



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:14 PM UTC

PDB ID : 6SH9 / pdb_00006sh9
Title : EngBF DARPin Fusion 4b D12
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Deposited on : 2019-08-06
Resolution : 2.40 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 : 4-5-2 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

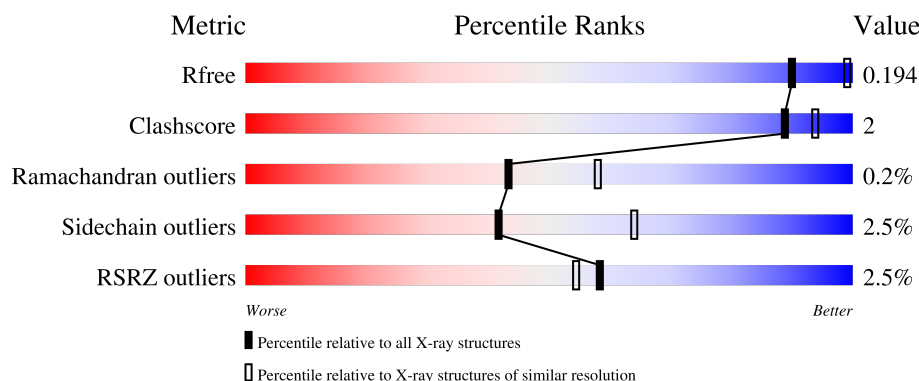
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	B	1357	2% 90% 8% ..
2	E	14	50% 64% 7% 29%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 11359 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 Endo-alpha-N-acetylgalactosaminidase,DARPin 4b D12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	1339	Total	C	N	O	S	0	7	0
			10334	6430	1773	2103	28			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	334	GLY	-	expression tag	UNP Q3T552
B	335	PRO	-	expression tag	UNP Q3T552
B	336	LEU	-	expression tag	UNP Q3T552
B	337	GLY	-	expression tag	UNP Q3T552
B	338	SER	-	expression tag	UNP Q3T552
B	339	MET	-	expression tag	UNP Q3T552
B	342	CYS	SER	conflict	UNP Q3T552
B	1123	SER	GLY	conflict	UNP Q3T552

- Molecule 2 is a protein called Envelope glycoprotein gp160.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	10	Total	C	N	O	0	0	0
			80	54	15	11			

- Molecule 3 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: C₆H₁₃NO₄S).

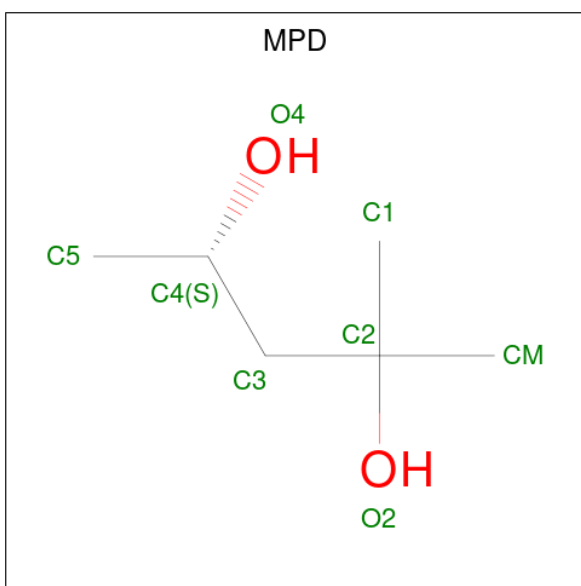


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 4 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	4	Total	Mn	0	0
			4	4		

- Molecule 5 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			8	6	2		

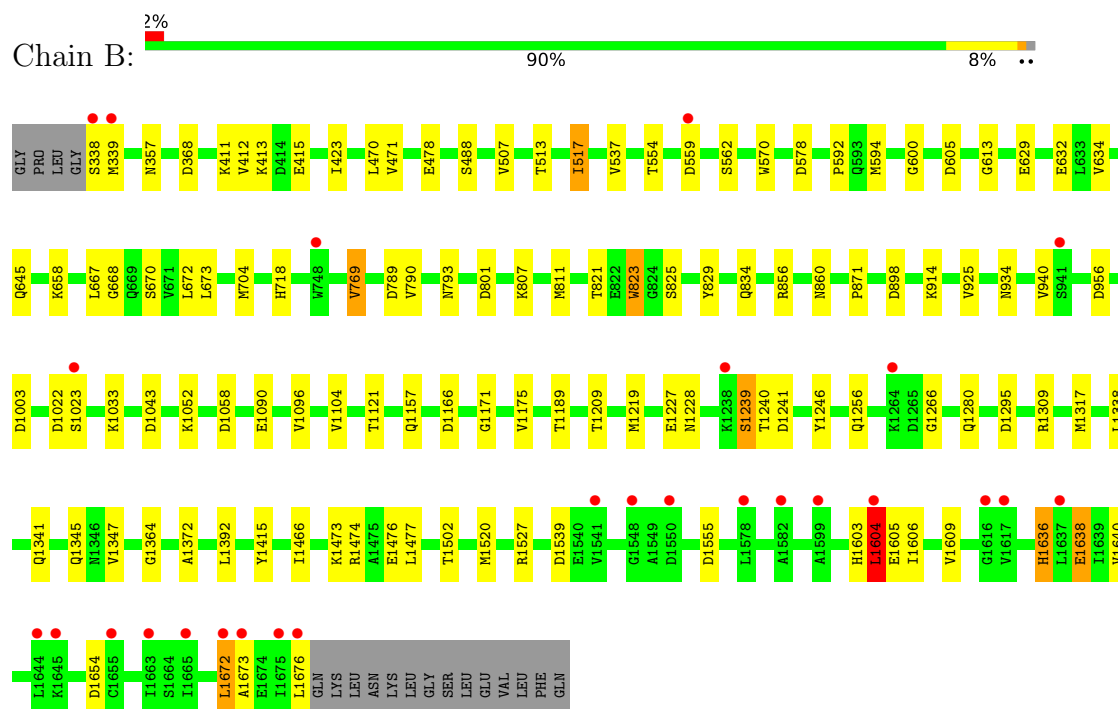
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	919	Total	O	0	0
			919	919		
6	E	2	Total	O	0	0
			2	2		

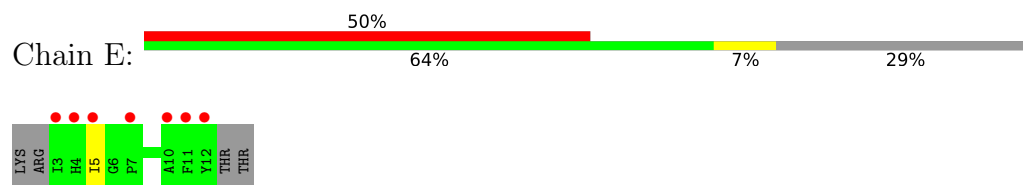
3 Residue-property plots [i](#)

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: Endo-alpha-N-acetylgalactosaminidase,DARPin 4b D12



- Molecule 2: Envelope glycoprotein gp160



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	192.01Å 192.01Å 122.05Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.20 – 2.40 49.20 – 2.40	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.20-2.40) 100.0 (49.20-2.40)	Depositor EDS
R_{merge}	0.37	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.60 (at 2.39Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.161 , 0.193 0.166 , 0.194	Depositor DCC
R_{free} test set	4991 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	52.2	Xtriage
Anisotropy	0.127	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 47.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.028 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	11359	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.97% 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: MN, MES, MPD

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	B	0.75	1/10532 (0.0%)	1.30	51/14286 (0.4%)
2	E	0.81	0/83	1.05	0/111
All	All	0.75	1/10615 (0.0%)	1.30	51/14397 (0.4%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1317	MET	SD-CE	-5.04	1.67	1.79

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1240	THR	CA-C-N	8.23	131.66	120.38
1	B	1240	THR	C-N-CA	8.23	131.66	120.38
1	B	1227	GLU	CA-C-N	7.85	131.13	120.38
1	B	1227	GLU	C-N-CA	7.85	131.13	120.38
1	B	1604	LEU	CA-C-N	6.69	129.57	120.54
1	B	1604	LEU	C-N-CA	6.69	129.57	120.54
1	B	1654	ASP	CA-CB-CG	6.60	119.20	112.60
1	B	1295	ASP	N-CA-C	-6.55	97.17	108.56
1	B	368	ASP	CA-CB-CG	6.19	118.79	112.60
1	B	1058	ASP	CA-CB-CG	6.12	118.72	112.60
1	B	1228	ASN	CA-CB-CG	6.02	118.62	112.60
1	B	629	GLU	CA-C-N	5.98	126.17	120.43
1	B	629	GLU	C-N-CA	5.98	126.17	120.43
1	B	605	ASP	CA-CB-CG	5.80	118.40	112.60
1	B	956	ASP	CA-CB-CG	5.78	118.38	112.60
1	B	513	THR	N-CA-C	-5.77	105.08	111.36
1	B	1636	HIS	CA-C-N	5.67	128.20	120.54
1	B	1636	HIS	C-N-CA	5.67	128.20	120.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1240	THR	N-CA-C	-5.60	103.84	111.56
1	B	1555	ASP	CA-CB-CG	5.59	118.19	112.60
1	B	578	ASP	CA-CB-CG	5.58	118.17	112.60
1	B	357	ASN	CA-CB-CG	5.56	118.16	112.60
1	B	934	ASN	CA-CB-CG	5.52	118.12	112.60
1	B	1673	ALA	CA-C-N	5.49	127.63	120.28
1	B	1673	ALA	C-N-CA	5.49	127.63	120.28
1	B	1603	HIS	CA-C-N	5.46	127.92	120.54
1	B	1603	HIS	C-N-CA	5.46	127.92	120.54
1	B	801	ASP	CA-CB-CG	5.45	118.05	112.60
1	B	823	TRP	CA-C-N	5.40	126.08	120.03
1	B	823	TRP	C-N-CA	5.40	126.08	120.03
1	B	1295	ASP	CA-C-N	5.40	128.44	120.82
1	B	1295	ASP	C-N-CA	5.40	128.44	120.82
1	B	600	GLY	N-CA-C	-5.33	104.99	112.13
1	B	871	PRO	CA-C-N	5.33	127.68	120.38
1	B	871	PRO	C-N-CA	5.33	127.68	120.38
1	B	807	LYS	CA-C-N	5.30	127.33	120.44
1	B	807	LYS	C-N-CA	5.30	127.33	120.44
1	B	1502	THR	CA-C-N	5.30	127.64	120.38
1	B	1502	THR	C-N-CA	5.30	127.64	120.38
1	B	793	ASN	CA-CB-CG	5.28	117.88	112.60
1	B	825	SER	CA-C-N	5.24	125.08	120.10
1	B	825	SER	C-N-CA	5.24	125.08	120.10
1	B	613	GLY	CA-C-N	5.18	127.64	120.29
1	B	613	GLY	C-N-CA	5.18	127.64	120.29
1	B	789	ASP	CA-C-N	5.11	131.16	121.97
1	B	789	ASP	C-N-CA	5.11	131.16	121.97
1	B	898	ASP	CA-CB-CG	5.09	117.69	112.60
1	B	829	TYR	N-CA-C	5.01	116.82	111.36
1	B	1520	MET	CA-C-N	5.00	126.94	120.44
1	B	1520	MET	C-N-CA	5.00	126.94	120.44
1	B	1209	THR	N-CA-C	-5.00	105.54	111.69

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	B	10334	0	9889	38	0
2	E	80	0	77	0	0
3	B	12	0	13	0	0
4	B	4	0	0	0	0
5	B	8	0	14	0	0
6	B	919	0	0	2	0
6	E	2	0	0	0	0
All	All	11359	0	9993	38	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 (38) 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:1189:THR:HB	1:B:1345:GLN:HB3	1.78	0.65
1:B:1157[A]:GLN:HE22	1:B:1256:GLN:HE22	1.50	0.59
1:B:634:VAL:HG11	1:B:667:LEU:HD13	1.85	0.57
1:B:925:VAL:HG12	1:B:940:VAL:HG12	1.87	0.56
1:B:1364:GLY:HA2	1:B:1392:LEU:HD13	1.87	0.54
1:B:1171:GLY:HA3	1:B:1239:SER:HB2	1.90	0.54
1:B:1175:VAL:HG12	1:B:1219:MET:HE3	1.90	0.53
1:B:821:THR:HG22	1:B:834:GLN:NE2	2.24	0.52
1:B:645:GLN:O	1:B:1280:GLN:HG2	2.10	0.51
1:B:1604:LEU:HD11	1:B:1638:GLU:HB3	1.92	0.51
1:B:1640:VAL:HG21	1:B:1672:LEU:HD21	1.93	0.51
1:B:823:TRP:O	1:B:834:GLN:HG3	2.11	0.51
1:B:634:VAL:HA	1:B:914:LYS:HG3	1.92	0.51
1:B:769:VAL:HG23	1:B:811:MET:HB2	1.93	0.51
1:B:570:TRP:CD2	1:B:592:PRO:HB3	2.47	0.50
1:B:507:VAL:HG22	1:B:554:THR:HG23	1.95	0.49
1:B:471:VAL:HB	1:B:517:ILE:HD11	1.94	0.48
1:B:1309:ARG:HD3	6:B:1997:HOH:O	2.14	0.48
1:B:673:LEU:HD11	1:B:704:MET:HE1	1.95	0.47
1:B:1309:ARG:HA	6:B:1997:HOH:O	2.17	0.45
1:B:554:THR:HA	1:B:562:SER:O	2.17	0.45
1:B:1052:LYS:HE2	1:B:1090:GLU:HG3	2.00	0.44
1:B:1606:ILE:HA	1:B:1609:VAL:HG12	2.00	0.44
1:B:632:GLU:O	1:B:668:GLY:HA3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1003:ASP:HB2	1:B:1033:LYS:HE2	2.00	0.44
1:B:1476:GLU:HG2	1:B:1527:ARG:HD2	2.00	0.44
1:B:658:LYS:HD3	1:B:1096:VAL:HG13	2.00	0.43
1:B:856:ARG:O	1:B:860:ASN:HB2	2.18	0.43
1:B:672:LEU:HD11	1:B:718:HIS:HB2	2.01	0.42
1:B:1636:HIS:O	1:B:1640:VAL:HG23	2.19	0.42
1:B:488:SER:HB2	1:B:537:VAL:HB	2.01	0.41
1:B:821:THR:HG22	1:B:834:GLN:HE21	1.85	0.41
1:B:821:THR:CG2	1:B:834:GLN:HE21	2.34	0.41
1:B:1338:LEU:HD21	1:B:1341:GLN:HB3	2.02	0.41
1:B:1372:ALA:HB2	1:B:1415:TYR:HB2	2.03	0.41
1:B:470:LEU:HD22	1:B:594:MET:HE2	2.02	0.40
1:B:1166:ASP:HB3	1:B:1246:TYR:HB2	2.02	0.40
1:B:411:LYS:HZ2	1:B:413:LYS:HB2	1.86	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	B	1344/1357 (99%)	1294 (96%)	47 (4%)	3 (0%)	43	58
2	E	8/14 (57%)	6 (75%)	2 (25%)	0	100	100
All	All	1352/1371 (99%)	1300 (96%)	49 (4%)	3 (0%)	43	58

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	790	VAL
1	B	1266	GLY
1	B	1473	LYS

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	B	1099/1107 (99%)	1072 (98%)	27 (2%)	42 64
2	E	7/11 (64%)	6 (86%)	1 (14%)	3 4
All	All	1106/1118 (99%)	1078 (98%)	28 (2%)	42 64

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	338	SER
1	B	339	MET
1	B	412	VAL
1	B	415	GLU
1	B	423	ILE
1	B	478	GLU
1	B	517	ILE
1	B	559	ASP
1	B	670	SER
1	B	769	VAL
1	B	1022	ASP
1	B	1023	SER
1	B	1043	ASP
1	B	1104	VAL
1	B	1121	THR
1	B	1239	SER
1	B	1241	ASP
1	B	1347	VAL
1	B	1466	ILE
1	B	1474	ARG
1	B	1477	LEU
1	B	1539	ASP
1	B	1604	LEU
1	B	1605	GLU
1	B	1638	GLU
1	B	1672	LEU
1	B	1676	LEU

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Mol	Chain	Res	Type
2	E	5	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	426	GLN
1	B	467	ASN
1	B	481	GLN
1	B	498	ASN
1	B	555	GLN
1	B	793	ASN
1	B	905	ASN
1	B	936	ASN
1	B	1025	GLN
1	B	1119	ASN
1	B	1228	ASN
1	B	1255	ASN
1	B	1256	GLN
1	B	1334	GLN
1	B	1346	ASN
1	B	1375	GLN
1	B	1429	ASN
1	B	1484	GLN
1	B	1497	ASN
1	B	1587	ASN
1	B	1629	HIS
1	B	1636	HIS
1	B	1667	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 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	$\# Z > 2$
5	MPD	B	1706	-	7,7,7	0.40	0	9,10,10	0.47	0
3	MES	B	1701	-	12,12,12	0.70	0	15,16,16	0.32	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
5	MPD	B	1706	-	-	2/5/5/5	-
3	MES	B	1701	-	-	5/6/14/14	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	1701	MES	C7-C8-S-O3S
3	B	1701	MES	C8-C7-N4-C3
3	B	1701	MES	C8-C7-N4-C5
3	B	1701	MES	C7-C8-S-O1S
3	B	1701	MES	C7-C8-S-O2S
5	B	1706	MPD	C2-C3-C4-C5
5	B	1706	MPD	C2-C3-C4-O4

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	B	1339/1357 (98%)	-0.21	27 (2%) 65 60	22, 54, 106, 171	7 (0%)
2	E	10/14 (71%)	2.60	7 (70%) 0 0	129, 132, 145, 147	0
All	All	1349/1371 (98%)	-0.18	34 (2%) 58 54	22, 54, 107, 171	7 (0%)

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1676	LEU	7.4
2	E	3	ILE	4.6
2	E	11	PHE	4.5
1	B	1675	ILE	3.7
1	B	1672	LEU	3.6
2	E	12	TYR	3.5
1	B	339	MET	3.1
1	B	1617	VAL	3.1
1	B	338	SER	3.0
1	B	1616	GLY	3.0
1	B	1238	LYS	2.8
1	B	1578	LEU	2.8
1	B	748	TRP	2.8
1	B	1541	VAL	2.7
1	B	941	SER	2.7
1	B	1665	ILE	2.6
1	B	1663	ILE	2.6
2	E	10	ALA	2.5
2	E	5	ILE	2.3
1	B	559	ASP	2.3
2	E	7	PRO	2.3
1	B	1023	SER	2.3
1	B	1637	LEU	2.2
1	B	1582	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	1673	ALA	2.2
1	B	1599	ALA	2.1
1	B	1604	LEU	2.1
1	B	1655	CYS	2.1
2	E	4	HIS	2.1
1	B	1644	LEU	2.1
1	B	1264	LYS	2.1
1	B	1548	GLY	2.0
1	B	1645	LYS	2.0
1	B	1550	ASP	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, 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($\text{\AA}^2$)	Q<0.9
5	MPD	B	1706	8/8	0.89	0.27	87,89,90,93	0
3	MES	B	1701	12/12	0.94	0.15	68,84,93,94	0
4	MN	B	1703	1/1	1.00	0.02	67,67,67,67	0
4	MN	B	1704	1/1	1.00	0.03	61,61,61,61	0
4	MN	B	1705	1/1	1.00	0.04	61,61,61,61	0
4	MN	B	1702	1/1	1.00	0.02	47,47,47,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.