



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:30 PM GMT

PDB ID : 4LU0
Title : Crystal structure of 2-Keto-3-deoxy-D-manno-octulosonate-8-phosphate synthase from *Pseudomonas aeruginosa*.
Authors : Asojo, O.A.
Deposited on : 2013-07-24
Resolution : 2.80 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

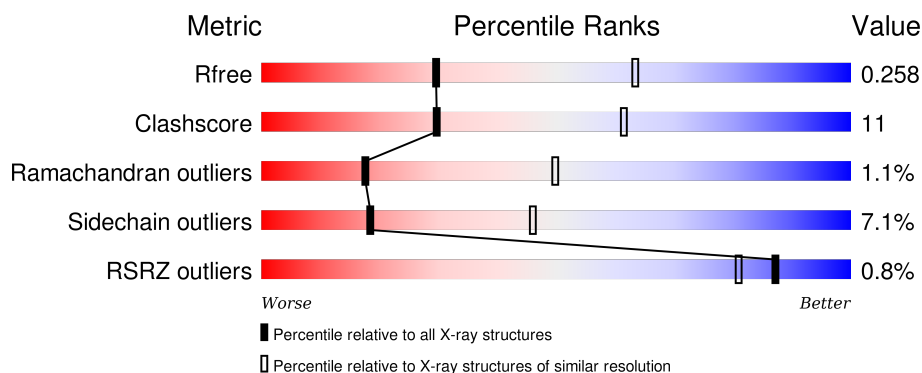
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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	287	<div> <div>%</div> <div> <div></div> <div>59%</div> <div>25%</div> <div>•</div> <div>14%</div> </div> </div>
1	B	287	<div> <div></div> <div> <div>62%</div> <div>21%</div> <div>•</div> <div>14%</div> </div> </div>
1	C	287	<div> <div>%</div> <div> <div></div> <div>58%</div> <div>24%</div> <div>5%</div> <div>13%</div> </div> </div>
1	D	287	<div> <div>%</div> <div> <div></div> <div>61%</div> <div>26%</div> <div>•</div> <div>12%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7875 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	247	Total	C	N	O	S	0	0	0
			1951	1258	330	352	11			
1	B	247	Total	C	N	O	S	0	0	0
			1939	1251	325	352	11			
1	C	250	Total	C	N	O	S	0	0	0
			1967	1267	331	358	11			
1	D	252	Total	C	N	O	S	0	0	0
			1992	1283	336	362	11			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	EXPRESSION TAG	UNP Q9ZFK4
A	2	HIS	-	EXPRESSION TAG	UNP Q9ZFK4
A	3	HIS	-	EXPRESSION TAG	UNP Q9ZFK4
A	4	HIS	-	EXPRESSION TAG	UNP Q9ZFK4
A	5	HIS	-	EXPRESSION TAG	UNP Q9ZFK4
A	6	HIS	-	EXPRESSION TAG	UNP Q9ZFK4
A	7	HIS	-	EXPRESSION TAG	UNP Q9ZFK4
B	1	MET	-	EXPRESSION TAG	UNP Q9ZFK4
B	2	HIS	-	EXPRESSION TAG	UNP Q9ZFK4
B	3	HIS	-	EXPRESSION TAG	UNP Q9ZFK4
B	4	HIS	-	EXPRESSION TAG	UNP Q9ZFK4
B	5	HIS	-	EXPRESSION TAG	UNP Q9ZFK4
B	6	HIS	-	EXPRESSION TAG	UNP Q9ZFK4
B	7	HIS	-	EXPRESSION TAG	UNP Q9ZFK4
C	1	MET	-	EXPRESSION TAG	UNP Q9ZFK4
C	2	HIS	-	EXPRESSION TAG	UNP Q9ZFK4
C	3	HIS	-	EXPRESSION TAG	UNP Q9ZFK4
C	4	HIS	-	EXPRESSION TAG	UNP Q9ZFK4
C	5	HIS	-	EXPRESSION TAG	UNP Q9ZFK4
C	6	HIS	-	EXPRESSION TAG	UNP Q9ZFK4
C	7	HIS	-	EXPRESSION TAG	UNP Q9ZFK4

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Chain	Residue	Modelled	Actual	Comment	Reference
D	1	MET	-	EXPRESSION TAG	UNP Q9ZFK4
D	2	HIS	-	EXPRESSION TAG	UNP Q9ZFK4
D	3	HIS	-	EXPRESSION TAG	UNP Q9ZFK4
D	4	HIS	-	EXPRESSION TAG	UNP Q9ZFK4
D	5	HIS	-	EXPRESSION TAG	UNP Q9ZFK4
D	6	HIS	-	EXPRESSION TAG	UNP Q9ZFK4
D	7	HIS	-	EXPRESSION TAG	UNP Q9ZFK4

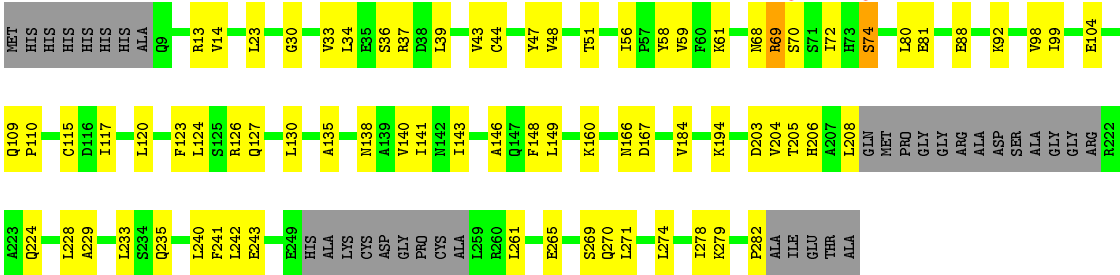
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	9	Total O 9 9	0	0
2	B	7	Total O 7 7	0	0
2	C	5	Total O 5 5	0	0
2	D	5	Total O 5 5	0	0

THR

ALA

• 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	79.27Å 95.10Å 145.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	57.69 – 2.80 57.69 – 2.80	Depositor EDS
% Data completeness (in resolution range)	95.5 (57.69-2.80) 95.5 (57.69-2.80)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.56 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.206 , 0.267 0.206 , 0.258	Depositor DCC
R_{free} test set	1321 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	48.9	Xtriage
Anisotropy	0.121	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 36.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 26456 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7875	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.20% 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](#)

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	0.81	2/1986 (0.1%)	0.79	0/2674
1	B	0.88	2/1972 (0.1%)	0.83	0/2655
1	C	0.77	1/2002 (0.0%)	0.75	0/2697
1	D	0.90	2/2028 (0.1%)	0.83	3/2732 (0.1%)
All	All	0.84	7/7988 (0.1%)	0.80	3/10758 (0.0%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	60	PHE	CG-CD2	6.54	1.48	1.38
1	D	104	GLU	CD-OE2	6.17	1.32	1.25
1	B	60	PHE	CE1-CZ	5.83	1.48	1.37
1	A	45	GLU	CD-OE1	5.32	1.31	1.25
1	C	63	SER	CB-OG	5.29	1.49	1.42
1	A	85	LYS	CD-CE	5.16	1.64	1.51
1	D	160	LYS	CD-CE	5.05	1.63	1.51

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	167	ASP	CB-CG-OD2	-5.85	113.04	118.30
1	D	224	GLN	N-CA-C	-5.53	96.08	111.00
1	D	240	LEU	CB-CG-CD2	-5.47	101.70	111.00

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	1951	0	1994	42	0
1	B	1939	0	1981	49	0
1	C	1967	0	2000	57	0
1	D	1992	0	2030	41	0
2	A	9	0	0	2	0
2	B	7	0	0	1	0
2	C	5	0	0	1	0
2	D	5	0	0	0	0
All	All	7875	0	8005	177	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 11.

All (177) 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:232:GLY:O	1:B:237:LEU:HD23	1.53	1.06
1:B:120:LEU:HD13	1:B:134:MET:HE1	1.31	1.05
1:A:144:LYS:NZ	1:A:172:CYS:SG	2.31	1.04
1:B:144:LYS:NZ	1:B:172:CYS:SG	2.41	0.94
1:A:203:ASP:HA	1:A:241:PHE:HB2	1.55	0.89
1:B:59:VAL:HG22	1:B:97:PRO:HG2	1.59	0.82
1:B:284:ILE:HG12	1:D:270:GLN:HE22	1.43	0.82
1:A:147:GLN:HG2	2:A:305:HOH:O	1.79	0.81
1:C:63:SER:HB3	1:C:101:ASP:OD1	1.82	0.79
1:C:203:ASP:HA	1:C:241:PHE:HB3	1.65	0.78
1:D:203:ASP:HA	1:D:241:PHE:HB2	1.66	0.77
1:B:232:GLY:O	1:B:237:LEU:CD2	2.36	0.73
1:A:102:VAL:HG23	1:A:134:MET:CE	2.20	0.72
1:B:203:ASP:HA	1:B:241:PHE:HB3	1.70	0.71
1:A:194:LYS:HE2	1:A:236:LYS:O	1.90	0.70
1:A:102:VAL:HG23	1:A:134:MET:HE1	1.74	0.68
1:C:61:LYS:NZ	1:C:243:GLU:OE2	2.25	0.68
1:A:132:VAL:O	1:A:136:ARG:HG2	1.92	0.68
1:B:277:LEU:HD12	1:B:281:PHE:CZ	2.29	0.68
1:A:101:ASP:HB3	1:A:119:GLN:HB3	1.75	0.67
1:D:241:PHE:O	1:D:242:LEU:HD12	1.95	0.67
1:B:222:ARG:HG3	1:B:223:ALA:H	1.58	0.67
1:A:231:ALA:HB2	1:C:235:GLN:NE2	2.12	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:51:THR:HG23	1:D:56:ILE:O	1.97	0.65
1:C:275:ASP:OD1	1:C:279:LYS:NZ	2.28	0.64
1:D:146:ALA:HB3	1:D:149:LEU:HD22	1.79	0.64
1:A:148:PHE:CD1	1:A:149:LEU:HD13	2.32	0.64
1:C:49:ARG:HB3	1:C:49:ARG:CZ	2.27	0.63
1:B:17:ILE:HG12	1:B:57:PRO:HB3	1.80	0.63
1:A:228:LEU:HD22	1:C:188:LEU:HD21	1.81	0.63
1:C:69:ARG:HE	1:C:70:SER:H	1.45	0.62
1:D:44:CYS:O	1:D:48:VAL:HG23	2.00	0.61
1:B:11:ILE:HG12	1:B:23:LEU:HD11	1.82	0.61
1:B:47:TYR:O	1:B:51:THR:OG1	2.17	0.60
1:B:119:GLN:NE2	1:B:144:LYS:HE2	2.15	0.60
1:D:135:ALA:HA	1:D:141:ILE:HD11	1.82	0.60
1:D:59:VAL:HG12	1:D:99:ILE:HG22	1.83	0.60
1:B:51:THR:HG22	1:B:56:ILE:HB	1.83	0.60
1:C:8:ALA:O	1:C:197:GLU:HG2	2.02	0.60
1:B:120:LEU:CD1	1:B:134:MET:HE1	2.22	0.59
1:A:275:ASP:OD1	1:A:279:LYS:NZ	2.35	0.59
1:C:197:GLU:O	1:C:198:TYR:HB2	2.01	0.58
1:D:98:VAL:HG23	1:D:115:CYS:SG	2.43	0.58
1:C:119:GLN:NE2	1:C:144:LYS:HG3	2.19	0.58
1:C:170:ILE:HG12	1:C:199:PRO:HB2	1.85	0.58
1:A:59:VAL:HG22	1:A:97:PRO:HB2	1.86	0.58
1:B:201:PHE:CE2	1:B:239:GLY:HA3	2.38	0.57
1:C:23:LEU:O	1:C:279:LYS:HE2	2.04	0.57
1:A:221:ARG:HG3	1:A:222:ARG:H	1.68	0.57
1:B:222:ARG:HG3	1:B:223:ALA:N	2.21	0.56
1:C:14:VAL:O	1:C:16:ASP:N	2.38	0.56
1:A:23:LEU:O	1:A:279:LYS:HE2	2.05	0.56
1:A:66:LYS:H	1:A:76:ARG:HB2	1.70	0.56
1:C:226:THR:HA	1:C:267:PHE:HE1	1.70	0.56
1:C:145:LYS:HG3	1:C:154:MET:SD	2.46	0.56
1:C:147:GLN:H	1:C:147:GLN:HE21	1.52	0.56
1:D:127:GLN:HE21	1:D:130:LEU:HB2	1.71	0.55
1:C:10:LYS:HB2	1:C:198:TYR:H	1.71	0.54
1:B:181:ASN:HB3	2:B:307:HOH:O	2.06	0.54
1:A:277:LEU:HD22	1:C:277:LEU:HD12	1.89	0.54
1:D:148:PHE:CE1	1:D:149:LEU:HD13	2.42	0.54
1:D:69:ARG:HD2	1:D:70:SER:H	1.73	0.53
1:A:130:LEU:O	1:A:134:MET:HG3	2.08	0.53
1:D:274:LEU:O	1:D:278:ILE:HG12	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:88:GLU:OE2	1:D:88:GLU:HA	2.09	0.53
1:A:224:GLN:HE21	1:C:188:LEU:HD22	1.73	0.53
1:C:144:LYS:NZ	1:C:172:CYS:SG	2.82	0.53
1:A:137:THR:O	1:A:139:ALA:N	2.42	0.52
1:A:45:GLU:HG3	1:A:94:PHE:HE1	1.74	0.52
1:C:37:ARG:HD2	1:C:89:GLU:OE2	2.08	0.52
1:D:148:PHE:CD1	1:D:149:LEU:HD13	2.45	0.52
1:C:245:HIS:H	1:C:260:ARG:HG2	1.75	0.52
1:B:36:SER:OG	1:B:39:LEU:HB2	2.10	0.51
1:C:226:THR:HG22	1:C:267:PHE:CD1	2.46	0.51
1:D:14:VAL:CG2	1:D:140:VAL:HG21	2.41	0.51
1:D:126:ARG:HE	1:D:149:LEU:HD11	1.76	0.50
1:B:51:THR:HG21	1:B:58:TYR:HB2	1.94	0.50
1:B:234:SER:HA	1:B:278:ILE:HG13	1.94	0.50
1:B:235:GLN:HB2	1:B:237:LEU:HD21	1.93	0.50
1:B:13:ARG:HB2	1:B:13:ARG:NH1	2.26	0.49
1:A:102:VAL:HG23	1:A:134:MET:HE2	1.92	0.49
1:A:27:LEU:HD11	1:A:242:LEU:HD12	1.93	0.49
1:B:54:LEU:HD23	1:B:56:ILE:HD11	1.94	0.49
1:C:119:GLN:HE21	1:C:144:LYS:HG3	1.77	0.49
1:C:277:LEU:HD22	1:C:281:PHE:CZ	2.48	0.49
1:B:78:PRO:O	1:B:82:GLU:HB3	2.12	0.49
1:C:72:ILE:C	1:C:74:SER:H	2.16	0.49
1:B:18:GLN:HB3	1:B:23:LEU:HD13	1.95	0.49
1:B:149:LEU:HG	1:B:153:GLU:HG2	1.95	0.49
1:C:72:ILE:HG22	1:C:73:HIS:H	1.79	0.48
1:A:117:ILE:HG12	1:A:140:VAL:HG13	1.96	0.48
1:D:30:GLY:HA3	1:D:61:LYS:O	2.13	0.48
1:C:148:PHE:CE1	1:C:149:LEU:HD22	2.49	0.48
1:C:98:VAL:HG23	1:C:115:CYS:HA	1.96	0.47
1:B:270:GLN:HE21	1:D:282:PRO:HD2	1.79	0.47
1:D:127:GLN:HG3	1:D:127:GLN:O	2.14	0.47
1:A:148:PHE:CE1	1:A:149:LEU:HD13	2.50	0.47
1:B:59:VAL:HG22	1:B:97:PRO:CG	2.39	0.47
1:C:14:VAL:HG23	1:C:17:ILE:HB	1.97	0.47
1:A:10:LYS:HA	1:A:197:GLU:O	2.15	0.47
1:A:72:ILE:HG23	1:A:73:HIS:H	1.79	0.47
1:B:76:ARG:NH1	1:C:128:THR:HB	2.30	0.47
1:C:205:THR:HG23	1:C:242:LEU:HD12	1.97	0.46
1:B:119:GLN:HE22	1:B:144:LYS:HE2	1.81	0.46
1:C:72:ILE:O	1:C:74:SER:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:ALA:HB1	1:A:90:ILE:HD11	1.98	0.45
1:A:233:LEU:HD12	1:A:271:LEU:HD22	1.98	0.45
1:D:204:VAL:HG11	1:D:229:ALA:HB2	1.97	0.45
1:B:13:ARG:HB2	1:B:13:ARG:HH11	1.80	0.45
1:A:109:GLN:N	1:A:110:PRO:HD2	2.32	0.45
1:C:117:ILE:HG12	1:C:140:VAL:CG1	2.47	0.45
1:C:267:PHE:CZ	1:C:271:LEU:HD11	2.52	0.45
1:D:36:SER:OG	1:D:39:LEU:HD13	2.17	0.45
1:A:137:THR:C	1:A:139:ALA:H	2.20	0.45
1:C:18:GLN:HB3	1:C:23:LEU:CD2	2.48	0.44
1:B:158:LEU:HD11	1:B:171:LEU:HD11	1.98	0.44
1:C:49:ARG:HB3	1:C:49:ARG:NH1	2.31	0.44
1:C:78:PRO:HB2	1:C:82:GLU:HB3	1.99	0.44
1:B:275:ASP:OD1	1:B:279:LYS:HE2	2.17	0.44
1:A:123:PHE:HE2	1:D:126:ARG:HD2	1.83	0.44
1:A:234:SER:HA	1:A:278:ILE:HG13	2.00	0.44
1:D:135:ALA:O	1:D:166:ASN:HB2	2.17	0.44
1:D:47:TYR:HB3	1:D:58:TYR:CZ	2.52	0.43
1:C:72:ILE:H	1:C:72:ILE:HG13	1.56	0.43
1:B:204:VAL:HG11	1:B:229:ALA:HB2	2.00	0.43
1:C:102:VAL:HG23	1:C:107:GLN:HG3	2.00	0.43
1:C:274:LEU:O	1:C:278:ILE:HG12	2.18	0.43
1:A:60:PHE:HB3	1:A:98:VAL:HG12	2.01	0.43
1:A:122:ALA:HB1	1:A:146:ALA:HA	2.00	0.43
1:D:265:GLU:O	1:D:269:SER:HB2	2.18	0.43
1:A:19:ILE:HG12	1:A:26:VAL:HG21	2.00	0.43
1:D:117:ILE:HG12	1:D:140:VAL:HB	2.01	0.42
1:C:197:GLU:O	1:C:198:TYR:CB	2.67	0.42
1:A:15:GLY:HA3	2:A:304:HOH:O	2.19	0.42
1:D:208:LEU:HD21	1:D:228:LEU:HD12	2.00	0.42
1:A:155:LYS:HA	1:A:158:LEU:HD12	1.99	0.42
1:D:205:THR:HG21	1:D:243:GLU:H	1.83	0.42
1:A:45:GLU:HG3	1:A:94:PHE:CE1	2.51	0.42
1:D:33:VAL:HG22	1:D:34:LEU:N	2.34	0.42
1:B:194:LYS:NZ	1:B:236:LYS:HB3	2.33	0.42
1:C:128:THR:O	1:C:132:VAL:HG23	2.18	0.42
1:C:117:ILE:HG12	1:C:140:VAL:HG13	2.02	0.42
1:B:44:CYS:O	1:B:48:VAL:HG23	2.19	0.42
1:D:23:LEU:O	1:D:279:LYS:NZ	2.43	0.42
1:D:120:LEU:HD23	1:D:143:ILE:HG23	2.01	0.42
1:D:92:LYS:HB2	1:D:92:LYS:HE3	1.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:25:PHE:HB2	1:B:239:GLY:HA2	2.01	0.41
1:A:126:ARG:HB3	1:D:68:ASN:HB2	2.02	0.41
1:B:284:ILE:HG12	1:D:270:GLN:NE2	2.23	0.41
1:B:26:VAL:HG13	1:B:57:PRO:HB2	2.02	0.41
1:C:87:PHE:HD1	1:C:98:VAL:HG11	1.85	0.41
1:B:123:PHE:HB3	1:C:123:PHE:O	2.19	0.41
1:C:242:LEU:HG	1:C:243:GLU:N	2.35	0.41
1:B:60:PHE:HB3	1:B:98:VAL:HG12	2.02	0.41
1:A:221:ARG:HG3	1:A:222:ARG:N	2.34	0.41
1:D:194:LYS:NZ	1:D:235:GLN:O	2.51	0.41
1:B:31:MET:HE3	1:B:43:VAL:HG21	2.02	0.41
1:B:149:LEU:HA	1:B:149:LEU:HD12	1.90	0.41
1:C:104:GLU:O	1:C:107:GLN:HG2	2.20	0.41
1:C:155:LYS:HD2	1:C:155:LYS:HA	1.84	0.41
1:B:119:GLN:HE21	1:B:144:LYS:HG3	1.85	0.41
1:C:41:MET:HE3	1:C:41:MET:HB3	1.91	0.41
1:D:233:LEU:HD12	1:D:271:LEU:HD22	2.01	0.41
1:B:47:TYR:HB3	1:B:58:TYR:CZ	2.55	0.41
1:D:99:ILE:HB	1:D:117:ILE:HB	2.03	0.41
1:A:78:PRO:HB2	1:A:82:GLU:HB3	2.03	0.41
1:B:184:VAL:HG11	1:D:184:VAL:HG11	2.02	0.41
1:B:72:ILE:HD11	1:B:73:HIS:CE1	2.56	0.41
1:D:43:VAL:HA	1:D:261:LEU:HD11	2.03	0.41
1:C:201:PHE:CE2	1:C:239:GLY:HA3	2.56	0.41
1:C:199:PRO:HB3	1:C:238:ALA:CB	2.51	0.40
1:C:233:LEU:HA	1:C:233:LEU:HD23	1.91	0.40
1:C:19:ILE:HA	2:C:304:HOH:O	2.21	0.40
1:B:109:GLN:O	1:B:113:GLU:HG2	2.22	0.40
1:C:152:GLN:CD	1:C:152:GLN:H	2.25	0.40
1:C:50:VAL:HG11	1:C:265:GLU:HA	2.03	0.40
1:D:109:GLN:HB3	1:D:110:PRO:CD	2.51	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	241/287 (84%)	224 (93%)	13 (5%)	4 (2%)	11	36
1	B	241/287 (84%)	230 (95%)	10 (4%)	1 (0%)	39	74
1	C	244/287 (85%)	223 (91%)	17 (7%)	4 (2%)	12	38
1	D	246/287 (86%)	226 (92%)	18 (7%)	2 (1%)	24	58
All	All	972/1148 (85%)	903 (93%)	58 (6%)	11 (1%)	17	50

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	75	PHE
1	A	138	ASN
1	C	15	GLY
1	C	73	HIS
1	A	34	LEU
1	D	74	SER
1	C	68	ASN
1	D	138	ASN
1	B	71	SER
1	C	198	TYR
1	A	72	ILE

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	213/241 (88%)	196 (92%)	17 (8%)	15	40
1	B	210/241 (87%)	196 (93%)	14 (7%)	20	50
1	C	214/241 (89%)	194 (91%)	20 (9%)	11	32
1	D	218/241 (90%)	208 (95%)	10 (5%)	33	67
All	All	855/964 (89%)	794 (93%)	61 (7%)	18	46

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	ARG
1	A	46	GLU
1	A	70	SER
1	A	76	ARG
1	A	93	THR
1	A	102	VAL
1	A	136	ARG
1	A	140	VAL
1	A	149	LEU
1	A	153	GLU
1	A	174	ARG
1	A	206	HIS
1	A	208	LEU
1	A	240	LEU
1	A	243	GLU
1	A	262	ASN
1	A	263	LYS
1	B	9	GLN
1	B	14	VAL
1	B	31	MET
1	B	39	LEU
1	B	51	THR
1	B	56	ILE
1	B	69	ARG
1	B	136	ARG
1	B	149	LEU
1	B	152	GLN
1	B	153	GLU
1	B	204	VAL
1	B	222	ARG
1	B	277	LEU
1	C	27	LEU
1	C	39	LEU
1	C	46	GLU
1	C	66	LYS
1	C	68	ASN
1	C	72	ILE
1	C	82	GLU
1	C	95	LYS
1	C	102	VAL
1	C	127	GLN
1	C	140	VAL

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Mol	Chain	Res	Type
1	C	147	GLN
1	C	149	LEU
1	C	172	CYS
1	C	181	ASN
1	C	240	LEU
1	C	260	ARG
1	C	262	ASN
1	C	272	LYS
1	C	277	LEU
1	D	13	ARG
1	D	37	ARG
1	D	69	ARG
1	D	72	ILE
1	D	74	SER
1	D	80	LEU
1	D	81	GLU
1	D	123	PHE
1	D	124	LEU
1	D	206	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	119	GLN
1	A	142	ASN
1	A	224	GLN
1	B	119	GLN
1	B	206	HIS
1	B	224	GLN
1	B	270	GLN
1	C	119	GLN
1	C	147	GLN
1	C	262	ASN
1	D	127	GLN
1	D	224	GLN
1	D	270	GLN

5.3.3 RNA ⓘ

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	247/287 (86%)	-0.16	3 (1%) 81 73	19, 41, 73, 117	0
1	B	247/287 (86%)	-0.29	0 100 100	21, 39, 65, 82	0
1	C	250/287 (87%)	-0.19	3 (1%) 81 73	21, 44, 73, 98	0
1	D	252/287 (87%)	-0.27	2 (0%) 87 81	17, 39, 68, 113	0
All	All	996/1148 (86%)	-0.23	8 (0%) 87 81	17, 41, 70, 117	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	74	SER	3.4
1	A	206	HIS	2.8
1	D	70	SER	2.6
1	A	74	SER	2.4
1	C	206	HIS	2.4
1	A	73	HIS	2.2
1	C	70	SER	2.1
1	C	81	GLU	2.1

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.