



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 21, 2024 – 08:17 AM EST

PDB ID : 4NXT
Title : Crystal structure of the cytosolic domain of human MiD51
Authors : Richter, V.; Ryan, M.T.; Kvensakul, M.
Deposited on : 2013-12-09
Resolution : 2.12 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 : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.36
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

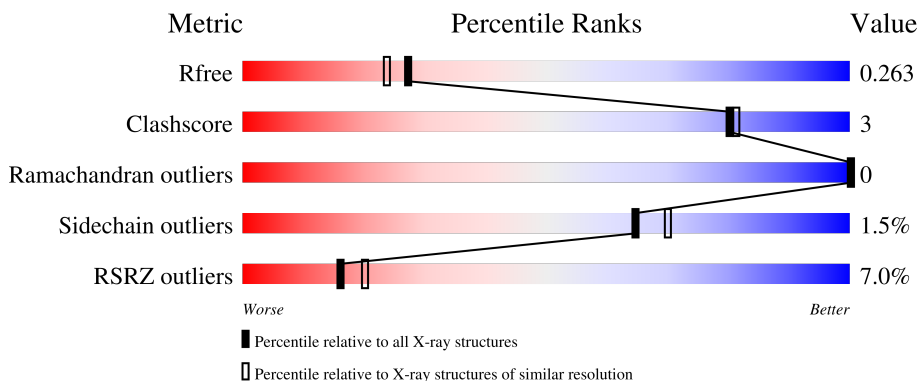
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.12 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	6241 (2.14-2.10)
Clashscore	141614	6778 (2.14-2.10)
Ramachandran outliers	138981	6705 (2.14-2.10)
Sidechain outliers	138945	6706 (2.14-2.10)
RSRZ outliers	127900	6112 (2.14-2.10)

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	347	 4% 90% 7% .
1	B	347	 6% 89% 6% 5%
1	C	347	 4% 88% 7% 5%
1	D	347	 12% 86% 7% 6%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 21243 atoms, of which 10351 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 Mitochondrial dynamic protein MID51.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	337	5217	1676	2606	444	479	12	0	1	0
1	B	331	5162	1661	2581	430	478	12	0	2	0
1	C	331	5176	1658	2594	438	474	12	0	0	0
1	D	326	5007	1615	2491	424	466	11	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	117	GLY	-	expression tag	UNP Q9NQG6
A	118	SER	-	expression tag	UNP Q9NQG6
B	117	GLY	-	expression tag	UNP Q9NQG6
B	118	SER	-	expression tag	UNP Q9NQG6
C	117	GLY	-	expression tag	UNP Q9NQG6
C	118	SER	-	expression tag	UNP Q9NQG6
D	117	GLY	-	expression tag	UNP Q9NQG6
D	118	SER	-	expression tag	UNP Q9NQG6

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			14	3	8	3		
2	B	1	Total	C	H	O	0	0
			14	3	8	3		
2	C	1	Total	C	H	O	0	0
			14	3	8	3		
2	C	1	Total	C	H	O	0	0
			14	3	8	3		
2	C	1	Total	C	H	O	0	0
			14	3	8	3		
2	C	1	Total	C	H	O	0	0
			14	3	8	3		
2	D	1	Total	C	H	O	0	0
			14	3	8	3		
2	D	1	Total	C	H	O	0	0
			14	3	8	3		
2	D	1	Total	C	H	O	0	0
			13	3	7	3		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0

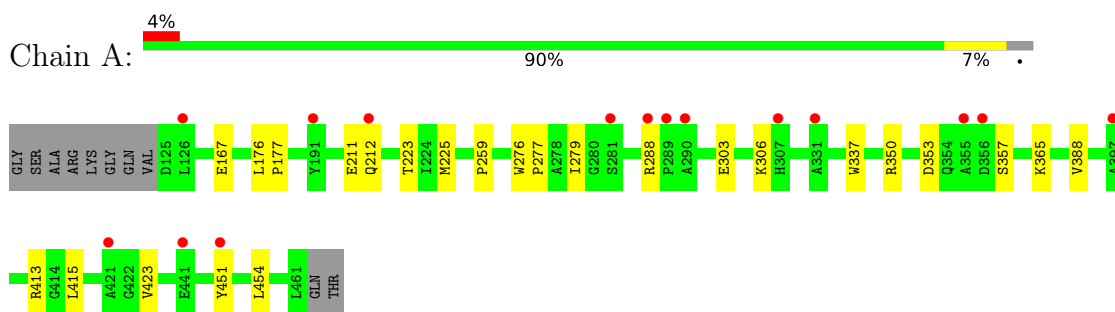
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	157	Total O 157 157	0	0
4	B	158	Total O 158 158	0	0
4	C	124	Total O 124 124	0	0
4	D	88	Total O 88 88	0	0

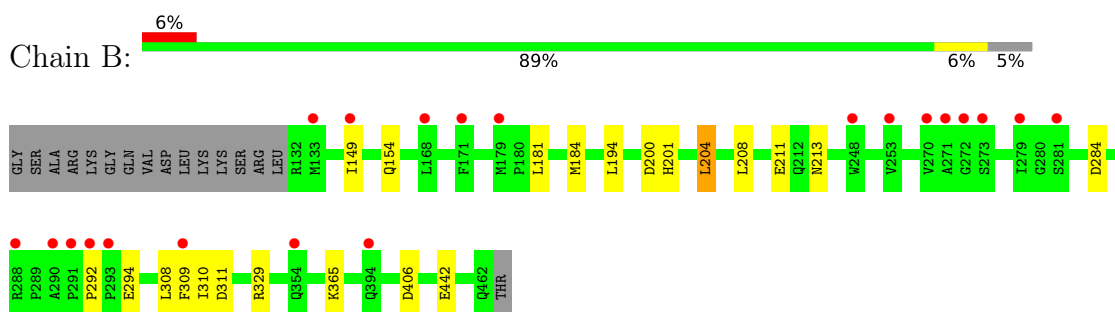
3 Residue-property plots [i](#)

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.

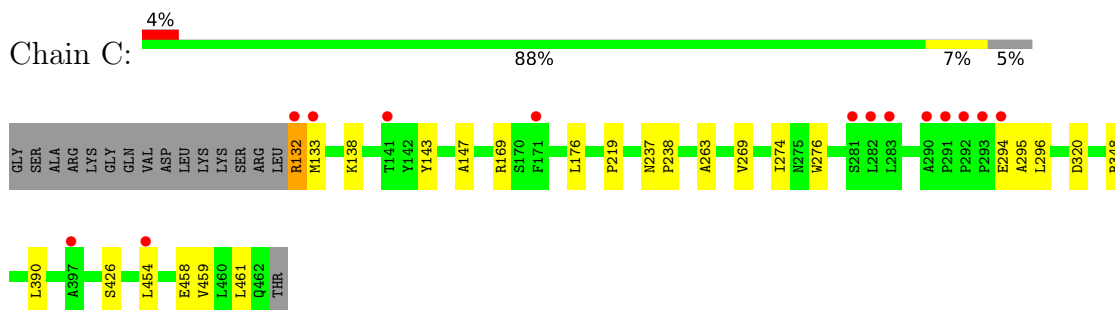
- Molecule 1: Mitochondrial dynamic protein MID51



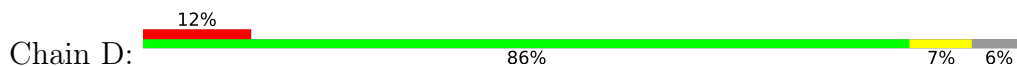
- Molecule 1: Mitochondrial dynamic protein MID51

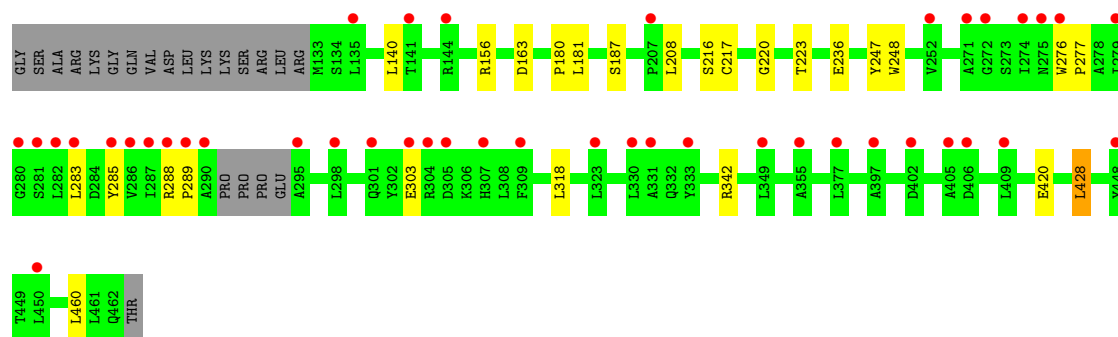


- Molecule 1: Mitochondrial dynamic protein MID51



- Molecule 1: Mitochondrial dynamic protein MID51





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	72.72Å 78.73Å 79.36Å 66.26° 84.93° 64.07°	Depositor
Resolution (Å)	39.01 – 2.12 39.01 – 2.12	Depositor EDS
% Data completeness (in resolution range)	97.3 (39.01-2.12) 97.3 (39.01-2.12)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.59 (at 2.12Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.223 , 0.263 0.224 , 0.263	Depositor DCC
R_{free} test set	3964 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	34.5	Xtriage
Anisotropy	0.176	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 51.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	21243	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.22% 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: GOL, SO4

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	0.24	0/2673	0.42	0/3648
1	B	0.25	0/2646	0.43	0/3616
1	C	0.23	0/2641	0.44	0/3604
1	D	0.24	0/2571	0.43	0/3510
All	All	0.24	0/10531	0.43	0/14378

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 [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	2611	2606	2615	12	0
1	B	2581	2581	2587	14	1
1	C	2582	2594	2599	13	0
1	D	2516	2491	2498	16	0
2	A	6	8	8	0	0
2	B	6	8	8	0	0
2	C	24	32	32	3	1
2	D	24	31	32	1	0
3	A	5	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	10	0	0	1	0
4	A	157	0	0	3	0
4	B	158	0	0	0	0
4	C	124	0	0	1	0
4	D	88	0	0	0	0
All	All	10892	10351	10379	56	1

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 3.

All (56) 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:D:156:ARG:NH1	1:D:303:GLU:OE2	2.23	0.72
1:C:294:GLU:CB	1:C:295:ALA:HA	2.21	0.70
1:B:200:ASP:OD1	1:B:201:HIS:ND1	2.17	0.67
1:A:413:ARG:NH2	4:A:721:HOH:O	2.28	0.66
1:D:220:GLY:O	1:D:223:THR:OG1	2.11	0.66
1:C:459:VAL:O	4:C:656:HOH:O	2.15	0.64
1:C:132:ARG:HA	1:C:132:ARG:HE	1.61	0.64
1:B:211:GLU:OE1	1:B:213:ASN:N	2.33	0.61
1:D:180:PRO:HG3	1:D:247:TYR:HB3	1.82	0.61
1:A:451:TYR:CD1	1:A:454:LEU:HD11	2.39	0.58
1:C:169:ARG:NH2	3:C:505:SO4:O3	2.35	0.57
1:A:211:GLU:OE2	4:A:745:HOH:O	2.18	0.56
1:A:167:GLU:HG2	1:A:279:ILE:HG23	1.89	0.55
1:D:276:TRP:N	1:D:277:PRO:HD2	2.23	0.54
1:B:184:MET:HB3	1:B:204:LEU:CD2	2.39	0.52
1:D:318:LEU:HD23	2:D:501:GOL:H11	1.91	0.52
1:B:329:ARG:NH2	1:B:442:GLU:OE1	2.44	0.51
1:B:194:LEU:HA	1:B:365:LYS:HE3	1.94	0.50
1:D:288:ARG:HD2	1:D:289:PRO:HD2	1.94	0.49
1:A:212:GLN:NE2	3:A:502:SO4:O4	2.44	0.48
1:C:348:ARG:HD3	1:C:390:LEU:HD22	1.97	0.47
1:D:163:ASP:HB3	1:D:283:LEU:HD22	1.96	0.47
1:C:237:ASN:N	1:C:238:PRO:HD3	2.29	0.47
2:C:501:GOL:O3	2:C:501:GOL:O1	2.30	0.47
1:B:292:PRO:HA	1:B:294:GLU:H	1.80	0.47
1:D:217:CYS:HB3	1:D:318:LEU:HD12	1.96	0.46
1:C:263:ALA:HB1	1:C:296:LEU:HD11	1.98	0.46
1:B:149[B]:ILE:HD13	1:B:154:GLN:HB2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:292:PRO:HA	1:B:294:GLU:N	2.32	0.45
1:D:181:LEU:HD23	1:D:208:LEU:HA	1.99	0.45
1:C:138:LYS:HG2	1:C:461:LEU:HD12	1.98	0.45
1:B:181:LEU:HD23	1:B:208:LEU:HA	1.99	0.45
2:C:504:GOL:H32	1:D:420:GLU:HB3	1.99	0.45
1:B:308:LEU:HD22	1:B:310:ILE:HG13	1.99	0.44
1:A:365:LYS:NZ	4:A:748:HOH:O	2.51	0.43
1:D:180:PRO:HG3	1:D:247:TYR:CB	2.47	0.43
1:A:276:TRP:HB2	1:A:277:PRO:HD3	2.00	0.42
1:D:283:LEU:HB3	1:D:285:TYR:CD2	2.54	0.42
1:B:204:LEU:HD12	1:B:310:ILE:HG21	2.02	0.42
1:B:308:LEU:HD23	1:B:309:PHE:N	2.34	0.42
1:C:176:LEU:HD13	1:C:269:VAL:HG12	2.01	0.42
1:D:216:SER:OG	1:D:236:GLU:OE2	2.34	0.41
1:C:143:TYR:HA	1:C:147:ALA:HB3	2.02	0.41
1:D:187:SER:OG	1:D:342:ARG:NH2	2.51	0.41
1:A:303:GLU:CG	1:A:306:LYS:HB2	2.50	0.41
1:A:388:VAL:HG21	1:A:415:LEU:HD12	2.02	0.41
1:C:274:ILE:HD13	1:C:276:TRP:CZ2	2.56	0.41
1:B:308:LEU:CD2	1:B:310:ILE:CG1	2.98	0.41
1:D:208:LEU:HG	1:D:248:TRP:CZ2	2.56	0.41
1:C:219:PRO:HB3	2:C:502:GOL:H12	2.03	0.41
1:C:132:ARG:HE	1:C:132:ARG:CA	2.31	0.41
1:A:353:ASP:O	1:A:357:SER:N	2.54	0.40
1:A:176:LEU:N	1:A:177:PRO:CD	2.85	0.40
1:A:259:PRO:HG3	1:A:337:TRP:CD1	2.56	0.40
1:B:149[B]:ILE:HD11	1:B:154:GLN:N	2.36	0.40
1:D:428:LEU:N	1:D:428:LEU:HD23	2.36	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:406:ASP:OD2	2:C:501:GOL:O3[1_554]	2.13	0.07

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	336/347 (97%)	327 (97%)	9 (3%)	0	100	100
1	B	331/347 (95%)	325 (98%)	6 (2%)	0	100	100
1	C	329/347 (95%)	320 (97%)	9 (3%)	0	100	100
1	D	322/347 (93%)	307 (95%)	15 (5%)	0	100	100
All	All	1318/1388 (95%)	1279 (97%)	39 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	279/298 (94%)	274 (98%)	5 (2%)	59	63
1	B	279/298 (94%)	276 (99%)	3 (1%)	73	79
1	C	279/298 (94%)	273 (98%)	6 (2%)	52	55
1	D	267/298 (90%)	264 (99%)	3 (1%)	73	79
All	All	1104/1192 (93%)	1087 (98%)	17 (2%)	65	70

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	223	THR
1	A	225	MET

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Mol	Chain	Res	Type
1	A	288	ARG
1	A	350	ARG
1	A	423	VAL
1	B	204	LEU
1	B	284	ASP
1	B	311	ASP
1	C	132	ARG
1	C	133	MET
1	C	320	ASP
1	C	426	SER
1	C	454	LEU
1	C	458	GLU
1	D	140	LEU
1	D	428	LEU
1	D	460	LEU

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](#)

13 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	A	502	-	4,4,4	0.13	0	6,6,6	0.08	0
2	GOL	B	501	-	5,5,5	0.38	0	5,5,5	0.24	0
2	GOL	C	501	-	5,5,5	0.37	0	5,5,5	0.37	0
2	GOL	A	501	-	5,5,5	0.38	0	5,5,5	0.24	0
3	SO4	C	505	-	4,4,4	0.13	0	6,6,6	0.06	0
2	GOL	C	503	-	5,5,5	0.36	0	5,5,5	0.20	0
2	GOL	D	503	-	5,5,5	0.36	0	5,5,5	0.25	0
3	SO4	C	506	-	4,4,4	0.13	0	6,6,6	0.06	0
2	GOL	D	504	-	5,5,5	0.42	0	5,5,5	0.41	0
2	GOL	D	502	-	5,5,5	0.39	0	5,5,5	0.20	0
2	GOL	C	502	-	5,5,5	0.45	0	5,5,5	0.16	0
2	GOL	D	501	-	5,5,5	0.33	0	5,5,5	0.47	0
2	GOL	C	504	-	5,5,5	0.41	0	5,5,5	0.14	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	GOL	B	501	-	-	0/4/4/4	-
2	GOL	C	501	-	-	2/4/4/4	-
2	GOL	A	501	-	-	2/4/4/4	-
2	GOL	C	503	-	-	2/4/4/4	-
2	GOL	D	503	-	-	2/4/4/4	-
2	GOL	D	504	-	-	3/4/4/4	-
2	GOL	D	502	-	-	4/4/4/4	-
2	GOL	C	502	-	-	0/4/4/4	-
2	GOL	D	501	-	-	2/4/4/4	-
2	GOL	C	504	-	-	3/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	501	GOL	O1-C1-C2-O2
2	C	501	GOL	O1-C1-C2-C3
2	D	501	GOL	O1-C1-C2-O2
2	D	501	GOL	O1-C1-C2-C3
2	D	502	GOL	O1-C1-C2-C3
2	D	502	GOL	C1-C2-C3-O3
2	A	501	GOL	O1-C1-C2-C3
2	C	503	GOL	C1-C2-C3-O3
2	C	504	GOL	O1-C1-C2-C3
2	C	504	GOL	C1-C2-C3-O3
2	D	504	GOL	O1-C1-C2-C3
2	A	501	GOL	O1-C1-C2-O2
2	C	504	GOL	O1-C1-C2-O2
2	D	502	GOL	O2-C2-C3-O3
2	D	502	GOL	O1-C1-C2-O2
2	C	503	GOL	O2-C2-C3-O3
2	D	503	GOL	O1-C1-C2-O2
2	D	504	GOL	O1-C1-C2-O2
2	D	504	GOL	O2-C2-C3-O3
2	D	503	GOL	O1-C1-C2-C3

There are no ring outliers.

6 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	502	SO4	1	0
2	C	501	GOL	1	1
3	C	505	SO4	1	0
2	C	502	GOL	1	0
2	D	501	GOL	1	0
2	C	504	GOL	1	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 [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	337/347 (97%)	0.44	15 (4%) 33 38	23, 45, 74, 104	0
1	B	331/347 (95%)	0.54	21 (6%) 20 24	24, 40, 69, 108	0
1	C	331/347 (95%)	0.41	14 (4%) 36 42	23, 39, 69, 121	0
1	D	326/347 (93%)	0.89	43 (13%) 3 4	34, 59, 95, 122	0
All	All	1325/1388 (95%)	0.57	93 (7%) 16 20	23, 45, 82, 122	0

All (93) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	283	LEU	8.3
1	D	355	ALA	7.9
1	B	272	GLY	5.7
1	B	291	PRO	5.7
1	B	293	PRO	5.7
1	A	355	ALA	5.4
1	D	397	ALA	5.0
1	D	287	ILE	4.8
1	B	290	ALA	4.5
1	D	305	ASP	4.4
1	A	397	ALA	4.4
1	B	270	VAL	4.2
1	D	271	ALA	4.1
1	D	331	ALA	4.1
1	D	274	ILE	4.0
1	D	280	GLY	3.7
1	D	290	ALA	3.6
1	C	133	MET	3.6
1	D	298	LEU	3.6
1	D	276	TRP	3.5
1	D	275	ASN	3.5

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Mol	Chain	Res	Type	RSRZ
1	D	288	ARG	3.4
1	D	330	LEU	3.4
1	D	307	HIS	3.4
1	C	132	ARG	3.4
1	B	171	PHE	3.4
1	D	286	VAL	3.2
1	D	282	LEU	3.2
1	D	279	ILE	3.2
1	C	281	SER	3.1
1	A	331	ALA	3.0
1	A	441	GLU	3.0
1	D	301	GLN	3.0
1	D	303	GLU	3.0
1	A	290	ALA	3.0
1	C	293	PRO	2.9
1	A	191	TYR	2.8
1	C	291	PRO	2.8
1	D	402	ASP	2.7
1	D	309	PHE	2.7
1	A	281	SER	2.7
1	C	171	PHE	2.7
1	D	448	TYR	2.7
1	B	288	ARG	2.7
1	B	273	SER	2.6
1	D	295	ALA	2.6
1	B	133	MET	2.6
1	C	141	THR	2.6
1	D	281	SER	2.6
1	B	271	ALA	2.6
1	B	354	GLN	2.6
1	D	349	LEU	2.5
1	B	292	PRO	2.5
1	A	451	TYR	2.5
1	D	135	LEU	2.5
1	D	289	PRO	2.5
1	D	333	TYR	2.4
1	A	356	ASP	2.4
1	B	279	ILE	2.4
1	C	397	ALA	2.4
1	D	409	LEU	2.3
1	B	394	GLN	2.3
1	C	283	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	292	PRO	2.3
1	D	272	GLY	2.3
1	A	126	LEU	2.3
1	D	406	ASP	2.3
1	B	309	PHE	2.3
1	A	307	HIS	2.3
1	C	282	LEU	2.3
1	B	179	MET	2.2
1	B	248	TRP	2.2
1	C	294	GLU	2.2
1	D	144	ARG	2.2
1	D	377	LEU	2.2
1	B	253	VAL	2.2
1	A	289	PRO	2.2
1	B	281	SER	2.2
1	D	450	LEU	2.2
1	D	304	ARG	2.2
1	A	212	GLN	2.1
1	A	288	ARG	2.1
1	B	149[A]	ILE	2.1
1	D	323	LEU	2.1
1	D	285	TYR	2.1
1	A	421	ALA	2.1
1	D	405	ALA	2.1
1	D	207	PRO	2.1
1	C	290	ALA	2.1
1	D	252	VAL	2.1
1	B	168	LEU	2.1
1	C	454	LEU	2.0
1	D	141	THR	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
2	GOL	C	501	6/6	0.69	0.33	72,87,94,96	0
2	GOL	D	501	6/6	0.73	0.26	67,80,83,84	0
2	GOL	D	504	6/6	0.80	0.18	16,20,33,34	0
3	SO4	A	502	5/5	0.80	0.30	73,76,76,79	0
2	GOL	D	502	6/6	0.81	0.22	65,78,80,81	0
2	GOL	C	503	6/6	0.81	0.23	59,71,78,79	0
2	GOL	B	501	6/6	0.81	0.22	81,98,98,98	0
2	GOL	C	502	6/6	0.83	0.15	62,74,77,77	0
2	GOL	A	501	6/6	0.86	0.17	66,79,80,80	0
2	GOL	D	503	6/6	0.87	0.23	63,76,79,81	0
3	SO4	C	506	5/5	0.87	0.23	81,81,81,82	0
2	GOL	C	504	6/6	0.90	0.22	53,64,73,75	0
3	SO4	C	505	5/5	0.94	0.14	61,62,63,64	0

6.5 Other polymers [i](#)

There are no such residues in this entry.