



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:54 PM GMT

PDB ID : 4JTI
Title : Crystal structure of F114R/R117Q/F139G mutant of 3-deoxy-D-manno-octulosonate 8-phosphate synthase (KDO8PS) from *Neisseria meningitidis*
Authors : Allison, T.M.; Cochran, F.C.; Jameson, G.B.; Parker, E.J.
Deposited on : 2013-03-23
Resolution : 1.75 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

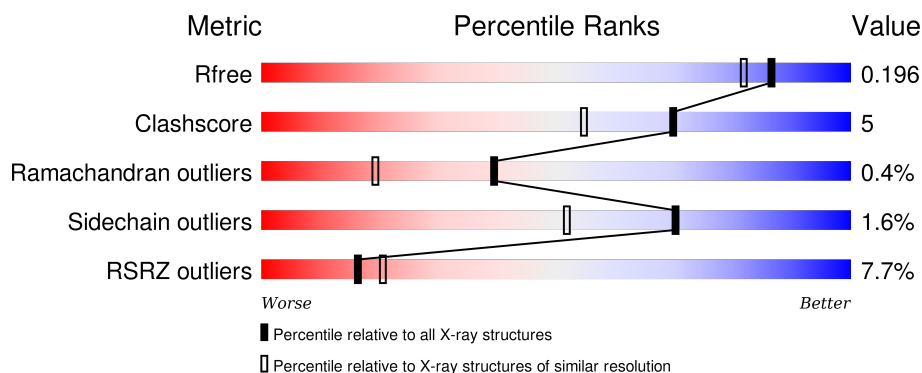
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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}	91344	1609 (1.76-1.76)
Clashscore	102246	1730 (1.76-1.76)
Ramachandran outliers	100387	1711 (1.76-1.76)
Sidechain outliers	100360	1711 (1.76-1.76)
RSRZ outliers	91569	1610 (1.76-1.76)

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. 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	280	<div> <div>9%</div> <div> <div></div> <div>80%</div> <div>10%</div> <div>10%</div> </div> </div>
1	B	280	<div> <div>5%</div> <div> <div></div> <div>84%</div> <div>8%</div> <div>8%</div> </div> </div>
1	C	280	<div> <div>6%</div> <div> <div></div> <div>83%</div> <div>9%</div> <div>8%</div> </div> </div>
1	D	280	<div> <div>8%</div> <div> <div></div> <div>81%</div> <div>10%</div> <div>8%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8642 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 2-dehydro-3-deoxyphosphooctonate aldolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	253	Total	C	N	O	S	0	1	0
			1943	1241	331	360	11			
1	B	257	Total	C	N	O	S	0	6	0
			2006	1283	343	369	11			
1	C	258	Total	C	N	O	S	0	2	0
			1986	1271	341	363	11			
1	D	258	Total	C	N	O	S	0	2	0
			1986	1269	339	367	11			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	114	ARG	PHE	ENGINEERED MUTATION	UNP Q9JZ55
A	117	GLN	ARG	ENGINEERED MUTATION	UNP Q9JZ55
A	139	GLY	PHE	ENGINEERED MUTATION	UNP Q9JZ55
B	114	ARG	PHE	ENGINEERED MUTATION	UNP Q9JZ55
B	117	GLN	ARG	ENGINEERED MUTATION	UNP Q9JZ55
B	139	GLY	PHE	ENGINEERED MUTATION	UNP Q9JZ55
C	114	ARG	PHE	ENGINEERED MUTATION	UNP Q9JZ55
C	117	GLN	ARG	ENGINEERED MUTATION	UNP Q9JZ55
C	139	GLY	PHE	ENGINEERED MUTATION	UNP Q9JZ55
D	114	ARG	PHE	ENGINEERED MUTATION	UNP Q9JZ55
D	117	GLN	ARG	ENGINEERED MUTATION	UNP Q9JZ55
D	139	GLY	PHE	ENGINEERED MUTATION	UNP Q9JZ55

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Cl	0	0
			1	1		
2	D	1	Total	Cl	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	3	Total	Cl	0	0
			3	3		

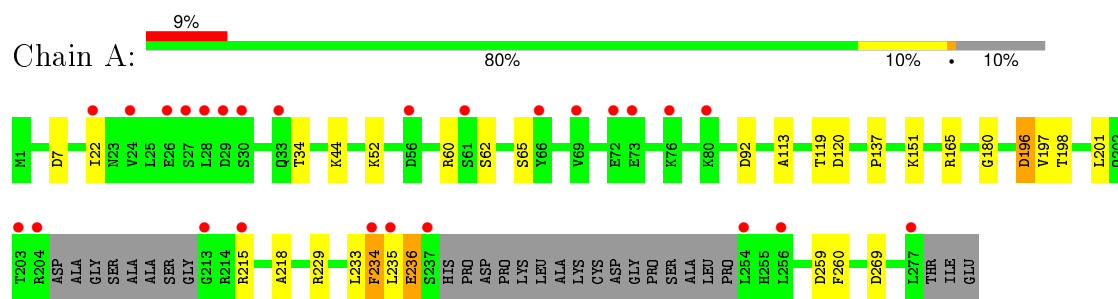
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	170	Total	O	0	0
			170	170		
3	B	193	Total	O	0	0
			193	193		
3	C	179	Total	O	0	0
			179	179		
3	D	174	Total	O	0	0
			174	174		

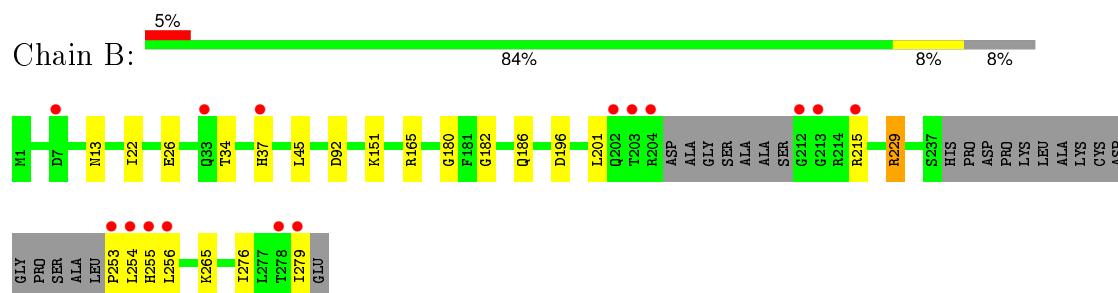
3 Residue-property plots [i](#)

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.

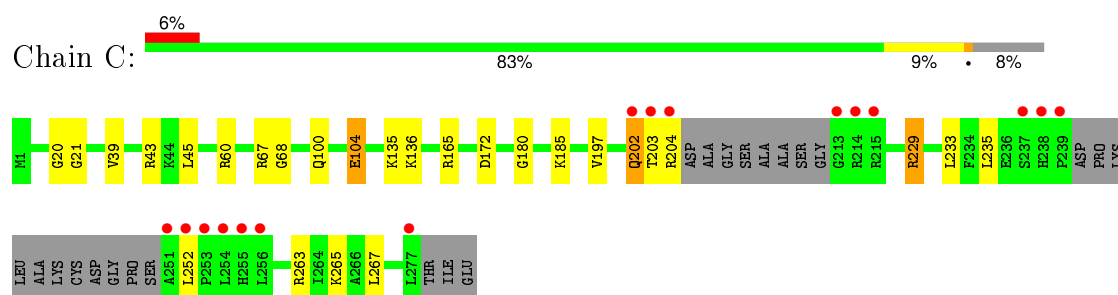
- Molecule 1: 2-dehydro-3-deoxyphosphooctonate aldolase



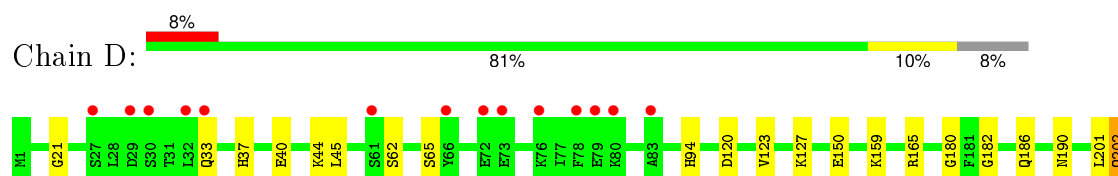
- Molecule 1: 2-dehydro-3-deoxyphosphooctonate aldolase

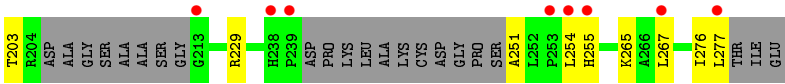


- Molecule 1: 2-dehydro-3-deoxyphosphooctonate aldolase



- Molecule 1: 2-dehydro-3-deoxyphosphooctonate aldolase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	81.67Å 85.20Å 162.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.82 – 1.75 40.84 – 1.75	Depositor EDS
% Data completeness (in resolution range)	99.9 (40.82-1.75) 99.9 (40.84-1.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.63 (at 1.75Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.159 , 0.188 0.171 , 0.196	Depositor DCC
R_{free} test set	5751 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	21.0	Xtriage
Anisotropy	0.491	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 45.7	EDS
Estimated twinning fraction	0.015 for k,h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 114952 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8642	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.34% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: CL

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	0.95	0/1976	0.95	5/2669 (0.2%)
1	B	1.00	0/2052	0.97	5/2771 (0.2%)
1	C	1.01	3/2025 (0.1%)	0.99	5/2738 (0.2%)
1	D	0.92	1/2022 (0.0%)	0.92	2/2734 (0.1%)
All	All	0.97	4/8075 (0.0%)	0.96	17/10912 (0.2%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	21	GLY	N-CA	-5.95	1.37	1.46
1	C	104	GLU	CD-OE2	-5.69	1.19	1.25
1	C	68	GLY	N-CA	-5.25	1.38	1.46
1	C	21	GLY	N-CA	-5.08	1.38	1.46

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	234	PHE	CB-CA-C	-5.94	98.53	110.40
1	C	252	LEU	CA-CB-CG	5.91	128.89	115.30
1	C	229	ARG	NE-CZ-NH2	-5.63	117.48	120.30
1	C	136	LYS	CD-CE-NZ	5.62	124.64	111.70
1	B	201	LEU	CA-CB-CG	5.60	128.17	115.30
1	D	201	LEU	CB-CA-C	-5.58	99.60	110.20
1	A	92	ASP	CB-CG-OD1	5.43	123.18	118.30
1	B	201	LEU	CB-CA-C	-5.41	99.93	110.20
1	A	259	ASP	CB-CG-OD1	5.38	123.14	118.30
1	C	172	ASP	CB-CG-OD2	-5.31	113.52	118.30
1	B	165	ARG	NE-CZ-NH2	5.23	122.92	120.30
1	B	196	ASP	CB-CG-OD2	-5.20	113.62	118.30
1	C	263	ARG	NE-CZ-NH2	-5.13	117.74	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	120	ASP	CB-CG-OD1	5.10	122.89	118.30
1	A	196	ASP	CB-CG-OD2	-5.04	113.77	118.30
1	A	269	ASP	CB-CG-OD1	5.03	122.83	118.30
1	B	92	ASP	CB-CG-OD2	5.02	122.82	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	1943	0	1991	20	0
1	B	2006	0	2075	15	0
1	C	1986	0	2044	22	0
1	D	1986	0	2032	22	0
2	B	1	0	0	0	0
2	C	3	0	0	0	0
2	D	1	0	0	0	0
3	A	170	0	0	6	0
3	B	193	0	0	3	0
3	C	179	0	0	4	0
3	D	174	0	0	9	0
All	All	8642	0	8142	73	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 5.

All (73) 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:253:PRO:HA	1:B:256:LEU:HB2	1.41	1.01
1:C:202:GLN:NE2	1:C:203:THR:HG23	1.82	0.94
1:D:94:HIS:HD2	3:D:505:HOH:O	1.54	0.91
1:D:251:ALA:HB2	3:D:491:HOH:O	1.74	0.86
1:B:13:ASN:HD21	1:B:229:ARG:HH21	1.23	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:43:ARG:HD3	3:C:533:HOH:O	1.77	0.83
1:D:276:ILE:O	1:D:277:LEU:HB2	1.81	0.81
1:C:135:LYS:HD2	1:C:165:ARG:HD2	1.61	0.80
1:B:182:GLY:O	1:B:186:GLN:HG2	1.89	0.73
1:C:202:GLN:HE21	1:C:203:THR:N	1.88	0.72
1:B:13:ASN:ND2	1:B:229:ARG:HH21	1.87	0.72
1:A:44:LYS:HB2	3:A:444:HOH:O	1.89	0.72
1:A:235:LEU:HD12	1:A:235:LEU:O	1.93	0.68
1:B:13:ASN:HD21	1:B:229:ARG:NH2	1.94	0.66
1:C:202:GLN:HE22	1:C:203:THR:HG23	1.62	0.64
1:C:267:LEU:CD1	1:D:267:LEU:HD13	2.28	0.64
1:C:267:LEU:HD13	1:D:267:LEU:CD1	2.29	0.62
1:A:215:ARG:O	1:A:260:PHE:HZ	1.83	0.62
1:B:37:HIS:CE1	1:B:254:LEU:HA	2.36	0.61
1:A:235:LEU:HD12	1:A:235:LEU:C	2.22	0.59
1:D:37:HIS:CD2	1:D:254:LEU:HG	2.37	0.59
1:C:204:ARG:NH1	3:C:504:HOH:O	2.32	0.59
1:A:52:LYS:HE2	3:A:404:HOH:O	2.03	0.58
1:D:190[B]:ASN:ND2	3:D:539:HOH:O	2.25	0.58
1:C:267:LEU:CD1	1:D:267:LEU:CD1	2.81	0.57
1:D:45:LEU:O	1:D:265:LYS:HE3	2.04	0.57
1:C:39:VAL:O	1:C:43:ARG:HG3	2.05	0.57
1:D:150:GLU:HG3	3:D:534:HOH:O	2.03	0.56
1:C:45:LEU:O	1:C:265:LYS:HE3	2.05	0.56
1:B:22:ILE:HG23	1:B:34:THR:HG21	1.90	0.54
1:D:94:HIS:CD2	3:D:505:HOH:O	2.39	0.54
1:A:196:ASP:HA	1:A:234:PHE:HB2	1.89	0.53
1:D:202:GLN:NE2	1:D:203:THR:HG23	2.23	0.53
1:A:22:ILE:HG23	1:A:34:THR:HG21	1.91	0.53
1:B:151:LYS:HD3	3:B:523:HOH:O	2.09	0.52
1:A:119:THR:HG22	3:A:439:HOH:O	2.08	0.52
1:B:45:LEU:O	1:B:265:LYS:HE3	2.09	0.52
1:D:33:GLN:NE2	3:D:513:HOH:O	2.43	0.51
1:D:159:LYS:HE3	3:D:522:HOH:O	2.09	0.51
1:A:215:ARG:O	1:A:260:PHE:CZ	2.63	0.51
1:B:22:ILE:CG2	1:B:34:THR:HG21	2.41	0.51
1:C:202:GLN:C	1:C:202:GLN:HE21	2.14	0.51
1:A:180:GLY:HA3	3:A:379:HOH:O	2.10	0.50
1:C:180:GLY:HA3	3:C:531:HOH:O	2.13	0.49
1:A:198:THR:HG21	1:A:236:GLU:HG2	1.95	0.49
1:C:267:LEU:HD11	1:D:267:LEU:HD13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:62:SER:HB3	1:D:65:SER:OG	2.13	0.49
1:A:62:SER:HB3	1:A:65:SER:OG	2.14	0.48
1:B:186:GLN:NE2	3:B:441:HOH:O	2.47	0.48
1:C:100:GLN:O	1:C:104:GLU:HG3	2.13	0.47
1:D:123:VAL:O	1:D:127:LYS:HG2	2.15	0.47
1:C:197[B]:VAL:HG11	1:C:233:LEU:HD11	1.96	0.47
1:B:13:ASN:OD1	1:B:276:ILE:HD11	2.16	0.46
1:C:197[B]:VAL:CG1	1:C:233:LEU:HD11	2.46	0.46
1:A:22:ILE:CG2	1:A:34:THR:HG21	2.46	0.46
1:A:120:ASP:OD1	1:C:67:ARG:NH1	2.38	0.45
1:B:180:GLY:HA3	3:B:460:HOH:O	2.15	0.45
1:A:197:VAL:HG21	1:A:233:LEU:HD11	1.97	0.45
1:C:267:LEU:HD13	1:D:267:LEU:HD11	1.97	0.45
1:A:235:LEU:C	1:A:235:LEU:CD1	2.85	0.45
1:A:52:LYS:CE	3:A:404:HOH:O	2.63	0.45
1:C:20:GLY:HA2	1:C:235:LEU:O	2.16	0.45
1:C:202:GLN:HE21	1:C:203:THR:HG23	1.76	0.43
1:A:151:LYS:NZ	3:A:372:HOH:O	2.50	0.43
1:D:159:LYS:CE	3:D:522:HOH:O	2.66	0.43
1:D:202:GLN:HE21	1:D:203:THR:HG23	1.82	0.43
1:B:26:GLU:O	1:B:26:GLU:HG3	2.18	0.42
1:A:201:LEU:HD11	1:A:218:ALA:HA	2.01	0.42
1:C:185:LYS:HA	3:C:549:HOH:O	2.20	0.41
1:D:182:GLY:O	1:D:186:GLN:HG3	2.20	0.41
1:A:113:ALA:HB1	1:A:137:PRO:HA	2.01	0.41
1:B:37:HIS:NE2	1:B:254:LEU:HA	2.36	0.41
1:D:180:GLY:HA3	3:D:563:HOH:O	2.20	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	248/280 (89%)	243 (98%)	4 (2%)	1 (0%)	39	19
1	B	257/280 (92%)	251 (98%)	5 (2%)	1 (0%)	39	19
1	C	254/280 (91%)	250 (98%)	3 (1%)	1 (0%)	39	19
1	D	254/280 (91%)	251 (99%)	2 (1%)	1 (0%)	39	19
All	All	1013/1120 (90%)	995 (98%)	14 (1%)	4 (0%)	39	19

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	229	ARG
1	B	229	ARG
1	C	229	ARG
1	A	229	ARG

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	215/235 (92%)	211 (98%)	4 (2%)	65	43
1	B	224/235 (95%)	221 (99%)	3 (1%)	76	60
1	C	220/235 (94%)	218 (99%)	2 (1%)	84	72
1	D	220/235 (94%)	215 (98%)	5 (2%)	58	33
All	All	879/940 (94%)	865 (98%)	14 (2%)	70	52

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

Mol	Chain	Res	Type
1	A	7	ASP
1	A	60	ARG
1	A	165	ARG
1	A	236	GLU
1	B	215	ARG
1	B	255	HIS
1	B	279	ILE

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Mol	Chain	Res	Type
1	C	60	ARG
1	C	202	GLN
1	D	40	GLU
1	D	44	LYS
1	D	165	ARG
1	D	202	GLN
1	D	255	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	ASN
1	A	23	ASN
1	A	94	HIS
1	A	138	GLN
1	A	144	GLN
1	B	13	ASN
1	B	37	HIS
1	B	144	GLN
1	B	147	ASN
1	B	186	GLN
1	B	202	GLN
1	B	217	GLN
1	C	100	GLN
1	C	118	GLN
1	C	138	GLN
1	C	202	GLN
1	D	186	GLN
1	D	202	GLN

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 [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

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	253/280 (90%)	0.36	26 (10%) 9 11	12, 27, 56, 73	1 (0%)
1	B	257/280 (91%)	0.02	15 (5%) 26 31	13, 21, 43, 74	0
1	C	258/280 (92%)	0.08	16 (6%) 24 29	14, 23, 46, 73	0
1	D	258/280 (92%)	0.38	22 (8%) 13 16	14, 26, 57, 72	0
All	All	1026/1120 (91%)	0.21	79 (7%) 16 20	12, 24, 55, 74	1 (0%)

All (79) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	254	LEU	11.3
1	D	277	LEU	7.6
1	B	279	ILE	7.4
1	C	239	PRO	7.2
1	B	253	PRO	6.7
1	B	255	HIS	5.7
1	D	239	PRO	5.7
1	C	254	LEU	5.2
1	A	66	TYR	5.2
1	C	204	ARG	5.1
1	C	238	HIS	5.0
1	B	278	THR	4.9
1	B	203	THR	4.8
1	B	212	GLY	4.7
1	A	277	LEU	4.7
1	D	238	HIS	4.6
1	C	252	LEU	4.4
1	C	202	GLN	4.2
1	B	256	LEU	4.1
1	A	203	THR	4.0
1	C	214	ARG	4.0

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Mol	Chain	Res	Type	RSRZ
1	C	237	SER	4.0
1	C	255	HIS	4.0
1	C	251	ALA	3.8
1	D	76	LYS	3.8
1	B	202	GLN	3.6
1	B	213	GLY	3.5
1	A	204	ARG	3.5
1	D	32	LEU	3.4
1	A	235	LEU	3.4
1	C	277	LEU	3.4
1	C	203	THR	3.4
1	A	26	GLU	3.3
1	D	66	TYR	3.3
1	A	69	VAL	3.2
1	C	213	GLY	3.2
1	D	254	LEU	3.1
1	C	253	PRO	3.0
1	A	27	SER	2.8
1	A	254	LEU	2.7
1	D	80	LYS	2.7
1	A	213	GLY	2.7
1	D	83	ALA	2.7
1	A	72	GLU	2.7
1	D	255	HIS	2.7
1	D	78	PHE	2.6
1	D	267	LEU	2.6
1	D	27	SER	2.6
1	D	253	PRO	2.5
1	A	24	VAL	2.5
1	A	215	ARG	2.5
1	D	29	ASP	2.5
1	C	215	ARG	2.4
1	A	33	GLN	2.4
1	A	234	PHE	2.4
1	B	215	ARG	2.4
1	A	29	ASP	2.4
1	A	80	LYS	2.4
1	B	204	ARG	2.3
1	C	256	LEU	2.3
1	A	73	GLU	2.3
1	A	30	SER	2.3
1	A	28	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	73	GLU	2.3
1	D	79	GLU	2.3
1	D	72	GLU	2.2
1	A	22	ILE	2.2
1	A	237	SER	2.1
1	A	256	LEU	2.1
1	B	7	ASP	2.1
1	A	76	LYS	2.1
1	A	61	SER	2.1
1	B	37	HIS	2.1
1	D	30	SER	2.1
1	A	56	ASP	2.1
1	D	61	SER	2.0
1	D	213	GLY	2.0
1	B	33	GLN	2.0
1	D	33	GLN	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 carbohydrates 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. 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	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	CL	D	301	1/1	0.95	0.08	-0.74	37,37,37,37	0
2	CL	C	303	1/1	0.98	0.04	-1.39	42,42,42,42	0
2	CL	C	302	1/1	0.97	0.05	-1.72	29,29,29,29	0
2	CL	C	301	1/1	0.98	0.04	-2.53	28,28,28,28	0
2	CL	B	301	1/1	0.99	0.08	-2.72	20,20,20,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.