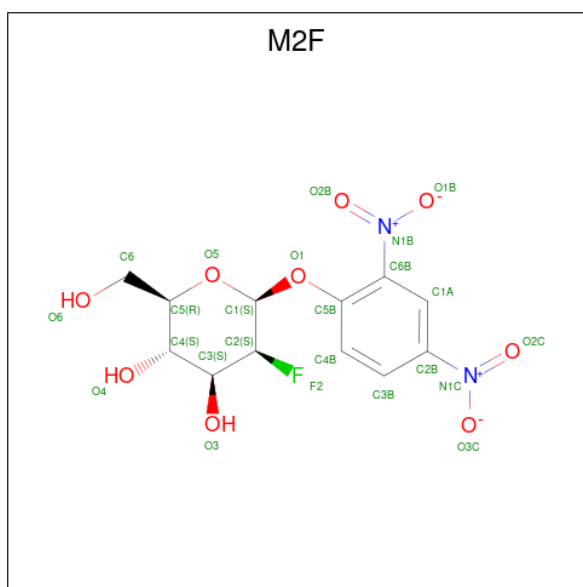
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	4	2	2	0	0

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

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	F	N			O
4	A	1	24	12	1	2	9	0	0
4	B	1	24	12	1	2	9	0	0

- Molecule 5 is BROMIDE ION (three-letter code: BR) (formula: Br).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Br		
5	A	6	6	6	0	0
5	B	6	6	6	0	0


- Molecule 6 is water.

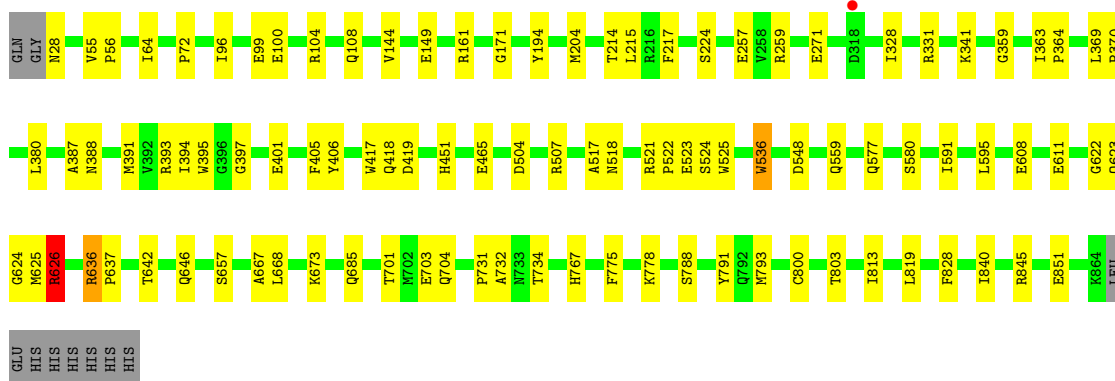
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	581	581	581	0	0
6	B	568	568	568	0	0

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.

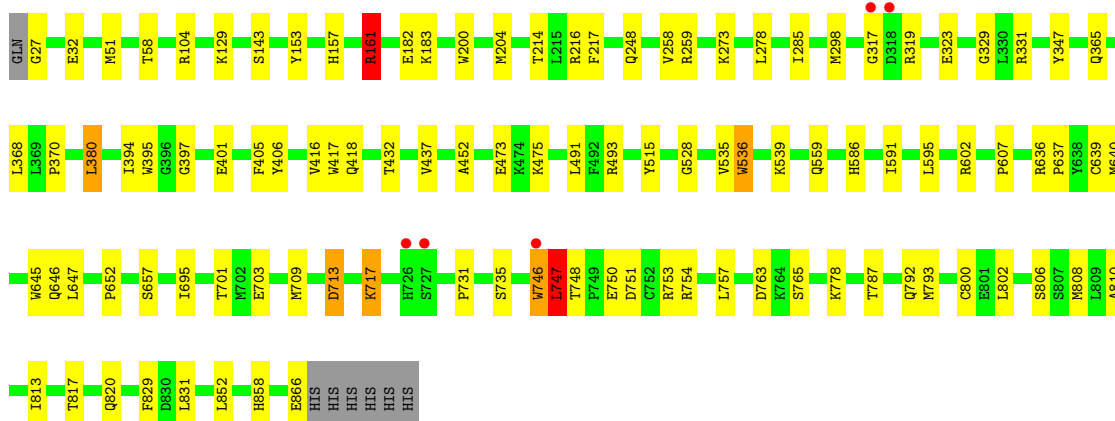
• Molecule 1: BETA-MANNOSIDASE

Chain A:  87% 11%



• Molecule 1: BETA-MANNOSIDASE

Chain B:  87% 12%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	91.45Å 115.50Å 97.70Å 90.00° 115.99° 90.00°	Depositor
Resolution (Å)	47.84 – 2.10 45.93 – 2.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.84-2.10) 100.0 (45.93-2.10)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.74 (at 2.10Å)	Xtrriage
Refinement program	REFMAC 5.5.0082	Depositor
R, R_{free}	0.169 , 0.232 0.170 , 0.233	Depositor DCC
R_{free} test set	5249 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	19.3	Xtrriage
Anisotropy	0.062	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 50.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.025 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	14932	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.45% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BR, CL, EDO, M2F

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	0.90	3/6996 (0.0%)	0.83	4/9520 (0.0%)
1	B	1.00	6/7025 (0.1%)	1.05	10/9554 (0.1%)
All	All	0.95	9/14021 (0.1%)	0.94	14/19074 (0.1%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	216	ARG	CZ-NH2	-30.73	0.93	1.33
1	B	746	TRP	CE3-CZ3	10.78	1.56	1.38
1	B	747	LEU	CG-CD1	-9.42	1.17	1.51
1	A	99	GLU	CD-OE2	-8.09	1.16	1.25
1	B	746	TRP	CD2-CE3	-5.77	1.31	1.40
1	A	611	GLU	CG-CD	5.62	1.60	1.51
1	B	639	CYS	CB-SG	-5.59	1.72	1.81
1	A	100	GLU	CB-CG	5.29	1.62	1.52
1	B	153	TYR	CE2-CZ	5.21	1.45	1.38

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	216	ARG	NE-CZ-NH2	53.47	147.03	120.30
1	B	216	ARG	NH1-CZ-NH2	-24.92	91.98	119.40
1	B	746	TRP	CE3-CZ3-CH2	-9.58	110.66	121.20
1	A	626	ARG	NE-CZ-NH2	-9.28	115.66	120.30
1	B	298	MET	CG-SD-CE	7.67	112.47	100.20
1	A	161	ARG	NE-CZ-NH2	-7.48	116.56	120.30
1	A	626	ARG	NE-CZ-NH1	7.38	123.99	120.30
1	B	161	ARG	NE-CZ-NH2	-7.21	116.70	120.30
1	B	746	TRP	CD2-CE3-CZ3	7.20	128.16	118.80
1	A	215	LEU	CB-CG-CD2	-7.13	98.89	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	51[A]	MET	CG-SD-CE	6.70	110.92	100.20
1	B	51[B]	MET	CG-SD-CE	6.70	110.92	100.20
1	B	713	ASP	CB-CG-OD2	-5.44	113.41	118.30
1	B	713	ASP	CB-CG-OD1	5.07	122.86	118.30

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	6767	0	6462	71	0
1	B	6797	0	6478	94	0
2	A	76	0	114	14	0
2	B	76	0	114	21	0
3	A	4	0	0	2	0
3	B	3	0	0	4	0
4	A	24	0	13	0	0
4	B	24	0	13	0	0
5	A	6	0	0	2	0
5	B	6	0	0	0	0
6	A	581	0	0	16	0
6	B	568	0	0	17	0
All	All	14932	0	13194	170	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 6.

All (170) 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)
3:A:1867:CL:CL	6:A:2390:HOH:O	1.97	1.18
3:B:1893:CL:CL	6:B:2078:HOH:O	2.02	1.14
1:B:709:MET:HB3	1:B:757:LEU:HD11	1.46	0.98
1:B:746:TRP:CD1	1:B:747:LEU:CD1	2.49	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1894:CL:CL	6:A:2056:HOH:O	2.21	0.95
1:B:161:ARG:HB3	6:B:2128:HOH:O	1.72	0.87
1:B:129:LYS:NZ	2:B:1877:EDO:H22	1.94	0.82
1:B:808:MET:CE	6:B:2507:HOH:O	2.29	0.81
1:B:746:TRP:CD1	1:B:747:LEU:HD11	2.18	0.78
1:A:328:ILE:HG23	2:A:1871:EDO:H22	1.64	0.78
1:B:746:TRP:CG	1:B:747:LEU:CD1	2.67	0.78
1:A:171:GLY:HA2	6:A:2148:HOH:O	1.84	0.77
1:A:624:GLY:HA2	2:A:1891:EDO:H21	1.68	0.75
1:B:380:LEU:HD11	1:B:647:LEU:HD21	1.67	0.75
1:B:129:LYS:HZ1	2:B:1877:EDO:H22	1.52	0.73
1:A:96:ILE:HG12	2:A:1886:EDO:H11	1.68	0.73
1:B:746:TRP:C	1:B:747:LEU:HD12	2.08	0.73
1:A:259:ARG:NH2	6:A:2229:HOH:O	2.22	0.72
1:B:636:ARG:HG2	1:B:637:PRO:HA	1.73	0.70
1:A:623:GLN:OE1	1:A:626:ARG:NH1	2.21	0.70
1:B:748:THR:HG23	1:B:751:ASP:H	1.56	0.69
1:B:746:TRP:CG	1:B:747:LEU:HD13	2.27	0.69
1:B:746:TRP:CD1	1:B:747:LEU:HD12	2.28	0.67
1:B:636:ARG:HD2	2:B:1871:EDO:H12	1.76	0.67
1:B:475:LYS:NZ	6:B:2332:HOH:O	2.28	0.67
1:B:401:GLU:O	1:B:406[A]:TYR:HE2	1.77	0.67
1:B:406[B]:TYR:OH	1:B:418:GLN:OE1	2.12	0.66
1:A:96:ILE:HG12	2:A:1886:EDO:C1	2.24	0.66
1:B:637:PRO:HD2	2:B:1870:EDO:O2	1.95	0.66
1:B:793:MET:HE2	1:B:800[A]:CYS:SG	2.36	0.65
1:A:257:GLU:OE1	1:A:259:ARG:HD3	1.99	0.63
1:B:695:ILE:CG2	2:B:1871:EDO:H21	2.28	0.63
1:B:161:ARG:CB	6:B:2128:HOH:O	2.39	0.63
1:A:401:GLU:O	1:A:406[A]:TYR:HE2	1.82	0.63
1:A:608:GLU:O	2:A:1873:EDO:H22	1.98	0.62
1:A:636[A]:ARG:HG2	1:A:637:PRO:HA	1.80	0.62
1:B:432:THR:HG22	6:B:2315:HOH:O	1.98	0.62
1:A:793:MET:SD	1:A:800[A]:CYS:SG	2.97	0.62
1:B:746:TRP:NE1	1:B:747:LEU:HD11	2.14	0.62
1:A:813:ILE:O	1:A:828:PHE:HA	2.00	0.61
1:B:866:GLU:C	6:B:2559:HOH:O	2.38	0.61
1:B:27:GLY:HA3	1:B:323:GLU:OE1	2.01	0.60
1:B:813:ILE:HD11	1:B:829:PHE:CZ	2.37	0.59
1:B:129:LYS:HZ3	2:B:1877:EDO:C2	2.16	0.59
1:B:258:VAL:HG21	1:B:285:ILE:HG21	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:767:HIS:NE2	1:B:32:GLU:OE2	2.30	0.59
1:A:406[B]:TYR:OH	1:A:418:GLN:OE1	2.18	0.58
1:B:713:ASP:OD2	1:B:717:LYS:HE2	2.03	0.58
1:B:792:GLN:CB	6:B:2512:HOH:O	2.50	0.58
1:B:793:MET:CE	1:B:800[A]:CYS:SG	2.91	0.58
1:A:517:ALA:HA	1:A:524:SER:HB2	1.86	0.57
1:B:129:LYS:HZ3	2:B:1877:EDO:H22	1.68	0.57
1:B:129:LYS:NZ	2:B:1877:EDO:C2	2.65	0.57
1:B:536:TRP:CH2	1:B:559:GLN:HB2	2.40	0.57
1:B:750:GLU:HG2	1:B:754:ARG:HD2	1.86	0.57
1:B:437:VAL:HG11	1:B:491:LEU:HD11	1.86	0.57
1:A:701:THR:HG23	1:A:731:PRO:HA	1.87	0.56
1:B:157:HIS:NE2	2:B:1877:EDO:H11	2.20	0.56
1:B:746:TRP:O	1:B:747:LEU:HD12	2.05	0.56
1:A:104:ARG:HG3	1:A:217:PHE:HB3	1.88	0.56
1:B:753:ARG:HD2	6:B:2490:HOH:O	2.06	0.56
1:A:626:ARG:HG3	6:A:2480:HOH:O	2.05	0.55
1:B:380:LEU:HD11	1:B:647:LEU:CD2	2.35	0.55
1:A:328:ILE:HG23	2:A:1871:EDO:C2	2.35	0.55
1:B:813:ILE:HG22	1:B:858:HIS:HB3	1.87	0.55
1:B:452:ALA:HA	2:B:1872:EDO:H22	1.89	0.55
1:A:271:GLU:HG2	6:A:2241:HOH:O	2.05	0.55
1:A:104:ARG:NH1	6:A:2082:HOH:O	2.29	0.55
1:B:713:ASP:OD2	1:B:717:LYS:CE	2.55	0.54
1:B:808:MET:HE1	6:B:2507:HOH:O	1.97	0.54
2:A:1873:EDO:O2	3:B:1886:CL:CL	2.63	0.54
1:A:775:PHE:HB2	2:A:1875:EDO:H22	1.90	0.53
1:A:778:LYS:HE2	6:A:2444:HOH:O	2.08	0.53
1:B:636:ARG:HD2	2:B:1871:EDO:C1	2.38	0.52
1:B:701:THR:HG23	1:B:731:PRO:HA	1.90	0.52
1:B:747:LEU:CD1	1:B:747:LEU:N	2.70	0.52
1:B:329:GLY:O	2:B:1872:EDO:H21	2.08	0.52
1:B:394:ILE:HD11	1:B:405:PHE:CE2	2.44	0.52
1:B:646:GLN:O	1:B:657:SER:HA	2.09	0.52
1:A:395:TRP:CH2	1:A:397:GLY:HA3	2.45	0.52
1:B:787:THR:HA	1:B:808:MET:HE3	1.92	0.52
1:B:157:HIS:CD2	2:B:1877:EDO:H11	2.45	0.51
1:A:625:MET:HB2	1:A:668:LEU:HD13	1.93	0.51
1:B:695:ILE:HG23	2:B:1871:EDO:H21	1.92	0.50
1:A:108:GLN:HG2	5:A:1882:BR:BR	2.66	0.50
1:B:746:TRP:C	1:B:747:LEU:CD1	2.78	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:787:THR:HG23	1:B:806[A]:SER:OG	2.11	0.50
1:A:819:LEU:HD11	1:A:845:ARG:HB2	1.92	0.50
1:A:591:ILE:HD13	1:A:595:LEU:HD22	1.92	0.50
2:B:1878:EDO:H21	6:B:2416:HOH:O	2.12	0.50
1:A:380:LEU:HD13	6:A:2308:HOH:O	2.11	0.50
1:B:182:GLU:HG2	6:B:2154:HOH:O	2.12	0.50
1:A:465:GLU:OE2	1:A:518:ASN:ND2	2.44	0.50
1:A:667:ALA:HB2	1:A:828:PHE:CD1	2.47	0.50
1:B:143:SER:HB3	2:B:1894:EDO:C1	2.41	0.50
1:A:149:GLU:CB	6:A:2135:HOH:O	2.60	0.49
1:A:387:ALA:O	1:A:388:ASN:HB2	2.10	0.49
1:A:504:ASP:OD2	1:A:507:ARG:HD2	2.13	0.49
1:A:577:GLN:HA	3:B:1886:CL:CL	2.49	0.49
3:B:1885:CL:CL	6:B:2462:HOH:O	2.57	0.49
1:A:451:HIS:CE1	2:A:1877:EDO:H22	2.48	0.49
1:A:522:PRO:HA	1:A:525:TRP:CE2	2.47	0.49
1:B:817:THR:HG21	1:B:852:LEU:HD21	1.95	0.49
1:A:622:GLY:O	1:A:626:ARG:HB3	2.13	0.48
1:A:144[B]:VAL:HG13	6:A:2100:HOH:O	2.13	0.48
1:B:104:ARG:HG3	1:B:217:PHE:HB3	1.95	0.48
1:B:200:TRP:HE1	1:B:645:TRP:HZ2	1.62	0.48
1:B:591:ILE:HD12	1:B:595:LEU:HD12	1.95	0.48
1:A:525:TRP:CE2	2:A:1870:EDO:H12	2.49	0.48
1:B:493:ARG:NH1	6:B:2343:HOH:O	2.20	0.48
1:B:735[B]:SER:OG	2:B:1871:EDO:H11	2.14	0.47
1:A:791:TYR:HA	1:A:803:THR:O	2.13	0.47
1:A:359:GLY:HA3	1:A:391:MET:O	2.14	0.47
1:A:548:ASP:O	2:A:1870:EDO:H22	2.14	0.47
1:B:204:MET:HE2	1:B:368:LEU:HD21	1.97	0.47
1:A:363:ILE:HB	1:A:364:PRO:HD2	1.96	0.47
1:A:642:THR:O	1:A:642:THR:HG23	2.15	0.47
1:B:143:SER:HB3	2:B:1894:EDO:H11	1.97	0.47
1:B:748:THR:HG22	1:B:751:ASP:CG	2.36	0.47
1:A:521:ARG:HG2	1:A:523:GLU:OE2	2.15	0.46
1:B:259:ARG:NH2	1:B:317:GLY:O	2.46	0.46
1:B:810:ALA:HB3	1:B:831:LEU:HB3	1.97	0.46
1:A:394:ILE:HD11	1:A:405:PHE:CE2	2.51	0.46
1:A:646:GLN:O	1:A:657:SER:HA	2.16	0.45
1:A:536:TRP:CH2	1:A:559:GLN:HB2	2.52	0.45
1:B:515:TYR:CE2	1:B:528:GLY:HA3	2.52	0.45
1:B:808:MET:HE3	1:B:808:MET:HB2	1.74	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:341:LYS:HG2	6:A:2274:HOH:O	2.15	0.45
1:B:248:GLN:OE1	1:B:278:LEU:HB3	2.17	0.44
1:B:602:ARG:O	1:B:778:LYS:HD3	2.16	0.44
1:A:793:MET:CG	1:A:800[A]:CYS:SG	3.05	0.44
1:A:204:MET:HB3	1:A:204:MET:HE2	1.91	0.44
1:A:685:GLN:HG2	5:A:1883:BR:BR	2.73	0.43
1:A:64:ILE:HD11	1:A:72:PRO:HG3	1.99	0.43
1:B:586:HIS:HD2	1:B:652:PRO:O	2.02	0.43
1:B:746:TRP:CE2	1:B:747:LEU:HD11	2.54	0.43
1:B:535:VAL:O	1:B:536:TRP:HB3	2.18	0.43
1:A:28:ASN:HB3	6:A:2001:HOH:O	2.18	0.43
1:A:845:ARG:HG2	6:B:2547:HOH:O	2.18	0.43
1:B:143:SER:HB3	2:B:1894:EDO:H12	2.01	0.43
1:A:96:ILE:HG12	2:A:1886:EDO:H12	2.00	0.42
1:B:747:LEU:HD12	1:B:747:LEU:N	2.33	0.42
1:A:636[B]:ARG:HD2	6:A:2464:HOH:O	2.19	0.42
1:B:763:ASP:OD2	1:B:765:SER:N	2.53	0.42
1:A:55:VAL:HA	1:A:56:PRO:C	2.40	0.42
1:A:840:ILE:O	2:A:1876:EDO:H12	2.20	0.42
1:B:607:PRO:O	2:B:1878:EDO:H22	2.20	0.42
1:A:214:THR:HG21	6:A:2042:HOH:O	2.20	0.41
1:A:703:GLU:C	1:A:704:GLN:HG2	2.40	0.41
1:B:182:GLU:HG3	1:B:183:LYS:HG3	2.02	0.41
1:B:401:GLU:C	1:B:406[A]:TYR:HE2	2.24	0.41
1:B:406[B]:TYR:CE1	1:B:416:VAL:HG11	2.55	0.41
1:A:673:LYS:CE	6:A:2482:HOH:O	2.67	0.41
1:B:214:THR:HG23	6:B:2088:HOH:O	2.20	0.41
1:A:393:ARG:NH2	1:A:419:ASP:OD2	2.52	0.41
1:B:347:TYR:HB3	1:B:640:MET:CB	2.50	0.41
1:B:750:GLU:CG	1:B:754:ARG:HD2	2.51	0.41
1:B:645:TRP:HA	1:B:646:GLN:HA	1.92	0.41
1:B:820:GLN:OE1	1:B:820:GLN:HA	2.21	0.41
1:B:515:TYR:CD1	2:B:1874:EDO:H22	2.55	0.41
1:A:793:MET:HG3	1:A:800[A]:CYS:SG	2.61	0.41
1:A:522:PRO:HA	1:A:525:TRP:CD2	2.56	0.40
1:A:577:GLN:HB2	1:A:580:SER:HB3	2.02	0.40
1:A:732:ALA:O	1:A:734:THR:HG23	2.21	0.40
1:B:58:THR:HG23	1:B:370:PRO:HD2	2.02	0.40
1:A:369:LEU:HB2	1:A:370:PRO:HD3	2.02	0.40
1:B:365:GLN:CD	1:B:380:LEU:HD23	2.42	0.40
1:A:624:GLY:CA	2:A:1891:EDO:H21	2.47	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:319:ARG:HD2	6:B:2006:HOH:O	2.21	0.40
1:B:395:TRP:CH2	1:B:397:GLY:HA3	2.56	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	848/847 (100%)	821 (97%)	25 (3%)	2 (0%)	47 49
1	B	852/847 (101%)	824 (97%)	26 (3%)	2 (0%)	47 49
All	All	1700/1694 (100%)	1645 (97%)	51 (3%)	4 (0%)	47 49

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	539	LYS
1	A	536	TRP
1	B	536	TRP
1	A	851	GLU

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	722/755 (96%)	713 (99%)	9 (1%)	71	77
1	B	723/755 (96%)	713 (99%)	10 (1%)	67	73
All	All	1445/1510 (96%)	1426 (99%)	19 (1%)	71	75

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	194	TYR
1	A	224[A]	SER
1	A	224[B]	SER
1	A	331	ARG
1	A	417	TRP
1	A	626	ARG
1	A	636[A]	ARG
1	A	636[B]	ARG
1	A	788	SER
1	B	161	ARG
1	B	273	LYS
1	B	331	ARG
1	B	380	LEU
1	B	417	TRP
1	B	473	GLU
1	B	703	GLU
1	B	717	LYS
1	B	747	LEU
1	B	802	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	584	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 59 ligands modelled in this entry, 19 are monoatomic - leaving 40 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	EDO	A	1865	-	3,3,3	0.47	0	2,2,2	0.54	0
2	EDO	B	1892	-	3,3,3	0.57	0	2,2,2	0.40	0
2	EDO	A	1876	-	3,3,3	0.49	0	2,2,2	0.40	0
2	EDO	B	1874	-	3,3,3	0.34	0	2,2,2	0.91	0
2	EDO	A	1875	-	3,3,3	0.48	0	2,2,2	0.27	0
2	EDO	B	1870	-	3,3,3	0.32	0	2,2,2	0.63	0
2	EDO	B	1889	-	3,3,3	0.37	0	2,2,2	0.73	0
4	M2F	A	1869	-	23,25,25	3.70	7 (30%)	28,36,36	2.13	7 (25%)
2	EDO	B	1891	-	3,3,3	0.22	0	2,2,2	0.81	0
2	EDO	B	1895	-	3,3,3	0.72	0	2,2,2	0.55	0
4	M2F	B	1868	-	23,25,25	3.55	6 (26%)	28,36,36	1.60	6 (21%)
2	EDO	A	1871	-	3,3,3	0.83	0	2,2,2	0.37	0
2	EDO	B	1878	-	3,3,3	0.25	0	2,2,2	1.08	0
2	EDO	A	1873	-	3,3,3	0.32	0	2,2,2	0.71	0
2	EDO	B	1879	-	3,3,3	0.47	0	2,2,2	0.63	0
2	EDO	A	1872	-	3,3,3	0.55	0	2,2,2	0.47	0
2	EDO	A	1879	-	3,3,3	0.89	0	2,2,2	0.15	0
2	EDO	B	1871	-	3,3,3	0.47	0	2,2,2	0.47	0
2	EDO	B	1869	-	3,3,3	0.47	0	2,2,2	0.20	0
2	EDO	A	1870	-	3,3,3	0.38	0	2,2,2	0.50	0
2	EDO	B	1867	-	3,3,3	0.46	0	2,2,2	0.30	0
2	EDO	B	1877	-	3,3,3	0.20	0	2,2,2	0.56	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	EDO	A	1887	-	3,3,3	0.38	0	2,2,2	0.43	0
2	EDO	B	1880	-	3,3,3	0.58	0	2,2,2	0.52	0
2	EDO	B	1894	-	3,3,3	0.37	0	2,2,2	0.11	0
2	EDO	B	1873	-	3,3,3	0.93	0	2,2,2	0.95	0
2	EDO	B	1875	-	3,3,3	0.61	0	2,2,2	0.74	0
2	EDO	A	1877	-	3,3,3	0.73	0	2,2,2	0.65	0
2	EDO	A	1892	-	3,3,3	0.74	0	2,2,2	0.76	0
2	EDO	A	1888	-	3,3,3	0.65	0	2,2,2	0.15	0
2	EDO	A	1886	-	3,3,3	0.42	0	2,2,2	0.68	0
2	EDO	B	1887	-	3,3,3	0.46	0	2,2,2	0.33	0
2	EDO	A	1868	-	3,3,3	0.94	0	2,2,2	0.27	0
2	EDO	B	1876	-	3,3,3	0.61	0	2,2,2	0.31	0
2	EDO	A	1889	-	3,3,3	0.42	0	2,2,2	0.81	0
2	EDO	A	1878	-	3,3,3	0.54	0	2,2,2	0.40	0
2	EDO	A	1891	-	3,3,3	0.75	0	2,2,2	0.26	0
2	EDO	B	1872	-	3,3,3	0.48	0	2,2,2	0.48	0
2	EDO	A	1866	-	3,3,3	0.77	0	2,2,2	0.35	0
2	EDO	A	1874	-	3,3,3	0.66	0	2,2,2	0.53	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
2	EDO	A	1865	-	-	1/1/1/1	-
2	EDO	B	1892	-	-	1/1/1/1	-
2	EDO	A	1876	-	-	1/1/1/1	-
2	EDO	B	1874	-	-	0/1/1/1	-
2	EDO	A	1875	-	-	1/1/1/1	-
2	EDO	B	1870	-	-	1/1/1/1	-
2	EDO	B	1889	-	-	1/1/1/1	-
4	M2F	A	1869	-	-	0/10/34/34	0/2/2/2
2	EDO	B	1891	-	-	1/1/1/1	-
2	EDO	B	1895	-	-	1/1/1/1	-
4	M2F	B	1868	-	-	0/10/34/34	0/2/2/2
2	EDO	A	1871	-	-	0/1/1/1	-
2	EDO	B	1878	-	-	1/1/1/1	-
2	EDO	A	1873	-	-	1/1/1/1	-
2	EDO	B	1879	-	-	1/1/1/1	-
2	EDO	A	1872	-	-	0/1/1/1	-
2	EDO	A	1879	-	-	0/1/1/1	-
2	EDO	B	1871	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EDO	B	1869	-	-	1/1/1/1	-
2	EDO	A	1870	-	-	1/1/1/1	-
2	EDO	B	1867	-	-	1/1/1/1	-
2	EDO	B	1877	-	-	1/1/1/1	-
2	EDO	A	1887	-	-	1/1/1/1	-
2	EDO	B	1880	-	-	0/1/1/1	-
2	EDO	B	1894	-	-	1/1/1/1	-
2	EDO	B	1873	-	-	1/1/1/1	-
2	EDO	B	1875	-	-	0/1/1/1	-
2	EDO	A	1877	-	-	0/1/1/1	-
2	EDO	A	1892	-	-	0/1/1/1	-
2	EDO	A	1888	-	-	0/1/1/1	-
2	EDO	A	1886	-	-	0/1/1/1	-
2	EDO	B	1887	-	-	1/1/1/1	-
2	EDO	A	1868	-	-	0/1/1/1	-
2	EDO	B	1876	-	-	0/1/1/1	-
2	EDO	A	1889	-	-	1/1/1/1	-
2	EDO	A	1878	-	-	1/1/1/1	-
2	EDO	A	1891	-	-	1/1/1/1	-
2	EDO	B	1872	-	-	1/1/1/1	-
2	EDO	A	1866	-	-	1/1/1/1	-
2	EDO	A	1874	-	-	1/1/1/1	-

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1869	M2F	O2C-N1C	12.08	1.43	1.22
4	B	1868	M2F	O2C-N1C	11.27	1.41	1.22
4	A	1869	M2F	O2B-N1B	9.62	1.39	1.22
4	B	1868	M2F	O2B-N1B	8.55	1.37	1.22
4	B	1868	M2F	C6B-N1B	-5.59	1.35	1.45
4	A	1869	M2F	C2-C3	4.65	1.56	1.52
4	B	1868	M2F	C2B-N1C	-4.64	1.34	1.45
4	B	1868	M2F	O1-C1	4.20	1.47	1.41
4	A	1869	M2F	C2B-N1C	-4.03	1.35	1.45
4	A	1869	M2F	C6B-N1B	-3.46	1.39	1.45
4	A	1869	M2F	O1-C1	2.44	1.44	1.41
4	A	1869	M2F	C6-C5	2.24	1.59	1.51
4	B	1868	M2F	O1-C5B	-2.12	1.33	1.37

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1869	M2F	C3B-C2B-N1C	6.65	124.38	119.38
4	A	1869	M2F	F2-C2-C3	4.04	112.44	108.85
4	B	1868	M2F	F2-C2-C3	3.90	112.32	108.85
4	A	1869	M2F	C1A-C2B-N1C	-3.80	115.40	118.75
4	B	1868	M2F	F2-C2-C1	3.58	111.58	107.57
4	A	1869	M2F	O2C-N1C-C2B	3.03	123.09	118.80
4	A	1869	M2F	C1-O5-C5	3.00	119.58	113.69
4	A	1869	M2F	C1A-C6B-C5B	-2.97	117.24	121.75
4	A	1869	M2F	C2B-C1A-C6B	2.81	123.02	119.29
4	B	1868	M2F	O1-C5B-C6B	2.61	120.46	117.31
4	B	1868	M2F	C1A-C6B-C5B	-2.41	118.08	121.75
4	B	1868	M2F	O1-C1-C2	-2.27	103.47	107.25
4	B	1868	M2F	C1A-C2B-N1C	2.03	120.54	118.75

There are no chirality outliers.

All (25) torsion outliers are listed below:

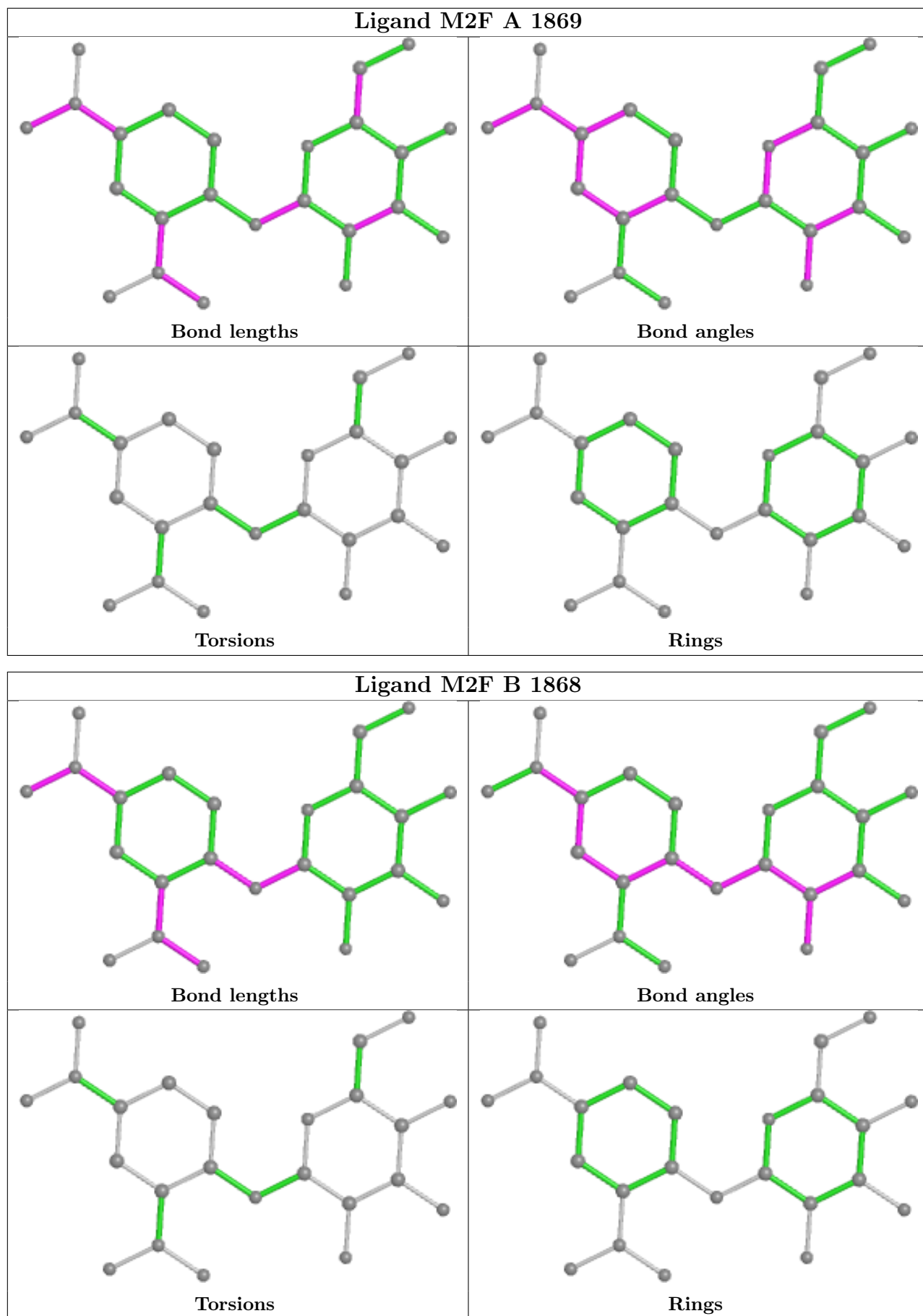
Mol	Chain	Res	Type	Atoms
2	A	1865	EDO	O1-C1-C2-O2
2	A	1873	EDO	O1-C1-C2-O2
2	A	1891	EDO	O1-C1-C2-O2
2	B	1867	EDO	O1-C1-C2-O2
2	B	1870	EDO	O1-C1-C2-O2
2	B	1891	EDO	O1-C1-C2-O2
2	B	1892	EDO	O1-C1-C2-O2
2	A	1889	EDO	O1-C1-C2-O2
2	A	1874	EDO	O1-C1-C2-O2
2	A	1887	EDO	O1-C1-C2-O2
2	B	1872	EDO	O1-C1-C2-O2
2	B	1877	EDO	O1-C1-C2-O2
2	B	1894	EDO	O1-C1-C2-O2
2	A	1866	EDO	O1-C1-C2-O2
2	A	1875	EDO	O1-C1-C2-O2
2	A	1870	EDO	O1-C1-C2-O2
2	A	1878	EDO	O1-C1-C2-O2
2	B	1895	EDO	O1-C1-C2-O2
2	B	1889	EDO	O1-C1-C2-O2
2	B	1869	EDO	O1-C1-C2-O2
2	B	1878	EDO	O1-C1-C2-O2
2	B	1879	EDO	O1-C1-C2-O2
2	B	1887	EDO	O1-C1-C2-O2
2	A	1876	EDO	O1-C1-C2-O2
2	B	1873	EDO	O1-C1-C2-O2

There are no ring outliers.

15 monomers are involved in 35 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1876	EDO	1	0
2	B	1874	EDO	1	0
2	A	1875	EDO	1	0
2	B	1870	EDO	1	0
2	A	1871	EDO	2	0
2	B	1878	EDO	2	0
2	A	1873	EDO	2	0
2	B	1871	EDO	5	0
2	A	1870	EDO	2	0
2	B	1877	EDO	7	0
2	B	1894	EDO	3	0
2	A	1877	EDO	1	0
2	A	1886	EDO	3	0
2	A	1891	EDO	2	0
2	B	1872	EDO	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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	837/847 (98%)	-0.42	1 (0%) 95 96	8, 19, 37, 49	5 (0%)
1	B	840/847 (99%)	-0.44	5 (0%) 89 91	8, 19, 36, 45	5 (0%)
All	All	1677/1694 (98%)	-0.43	6 (0%) 92 93	8, 19, 37, 49	10 (0%)

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	727	SER	3.4
1	B	318	ASP	3.2
1	A	318	ASP	2.7
1	B	317	GLY	2.6
1	B	726	HIS	2.4
1	B	746	TRP	2.4

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(\AA^2)	Q<0.9
2	EDO	A	1868	4/4	0.74	0.22	32,33,34,34	0
3	CL	A	1894	1/1	0.74	0.14	33,33,33,33	1
5	BR	B	1888	1/1	0.77	0.12	79,79,79,79	1
5	BR	B	1890	1/1	0.80	0.13	51,51,51,51	1
2	EDO	B	1892	4/4	0.82	0.15	38,41,41,42	0
2	EDO	B	1889	4/4	0.84	0.23	41,41,43,43	0
2	EDO	A	1873	4/4	0.86	0.26	29,31,33,36	0
2	EDO	A	1866	4/4	0.86	0.16	28,32,33,33	0
2	EDO	A	1886	4/4	0.87	0.17	33,39,40,40	0
2	EDO	A	1865	4/4	0.87	0.21	14,15,18,19	4
2	EDO	B	1880	4/4	0.89	0.12	32,35,36,39	0
2	EDO	A	1876	4/4	0.89	0.11	30,31,31,33	0
2	EDO	A	1891	4/4	0.89	0.12	23,24,26,30	0
2	EDO	A	1892	4/4	0.91	0.13	20,24,29,30	0
2	EDO	A	1888	4/4	0.92	0.18	35,37,38,39	0
5	BR	B	1882	1/1	0.92	0.06	42,42,42,42	1
2	EDO	A	1871	4/4	0.93	0.11	15,25,28,33	0
2	EDO	A	1875	4/4	0.93	0.12	25,29,29,29	0
2	EDO	B	1870	4/4	0.94	0.11	33,34,35,35	0
2	EDO	B	1873	4/4	0.94	0.12	20,20,24,24	0
2	EDO	A	1889	4/4	0.94	0.24	29,31,31,32	0
2	EDO	B	1878	4/4	0.95	0.15	35,36,37,39	0
2	EDO	A	1870	4/4	0.95	0.12	23,25,25,32	0
2	EDO	A	1872	4/4	0.95	0.10	17,17,20,22	0
2	EDO	B	1891	4/4	0.95	0.14	28,30,30,32	0
2	EDO	B	1871	4/4	0.95	0.12	29,30,31,31	0
2	EDO	B	1895	4/4	0.95	0.19	22,25,28,30	0
2	EDO	A	1887	4/4	0.95	0.12	31,32,33,34	0
3	CL	B	1886	1/1	0.95	0.16	37,37,37,37	1
4	M2F	A	1869	24/24	0.95	0.10	12,19,28,32	0
5	BR	A	1883	1/1	0.95	0.04	42,42,42,42	1
5	BR	A	1884	1/1	0.95	0.07	35,35,35,35	1
2	EDO	B	1874	4/4	0.95	0.13	26,26,27,27	0
2	EDO	B	1875	4/4	0.95	0.08	18,22,24,24	0
2	EDO	B	1877	4/4	0.95	0.13	20,23,26,29	0
2	EDO	A	1874	4/4	0.96	0.12	18,18,19,22	0
4	M2F	B	1868	24/24	0.96	0.10	11,20,29,31	0
2	EDO	B	1879	4/4	0.96	0.09	25,26,27,28	1
2	EDO	B	1894	4/4	0.96	0.16	30,32,32,32	0
5	BR	A	1890	1/1	0.96	0.09	35,35,35,35	1
2	EDO	B	1876	4/4	0.96	0.12	21,23,25,25	0
5	BR	B	1884	1/1	0.96	0.07	56,56,56,56	0
2	EDO	B	1887	4/4	0.96	0.12	28,29,31,32	0

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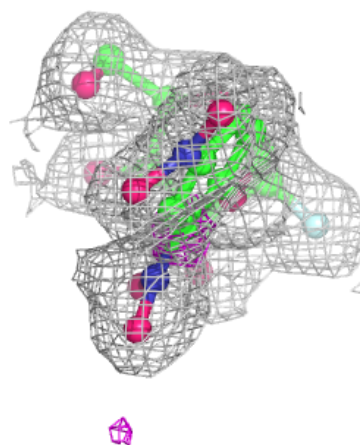
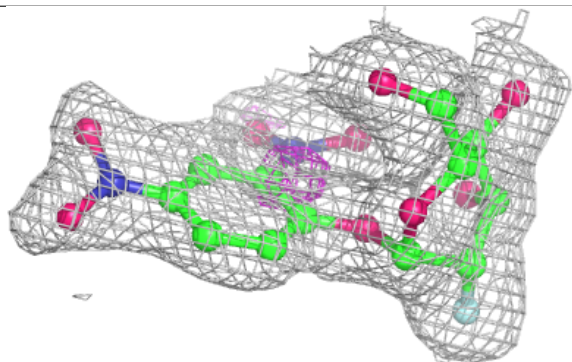
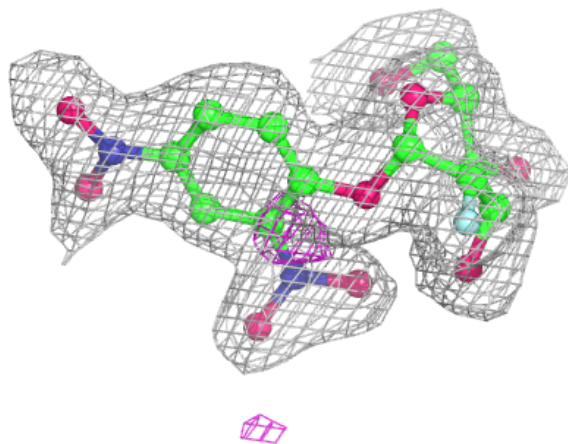
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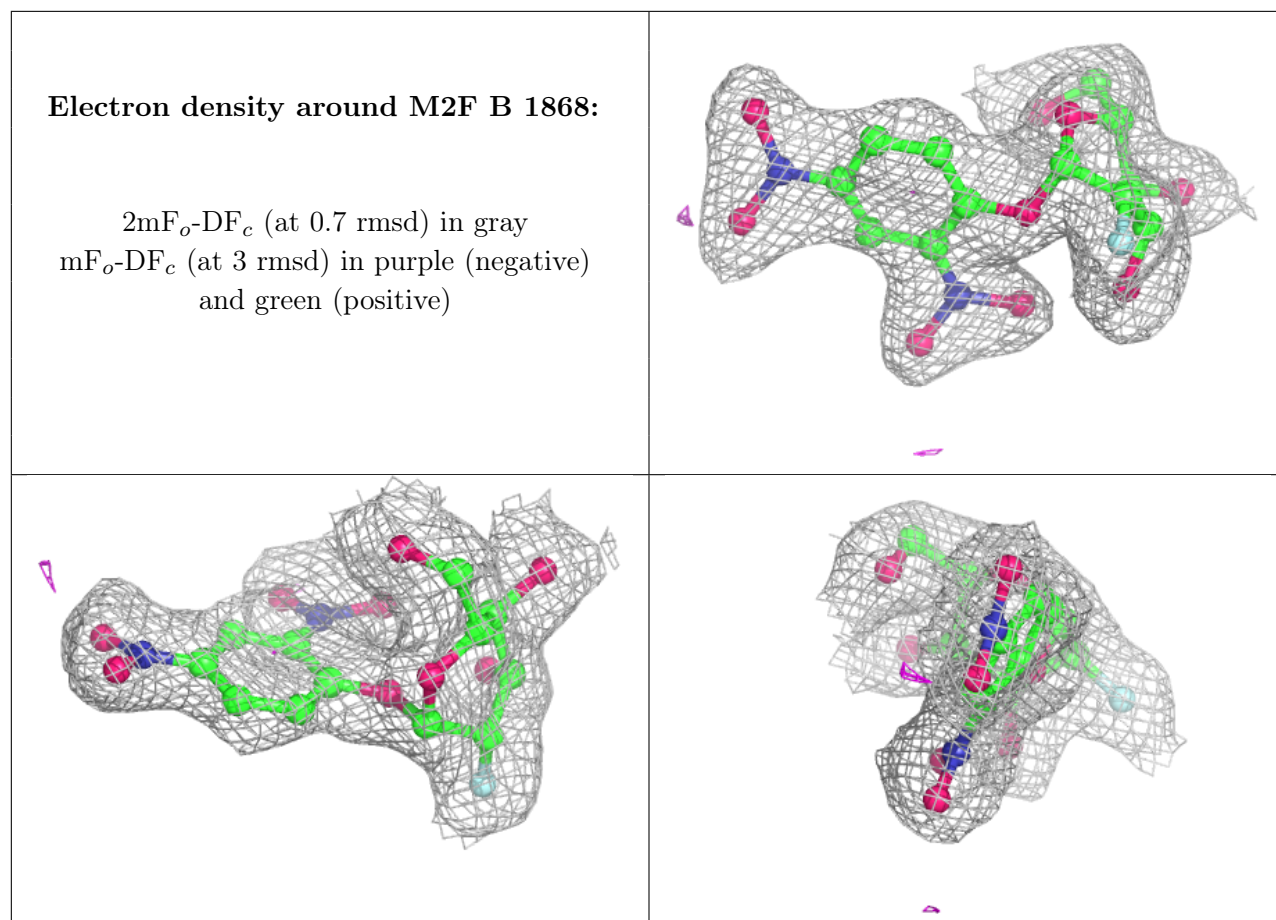
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	EDO	B	1869	4/4	0.96	0.16	21,22,22,23	0
3	CL	A	1880	1/1	0.97	0.06	37,37,37,37	0
2	EDO	B	1867	4/4	0.97	0.15	27,27,30,30	0
3	CL	B	1885	1/1	0.97	0.09	22,22,22,22	1
2	EDO	B	1872	4/4	0.97	0.26	16,24,26,28	0
2	EDO	A	1877	4/4	0.97	0.09	11,14,16,20	0
2	EDO	A	1878	4/4	0.97	0.10	25,27,27,28	0
5	BR	A	1882	1/1	0.97	0.04	29,29,29,29	1
3	CL	A	1893	1/1	0.98	0.06	31,31,31,31	0
2	EDO	A	1879	4/4	0.98	0.07	11,12,19,19	0
3	CL	A	1867	1/1	0.99	0.08	18,18,18,18	1
5	BR	B	1883	1/1	0.99	0.03	25,25,25,25	1
5	BR	A	1885	1/1	0.99	0.06	10,10,10,10	1
3	CL	B	1893	1/1	0.99	0.17	8,8,8,8	1
5	BR	B	1881	1/1	0.99	0.03	21,21,21,21	0
5	BR	A	1881	1/1	1.00	0.02	25,25,25,25	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 M2F A 1869:

$2mF_o-DF_c$ (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.