



Full wwPDB X-ray Structure Validation Report

Mar 12, 2014 – 03:07 PM GMT

PDB ID : 4LZJ
Title : Crystal Structure of MurQ from H.influenzae with bound inhibitor
Authors : Hazra, S.; Blanchard, J.
Deposited on : 2013-07-31
Resolution : 2.40 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

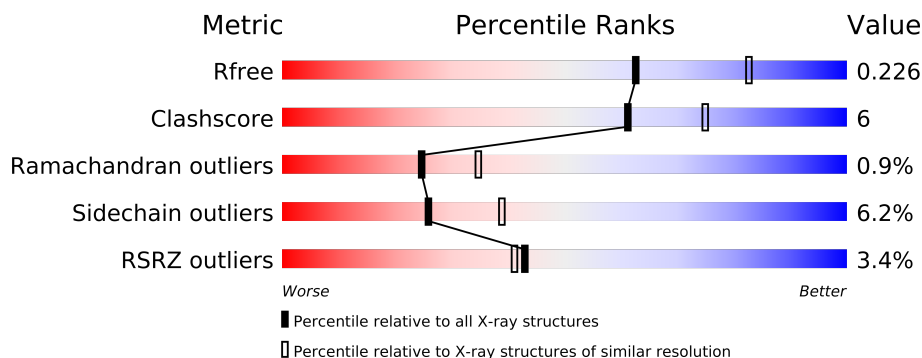
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : dev-1323
EDS : trunk22714
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk22714

1 Overall quality at a glance

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}	66092	2207 (2.40-2.40)
Clashscore	79885	2789 (2.40-2.40)
Ramachandran outliers	78287	2736 (2.40-2.40)
Sidechain outliers	78261	2737 (2.40-2.40)
RSRZ outliers	66119	2210 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	303	
1	B	303	
1	C	303	
1	D	303	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	PO4	D	401	-	X

2 Entry composition i

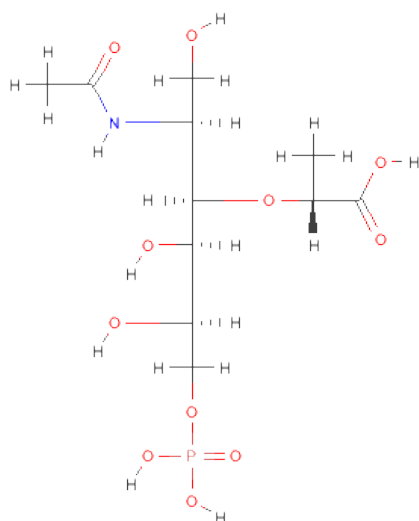
There are 4 unique types of molecules in this entry. The entry contains 9390 atoms, of which 0 are hydrogen and 0 are deuterium.

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 N-acetylmuramic acid 6-phosphate etherase.

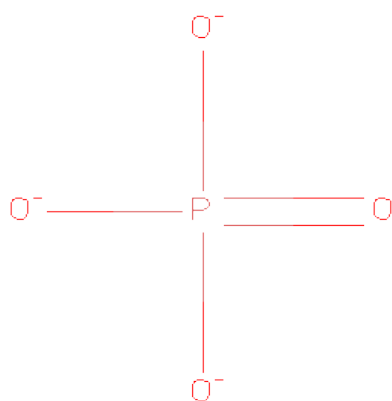
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	293	Total	C	N	O	S	0	1	0
			2200	1371	381	433	15			
1	B	299	Total	C	N	O	S	0	0	0
			2237	1397	386	439	15			
1	C	285	Total	C	N	O	S	0	1	0
			2131	1330	364	422	15			
1	D	297	Total	C	N	O	S	0	3	0
			2235	1392	388	440	15			

- Molecule 2 is 2-(ACETYLAMINO)-3-O-[(1R)-1-CARBOXYETHYL]-2-DEOXY-6-O-PHOSPHONO-D-GLUCITOL (three-letter code: 22H) (formula: C₁₁H₂₂NO₁₁P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			24	11	1	11	1		
2	D	1	Total	C	N	O	P	0	0
			24	11	1	11	1		

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	O	P	0	0
			5	4	1		
3	D	1	Total	O	P	0	0
			5	4	1		

- Molecule 4 is water.

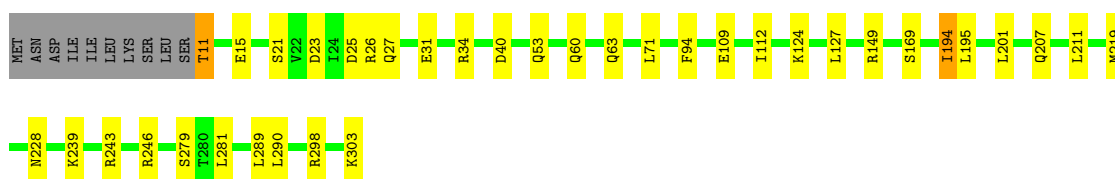
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	162	Total	O	0	0
			162	162		
4	B	117	Total	O	0	0
			117	117		
4	C	113	Total	O	0	0
			113	113		
4	D	137	Total	O	0	0
			137	137		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

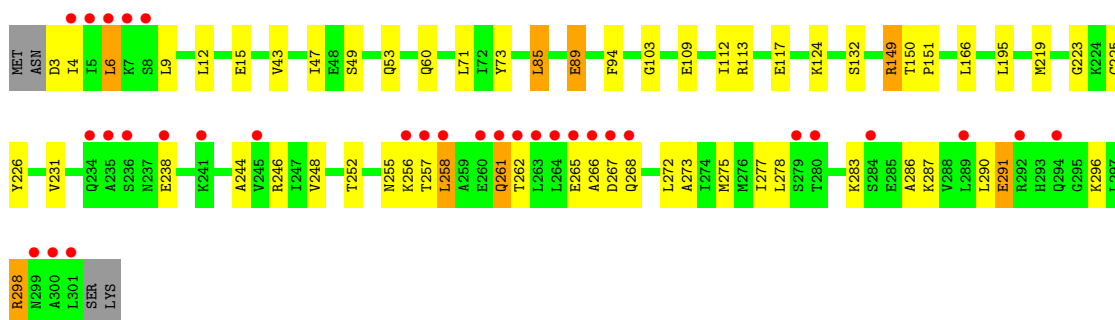
- Molecule 1: N-acetylmuramic acid 6-phosphate etherase

Chain A:



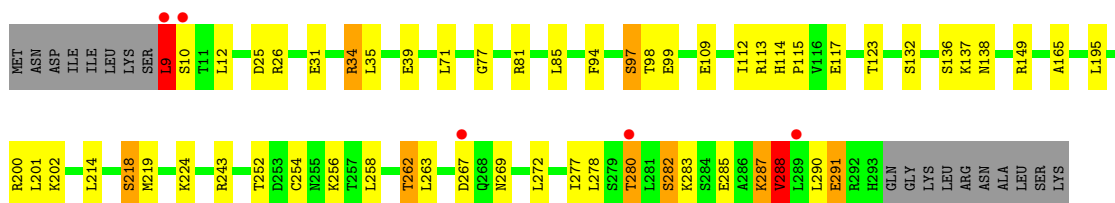
- Molecule 1: N-acetylmuramic acid 6-phosphate etherase

Chain B:



- Molecule 1: N-acetylmuramic acid 6-phosphate etherase

Chain C:



- Molecule 1: N-acetylmuramic acid 6-phosphate etherase

Chain D:



Q234	A235	S236	V245	H249	T262	L263	L264	Q268	I277	L281	K287	L297	R298	S302	LYS
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4 Data and refinement statistics

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α , β , γ	76.49Å 113.33Å 143.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.52 – 2.40 44.52 – 2.40	Depositor EDS
% Data completeness (in resolution range)	97.3 (44.52-2.40) 97.3 (44.52-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.69 (at 2.39Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.166 , 0.225 0.168 , 0.226	Depositor DCC
R_{free} test set	2421 reflections (5.04%)	DCC
Wilson B-factor (Å ²)	28.2	Xtriage
Anisotropy	0.025	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 10.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 48051 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9390	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.35% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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: PO4, 22H

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	0.39	0/2218	0.57	0/2996
1	B	0.41	0/2255	0.57	0/3047
1	C	0.40	0/2149	0.59	1/2907 (0.0%)
1	D	0.40	0/2257	0.57	0/3050
All	All	0.40	0/8879	0.58	1/12000 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	9	LEU	CA-CB-CG	6.51	130.26	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2200	0	2291	24	0
1	B	2237	0	2339	36	0
1	C	2131	0	2210	38	0
1	D	2235	0	2324	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	24	0	0	1	0
2	D	24	0	0	1	0
3	C	5	0	0	0	0
3	D	5	0	0	2	0
4	A	162	0	0	7	0
4	B	117	0	0	4	0
4	C	113	0	0	9	0
4	D	137	0	0	2	0
All	All	9390	0	9164	105	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 6.

All (105) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:114:HIS:NE2	4:C:542:HOH:O	2.17	0.78
2:B:401:22H:CAA	1:C:243:ARG:HH12	2.04	0.71
1:A:298:ARG:NH2	4:A:548:HOH:O	2.25	0.70
1:B:109:GLU:OE2	1:C:113:ARG:NE	2.23	0.66
1:B:9:LEU:HD22	1:B:15:GLU:HG3	1.77	0.65
1:A:40:ASP:OD1	4:A:427:HOH:O	2.15	0.64
1:C:267:ASP:OD2	1:C:283:LYS:NZ	2.27	0.63
1:C:269:ASN:OD1	1:C:272:LEU:N	2.24	0.63
1:C:99:GLU:OE1	4:C:601:HOH:O	2.16	0.62
1:A:63:GLN:NE2	4:A:411:HOH:O	2.26	0.61
1:A:246:ARG:HH21	1:D:10:SER:HA	1.65	0.61
1:B:60:GLN:HB3	1:B:166:LEU:HD22	1.81	0.60
1:A:53:GLN:HG2	4:A:404:HOH:O	2.01	0.60
1:D:235:ALA:HB3	1:D:268:GLN:HG3	1.85	0.59
1:A:21:SER:HB3	1:A:194:ILE:HD12	1.85	0.59
1:C:9:LEU:HG	1:C:10:SER:H	1.68	0.58
1:C:39:GLU:HB3	1:C:202:LYS:HD3	1.85	0.58
1:B:266:ALA:O	1:B:268:GLN:N	2.36	0.58
1:B:94:PHE:CD2	1:B:219:MET:HG3	2.39	0.58
1:B:226:TYR:HB3	1:B:231:VAL:HG11	1.85	0.57
1:B:149:ARG:NH1	4:B:529:HOH:O	2.37	0.57
1:A:298:ARG:HD2	1:C:26:ARG:HH12	1.69	0.57
1:C:285:GLU:O	4:C:510:HOH:O	2.17	0.57
1:A:243:ARG:HH12	2:D:402:22H:CAA	2.17	0.57
1:A:228:ASN:HB3	1:D:21:SER:O	2.04	0.57
1:A:60:GLN:NE2	4:A:544:HOH:O	2.37	0.57
1:C:94:PHE:HB3	1:C:224:LYS:HG2	1.86	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:136:SER:OG	1:C:138:ASN:OD1	2.22	0.56
1:B:257:THR:O	1:B:261:GLN:HB2	2.09	0.53
1:B:298:ARG:HG3	1:C:25:ASP:OD2	2.10	0.52
1:D:60:GLN:HB3	1:D:166:LEU:HD22	1.92	0.52
1:B:262:THR:HG21	1:B:277:ILE:HD11	1.92	0.52
1:D:39:GLU:HB3	1:D:202:LYS:HD3	1.91	0.52
1:B:272:LEU:HD21	1:B:287:LYS:HE2	1.92	0.51
1:A:246:ARG:NH2	1:D:10:SER:HA	2.25	0.51
1:B:262:THR:HG23	1:B:273:ALA:HB1	1.93	0.51
1:C:214:LEU:O	1:C:218:SER:HB2	2.10	0.50
1:B:113:ARG:NE	1:C:109:GLU:OE2	2.30	0.50
1:A:15:GLU:OE2	4:A:443:HOH:O	2.18	0.50
1:C:123:THR:HA	4:C:592:HOH:O	2.11	0.49
1:C:262:THR:HG21	1:C:277:ILE:HD11	1.95	0.49
1:A:279:SER:HB3	1:A:281:LEU:HG	1.95	0.48
1:B:53:GLN:OE1	4:B:527:HOH:O	2.20	0.48
1:C:9:LEU:HG	1:C:10:SER:N	2.28	0.48
1:C:115:PRO:O	4:C:600:HOH:O	2.20	0.48
1:A:31:GLU:HG2	1:A:34:ARG:HH22	1.79	0.48
1:B:290:LEU:O	1:B:291:GLU:HB2	2.13	0.48
1:A:23:ASP:O	1:A:27:GLN:HG3	2.14	0.48
1:C:254:CYS:HB2	1:C:258:LEU:HD23	1.96	0.48
1:D:141:LEU:HD23	1:D:157:LEU:HD23	1.96	0.48
1:B:43:VAL:O	1:B:47:ILE:HG12	2.14	0.47
1:B:6:LEU:HG	1:C:256:LYS:HE2	1.97	0.47
1:D:298:ARG:NH2	4:D:628:HOH:O	2.34	0.47
1:D:77:GLY:O	1:D:81:ARG:HG3	2.14	0.47
1:D:194:ILE:HD12	1:D:194:ILE:HA	1.61	0.46
1:D:57:ALA:HB1	1:D:168:ILE:HD13	1.97	0.46
1:C:291:GLU:HA	4:C:578:HOH:O	2.15	0.46
1:B:252:THR:HG22	1:B:278:LEU:HG	1.96	0.46
1:C:149:ARG:NH2	4:C:567:HOH:O	2.49	0.46
1:B:112:ILE:CG2	1:C:112:ILE:HG21	2.46	0.46
1:B:12:LEU:HA	4:B:593:HOH:O	2.15	0.45
1:C:287:LYS:HG2	1:C:288:VAL:HG22	1.97	0.45
1:A:109:GLU:OE2	1:D:113:ARG:NE	2.50	0.45
1:B:244:ALA:O	1:B:248:VAL:HG23	2.17	0.45
1:B:246:ARG:NH2	1:C:10:SER:HA	2.32	0.45
1:B:298:ARG:HD2	1:C:26:ARG:HE	1.82	0.45
1:B:275:MET:HG3	1:B:286:ALA:HB1	1.98	0.45
1:C:137:LYS:HA	1:C:165:ALA:HB2	2.00	0.44
1:B:225:CYS:HA	1:B:231:VAL:HG22	2.00	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:149:ARG:NH2	3:D:401:PO4:O3	2.51	0.44
1:A:25:ASP:OD2	1:D:298:ARG:HD3	2.17	0.43
1:D:145:ALA:HB3	1:D:178:MET:SD	2.58	0.43
1:C:94:PHE:CD2	1:C:219:MET:HG3	2.54	0.43
1:A:94:PHE:CD2	1:A:219:MET:HG3	2.53	0.43
1:A:11:THR:HA	4:A:403:HOH:O	2.19	0.43
1:C:97:SER:HB3	4:C:607:HOH:O	2.18	0.43
1:B:255:ASN:HB2	1:B:258:LEU:HB2	2.01	0.43
1:A:239:LYS:HB2	3:D:401:PO4:O1	2.19	0.43
1:D:132:SER:HB3	4:D:552:HOH:O	2.18	0.43
1:B:265:GLU:HG2	1:B:283:LYS:HB2	2.01	0.43
1:B:73:TYR:HB2	1:B:103:GLY:HA2	2.01	0.42
1:B:223:GLY:HA3	1:B:296:LYS:HG2	2.02	0.42
1:C:252:THR:HG22	1:C:278:LEU:HG	2.01	0.42
1:B:85:LEU:O	1:B:85:LEU:HD22	2.20	0.42
1:B:255:ASN:HB2	1:B:258:LEU:H	1.84	0.42
1:C:31:GLU:OE1	1:C:34:ARG:NH1	2.52	0.42
1:C:149:ARG:HG2	1:C:149:ARG:O	2.20	0.42
1:B:89:GLU:HG2	1:C:200:ARG:HD3	2.01	0.41
1:B:53:GLN:HG2	4:B:525:HOH:O	2.20	0.41
1:A:239:LYS:HB3	1:A:239:LYS:HE2	1.91	0.41
1:D:262:THR:HG21	1:D:277:ILE:HG13	2.02	0.41
1:B:283:LYS:HB3	1:B:283:LYS:HE2	1.84	0.41
1:C:98:THR:HG23	4:C:601:HOH:O	2.21	0.41
1:D:245:VAL:O	1:D:249:MET:HG3	2.20	0.41
1:B:283:LYS:O	1:B:287:LYS:HB2	2.21	0.41
1:D:166:LEU:HG	1:D:167:THR:N	2.35	0.40
1:D:39:GLU:HG3	1:D:194:ILE:HD13	2.03	0.40
1:C:252:THR:HA	1:C:278:LEU:HD21	2.03	0.40
1:A:112:ILE:HG21	1:D:112:ILE:CG2	2.51	0.40
1:A:207:GLN:O	1:A:211:LEU:HG	2.21	0.40
1:C:77:GLY:O	1:C:81:ARG:HG3	2.22	0.40
1:B:150:THR:HA	1:B:151:PRO:HD3	1.84	0.40
1:C:12:LEU:HD23	1:C:12:LEU:HA	1.87	0.40
1:A:290:LEU:HD23	1:A:290:LEU:HA	1.83	0.40
1:D:52:PRO:O	1:D:56:LEU:HD13	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	292/303 (96%)	286 (98%)	5 (2%)	1 (0%)	50	68
1	B	297/303 (98%)	290 (98%)	5 (2%)	2 (1%)	30	43
1	C	284/303 (94%)	268 (94%)	10 (4%)	6 (2%)	11	12
1	D	298/303 (98%)	292 (98%)	5 (2%)	1 (0%)	50	68
All	All	1171/1212 (97%)	1136 (97%)	25 (2%)	10 (1%)	25	35

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	267	ASP
1	B	291	GLU
1	C	280	THR
1	D	8	SER
1	A	201	LEU
1	C	290	LEU
1	C	201	LEU
1	C	287	LYS
1	C	282	SER
1	C	288	VAL

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	A	244/253 (96%)	233 (96%)	11 (4%)	38	57
1	B	249/253 (98%)	232 (93%)	17 (7%)	22	34
1	C	237/253 (94%)	221 (93%)	16 (7%)	22	34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	249/253 (98%)	233 (94%)	16 (6%)	25	37
All	All	979/1012 (97%)	919 (94%)	60 (6%)	26	40

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	THR
1	A	26	ARG
1	A	71	LEU
1	A	124	LYS
1	A	127	LEU
1	A	149	ARG
1	A	169	SER
1	A	194	ILE
1	A	195	LEU
1	A	289	LEU
1	A	303	LYS
1	B	3	ASP
1	B	4	ILE
1	B	6	LEU
1	B	49	SER
1	B	71	LEU
1	B	85	LEU
1	B	89	GLU
1	B	117	GLU
1	B	124	LYS
1	B	132	SER
1	B	149	ARG
1	B	195	LEU
1	B	238	GLU
1	B	256	LYS
1	B	258	LEU
1	B	261	GLN
1	B	298	ARG
1	C	9	LEU
1	C	34	ARG
1	C	35	LEU
1	C	71	LEU
1	C	85	LEU
1	C	97	SER
1	C	117	GLU
1	C	132	SER

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Mol	Chain	Res	Type
1	C	195	LEU
1	C	218	SER
1	C	262	THR
1	C	263	LEU
1	C	280	THR
1	C	282	SER
1	C	288	VAL
1	C	291	GLU
1	D	11	THR
1	D	22	VAL
1	D	55	SER
1	D	71	LEU
1	D	85	LEU
1	D	97	SER
1	D	194	ILE
1	D	195	LEU
1	D	233	VAL
1	D	234	GLN
1	D	236	SER
1	D	263	LEU
1	D	264	LEU
1	D	281	LEU
1	D	287	LYS
1	D	297	LEU

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

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry

4 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$
2	22H	B	401	-	23,23,23	1.72	5 (21%)	32,32,32	2.05	11 (34%)
3	PO4	C	401	-	4,4,4	0.26	0	6,6,6	0.28	0
3	PO4	D	401	-	4,4,4	0.29	0	6,6,6	0.30	0
2	22H	D	402	-	23,23,23	1.63	5 (21%)	32,32,32	1.89	7 (21%)

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	22H	B	401	-	-	0/32/32/32	0/0/0/0
3	PO4	C	401	-	-	0/0/0/0	0/0/0/0
3	PO4	D	401	-	-	0/0/0/0	0/0/0/0
2	22H	D	402	-	-	0/32/32/32	0/0/0/0

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	402	22H	OAF-CAL	-4.14	1.24	1.42
2	B	401	22H	OAF-CAL	-4.13	1.24	1.42
2	B	401	22H	CAV-CAW	-3.31	1.48	1.52
2	D	402	22H	CAQ-NAN	2.53	1.44	1.34
2	D	402	22H	OAP-CAS	-2.43	1.38	1.44
2	B	401	22H	OAH-CAT	-2.40	1.37	1.43
2	B	401	22H	OAP-CAS	-2.40	1.38	1.44
2	D	402	22H	OAP-CAW	-2.35	1.38	1.43
2	B	401	22H	CAQ-NAN	2.25	1.43	1.34
2	D	402	22H	OAH-CAT	-2.07	1.38	1.43

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	22H	OAF-CAL-CAU	4.63	123.06	111.17
2	D	402	22H	OAF-CAL-CAU	4.50	122.71	111.17
2	D	402	22H	CAW-OAP-CAS	4.20	123.29	115.33
2	D	402	22H	CAL-CAU-NAN	3.99	116.40	109.35
2	B	401	22H	CAL-CAU-NAN	3.49	115.52	109.35
2	B	401	22H	CAB-CAS-CAR	3.48	112.87	109.21
2	B	401	22H	CAT-CAV-CAW	-3.25	106.65	113.02
2	B	401	22H	CAA-CAQ-NAN	3.17	122.12	116.12
2	B	401	22H	CAW-OAP-CAS	3.12	121.24	115.33
2	B	401	22H	OAO-CAM-CAT	3.11	117.90	109.23
2	D	402	22H	OAG-CAR-CAS	3.03	120.31	113.63
2	D	402	22H	CAL-CAU-CAW	3.00	118.38	112.57
2	B	401	22H	OAG-CAR-CAS	2.76	119.72	113.63
2	D	402	22H	CAA-CAQ-NAN	2.75	121.32	116.12
2	B	401	22H	CAL-CAU-CAW	2.62	117.64	112.57
2	B	401	22H	OAC-CAQ-NAN	-2.51	116.78	121.90
2	B	401	22H	CAU-NAN-CAQ	2.27	126.33	123.42
2	D	402	22H	CAM-CAT-CAV	-2.04	108.20	112.06

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	A	293/303 (96%)	-0.69	0 100 100	4, 15, 30, 59	0
1	B	299/303 (98%)	0.05	32 (10%) 6 6	6, 21, 82, 91	0
1	C	285/303 (94%)	-0.37	5 (1%) 65 63	6, 23, 56, 77	0
1	D	297/303 (98%)	-0.60	2 (0%) 84 84	6, 16, 39, 62	0
All	All	1174/1212 (96%)	-0.40	39 (3%) 43 42	4, 18, 65, 91	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	6	LEU	11.9
1	B	289	LEU	5.5
1	B	264	LEU	5.4
1	B	5	ILE	5.0
1	B	279	SER	4.4
1	B	235	ALA	4.2
1	D	8	SER	4.1
1	B	301	LEU	4.0
1	B	257	THR	3.9
1	B	265	GLU	3.7
1	C	10	SER	3.7
1	B	263	LEU	3.6
1	B	4	ILE	3.4
1	B	300	ALA	3.3
1	B	280	THR	3.3
1	C	289	LEU	3.3
1	B	8	SER	3.3
1	B	294	GLN	3.2
1	B	262	THR	3.1
1	B	256	LYS	3.1
1	B	6	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	9	LEU	3.0
1	B	299	ASN	3.0
1	C	280	THR	2.8
1	B	267	ASP	2.8
1	B	261	GLN	2.6
1	B	236	SER	2.6
1	C	267	ASP	2.5
1	B	292	ARG	2.5
1	B	7	LYS	2.5
1	B	260	GLU	2.4
1	B	245	VAL	2.4
1	B	266	ALA	2.4
1	B	241	LYS	2.3
1	B	238	GLU	2.3
1	B	258	LEU	2.2
1	B	234	GLN	2.2
1	B	268	GLN	2.2
1	B	284	SER	2.1

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	PO4	D	401	5/5	0.42	5.39	46,55,76,87	0
3	PO4	C	401	5/5	0.19	1.68	16,23,62,64	0
2	22H	B	401	24/24	0.11	-0.03	11,29,37,44	0
2	22H	D	402	24/24	0.11	-0.37	8,24,31,38	0

6.5 Other polymers ⓘ

There are no such residues in this entry.