



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:33 AM GMT

PDB ID : 2R88
Title : Crystal structure of the long-chain fatty acid transporter FadL mutant delta S3 kink
Authors : Hearn, E.M.; Patel, D.R.; Lepore, B.W.; Indic, M.; van den Berg, B.
Deposited on : 2007-09-10
Resolution : 2.60 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

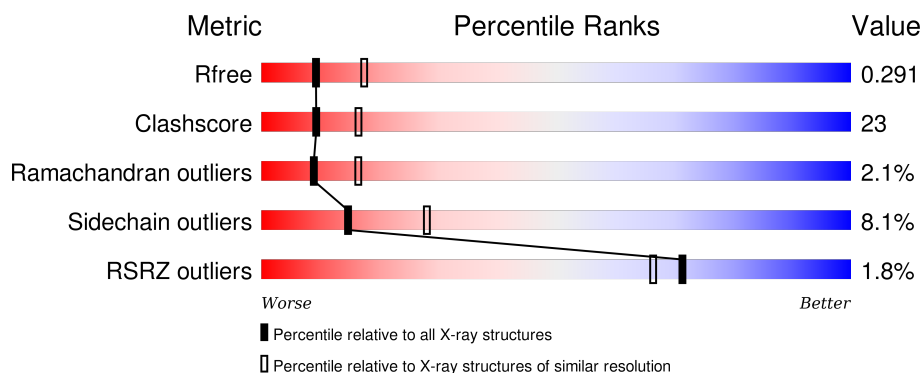
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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	426	<div> <div>2%</div> <div>51% 30% • 14%</div> </div>
1	B	426	<div> <div>%</div> <div>51% 31% • 14%</div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 5624 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 Long-chain fatty acid transport protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	365	Total	C	N	O	S	0	0	0
			2812	1776	479	551	6			
1	B	365	Total	C	N	O	S	0	0	0
			2812	1776	479	551	6			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	SER	SEE REMARK 999	UNP P10384
A	100	ALA	ASN	SEE REMARK 999	UNP P10384
A	101	ASN	TYR	SEE REMARK 999	UNP P10384
A	102	ASP	GLY	SEE REMARK 999	UNP P10384
A	196	THR	ILE	CONFLICT	UNP P10384
A	421	HIS	-	EXPRESSION TAG	UNP P10384
A	422	HIS	-	EXPRESSION TAG	UNP P10384
A	423	HIS	-	EXPRESSION TAG	UNP P10384
A	424	HIS	-	EXPRESSION TAG	UNP P10384
A	425	HIS	-	EXPRESSION TAG	UNP P10384
A	426	HIS	-	EXPRESSION TAG	UNP P10384
B	?	-	SER	SEE REMARK 999	UNP P10384
B	100	ALA	ASN	SEE REMARK 999	UNP P10384
B	101	ASN	TYR	SEE REMARK 999	UNP P10384
B	102	ASP	GLY	SEE REMARK 999	UNP P10384
B	196	THR	ILE	CONFLICT	UNP P10384
B	421	HIS	-	EXPRESSION TAG	UNP P10384
B	422	HIS	-	EXPRESSION TAG	UNP P10384
B	423	HIS	-	EXPRESSION TAG	UNP P10384
B	424	HIS	-	EXPRESSION TAG	UNP P10384
B	425	HIS	-	EXPRESSION TAG	UNP P10384
B	426	HIS	-	EXPRESSION TAG	UNP P10384

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	91.33Å 91.37Å 267.32Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.60 31.90 – 2.55	Depositor EDS
% Data completeness (in resolution range)	92.3 (10.00-2.60) 91.8 (31.90-2.55)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.94 (at 2.54Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.262 , 0.294 0.263 , 0.291	Depositor DCC
R_{free} test set	1618 reflections (5.13%)	DCC
Wilson B-factor (Å ²)	49.3	Xtriage
Anisotropy	0.434	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 19.7	EDS
Estimated twinning fraction	0.488 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 33907 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	5624	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.65% 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

5.1 Standard geometry

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	0.43	0/2887	0.68	3/3930 (0.1%)
1	B	0.43	0/2887	0.68	2/3930 (0.1%)
All	All	0.43	0/5774	0.68	5/7860 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	4	GLN	N-CA-C	7.48	131.21	111.00
1	B	5	LEU	N-CA-C	-5.60	95.89	111.00
1	A	6	ASN	N-CA-C	5.36	125.46	111.00
1	A	5	LEU	N-CA-C	-5.24	96.86	111.00
1	A	4	GLN	N-CA-C	5.18	124.98	111.00

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	2812	0	2606	124	0
1	B	2812	0	2606	127	0
All	All	5624	0	5212	247	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 23.

All (247) 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:89:ASN:ND2	1:B:90:ASP:H	1.60	1.00
1:A:89:ASN:ND2	1:A:90:ASP:H	1.60	0.97
1:B:57:ASN:ND2	1:B:72:ASN:H	1.63	0.95
1:A:57:ASN:ND2	1:A:72:ASN:H	1.63	0.95
1:A:156:ARG:HB2	1:A:197:ALA:HB3	1.58	0.85
1:B:156:ARG:HB2	1:B:197:ALA:HB3	1.59	0.84
1:B:136:ASN:HD21	1:B:139:TRP:H	1.25	0.83
1:A:136:ASN:HD21	1:A:139:TRP:H	1.25	0.82
1:B:177:THR:HB	1:B:180:GLY:H	1.49	0.76
1:A:322:ASP:O	1:A:350:PRO:HA	1.86	0.75
1:A:177:THR:HB	1:A:180:GLY:H	1.49	0.75
1:B:322:ASP:O	1:B:350:PRO:HA	1.86	0.74
1:A:219:ASN:HB3	1:A:281:ARG:HB3	1.70	0.73
1:B:219:ASN:HB3	1:B:281:ARG:HB3	1.71	0.73
1:A:277:SER:HB3	1:A:291:SER:HB3	1.69	0.73
1:A:89:ASN:ND2	1:A:90:ASP:N	2.37	0.72
1:B:120:THR:HG23	1:B:154:ILE:HD11	1.69	0.72
1:B:277:SER:HB3	1:B:291:SER:HB3	1.69	0.72
1:A:6:ASN:N	1:A:6:ASN:ND2	2.33	0.72
1:B:6:ASN:N	1:B:6:ASN:ND2	2.34	0.72
1:A:89:ASN:HD22	1:A:90:ASP:H	1.36	0.72
1:B:136:ASN:ND2	1:B:138:ALA:H	1.88	0.71
1:A:120:THR:HG23	1:A:154:ILE:HD11	1.71	0.71
1:A:136:ASN:ND2	1:A:138:ALA:H	1.88	0.71
1:B:136:ASN:ND2	1:B:139:TRP:H	1.89	0.71
1:A:136:ASN:ND2	1:A:139:TRP:H	1.89	0.71
1:A:57:ASN:HD22	1:A:72:ASN:H	1.38	0.70
1:B:89:ASN:HD22	1:B:90:ASP:H	1.36	0.70
1:B:57:ASN:HD22	1:B:72:ASN:H	1.38	0.70
1:B:89:ASN:ND2	1:B:90:ASP:N	2.37	0.69
1:A:106:GLU:HG3	1:A:119:THR:HG22	1.75	0.67
1:B:106:GLU:HG3	1:B:119:THR:HG22	1.76	0.66
1:A:379:ASP:O	1:A:418:TYR:HA	1.97	0.65
1:A:46:SER:OG	1:A:417:ASN:ND2	2.30	0.65
1:B:379:ASP:O	1:B:418:TYR:HA	1.97	0.64
1:A:158:ALA:O	1:A:192:SER:HA	1.98	0.64
1:B:158:ALA:O	1:B:192:SER:HA	1.97	0.64
1:A:89:ASN:HD22	1:A:90:ASP:N	1.96	0.64
1:B:46:SER:OG	1:B:417:ASN:ND2	2.31	0.62
1:B:215:GLU:HG2	1:B:221:ARG:HG2	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:ARG:HD2	1:A:20:GLU:OE1	2.01	0.61
1:B:15:ARG:HD2	1:B:20:GLU:OE1	2.00	0.61
1:A:130:SER:HB3	1:A:144:GLY:HA2	1.82	0.61
1:A:130:SER:HB3	1:A:144:GLY:CA	2.31	0.61
1:B:130:SER:HB3	1:B:144:GLY:HA2	1.83	0.61
1:B:57:ASN:HD21	1:B:72:ASN:H	1.46	0.60
1:A:136:ASN:HD22	1:A:136:ASN:C	2.05	0.60
1:A:281:ARG:HH11	1:A:281:ARG:HG3	1.66	0.60
1:A:57:ASN:HD21	1:A:72:ASN:H	1.47	0.60
1:B:136:ASN:HD22	1:B:136:ASN:C	2.05	0.60
1:B:151:ARG:HG2	1:B:202:ASN:OD1	2.02	0.60
1:B:130:SER:HB3	1:B:144:GLY:CA	2.32	0.60
1:A:215:GLU:HG2	1:A:221:ARG:HG2	1.83	0.60
1:A:122:LEU:HD21	1:A:268:LEU:HD22	1.84	0.59
1:A:328:LEU:HD23	1:A:329:GLY:N	2.17	0.59
1:B:89:ASN:HD22	1:B:90:ASP:N	1.96	0.59
1:B:281:ARG:HH11	1:B:281:ARG:HG3	1.67	0.59
1:A:151:ARG:HG2	1:A:202:ASN:OD1	2.01	0.59
1:B:122:LEU:HD21	1:B:268:LEU:HD22	1.84	0.58
1:B:328:LEU:HD23	1:B:329:GLY:N	2.17	0.58
1:A:106:GLU:HG3	1:A:119:THR:CG2	2.34	0.58
1:B:268:LEU:HD12	1:B:269:ASN:N	2.19	0.58
1:A:268:LEU:HD12	1:A:269:ASN:N	2.19	0.57
1:A:297:TRP:NE1	1:A:350:PRO:HB3	2.20	0.57
1:A:219:ASN:HB3	1:A:281:ARG:CB	2.34	0.57
1:B:198:HIS:C	1:B:199:LEU:HD12	2.25	0.57
1:A:198:HIS:C	1:A:199:LEU:HD12	2.24	0.57
1:B:271:PRO:HG2	1:B:297:TRP:CD2	2.40	0.57
1:B:297:TRP:NE1	1:B:350:PRO:HB3	2.20	0.57
1:A:271:PRO:HG2	1:A:297:TRP:CD2	2.40	0.56
1:A:268:LEU:HD12	1:A:269:ASN:H	1.70	0.56
1:B:219:ASN:HB3	1:B:281:ARG:CB	2.35	0.56
1:B:410:TRP:O	1:B:411:LEU:HD23	2.05	0.56
1:B:106:GLU:HG3	1:B:119:THR:CG2	2.34	0.56
1:B:268:LEU:HD12	1:B:269:ASN:H	1.70	0.56
1:A:140:SER:HB2	1:A:213:LEU:HB3	1.88	0.56
1:A:410:TRP:C	1:A:411:LEU:HD23	2.25	0.56
1:A:6:ASN:HD22	1:A:6:ASN:N	2.02	0.56
1:A:37:ILE:HB	1:A:132:ALA:HB3	1.88	0.56
1:B:37:ILE:HB	1:B:132:ALA:HB3	1.88	0.56
1:B:140:SER:HB2	1:B:213:LEU:HB3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:410:TRP:O	1:A:411:LEU:HD23	2.05	0.55
1:B:66:ARG:HH11	1:B:66:ARG:HG3	1.72	0.55
1:B:410:TRP:C	1:B:411:LEU:HD23	2.26	0.55
1:B:6:ASN:N	1:B:6:ASN:HD22	2.04	0.55
1:A:66:ARG:HH11	1:A:66:ARG:HG3	1.72	0.54
1:A:165:VAL:O	1:A:169:ILE:HG13	2.08	0.54
1:B:165:VAL:O	1:B:169:ILE:HG13	2.08	0.54
1:B:178:GLN:HE21	1:B:178:GLN:HA	1.73	0.54
1:A:120:THR:OG1	1:A:156:ARG:NH2	2.41	0.54
1:A:281:ARG:HG3	1:A:281:ARG:NH1	2.22	0.54
1:A:19:GLY:HA2	1:A:277:SER:CB	2.38	0.53
1:B:17:TYR:HA	1:B:20:GLU:OE1	2.08	0.53
1:A:57:ASN:HD22	1:A:72:ASN:N	2.07	0.53
1:B:19:GLY:HA2	1:B:277:SER:CB	2.39	0.53
1:A:17:TYR:HA	1:A:20:GLU:OE1	2.08	0.53
1:B:120:THR:OG1	1:B:156:ARG:NH2	2.41	0.52
1:A:178:GLN:HA	1:A:178:GLN:HE21	1.74	0.52
1:A:343:GLY:O	1:A:344:ILE:HD12	2.09	0.52
1:B:343:GLY:O	1:B:344:ILE:HD12	2.10	0.52
1:A:37:ILE:HB	1:A:132:ALA:CB	2.40	0.52
1:B:126:ASN:HD22	1:B:148:VAL:HG22	1.74	0.52
1:B:15:ARG:NH1	1:B:20:GLU:OE2	2.42	0.52
1:B:281:ARG:NH1	1:B:281:ARG:HG3	2.23	0.51
1:A:15:ARG:NH1	1:A:20:GLU:OE2	2.43	0.51
1:B:37:ILE:HB	1:B:132:ALA:CB	2.41	0.51
1:B:98:ILE:HD12	1:B:127:LEU:CD2	2.41	0.51
1:B:227:ARG:HB3	1:B:273:MET:HB3	1.93	0.51
1:B:17:TYR:HB2	1:B:325:ARG:NH2	2.26	0.51
1:B:19:GLY:HA2	1:B:277:SER:HB3	1.93	0.50
1:A:126:ASN:HD22	1:A:148:VAL:HG22	1.75	0.50
1:A:17:TYR:HB2	1:A:325:ARG:NH2	2.26	0.50
1:A:366:PHE:HB2	1:A:390:HIS:CD2	2.47	0.50
1:A:276:VAL:HG11	1:B:82:MET:SD	2.51	0.50
1:A:98:ILE:HD12	1:A:127:LEU:CD2	2.42	0.50
1:A:227:ARG:HB3	1:A:273:MET:HB3	1.94	0.50
1:B:231:LYS:N	1:B:231:LYS:HD3	2.26	0.49
1:A:294:TYR:HD1	1:B:420:PHE:CE1	2.30	0.49
1:A:19:GLY:HA2	1:A:277:SER:HB3	1.92	0.49
1:A:231:LYS:HD3	1:A:231:LYS:N	2.26	0.49
1:B:325:ARG:HG3	1:B:347:ASP:HB3	1.94	0.49
1:A:325:ARG:HG3	1:A:347:ASP:HB3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:216:LEU:HD11	1:B:125:MET:CE	2.42	0.49
1:A:43:PRO:HB2	1:A:420:PHE:CD2	2.48	0.49
1:B:57:ASN:HD22	1:B:72:ASN:N	2.06	0.48
1:B:352:PRO:HD2	1:B:355:ASN:HB2	1.95	0.48
1:B:366:PHE:HB2	1:B:390:HIS:CD2	2.47	0.48
1:A:174:ALA:C	1:A:176:GLN:H	2.17	0.48
1:B:43:PRO:HB2	1:B:420:PHE:CD2	2.49	0.48
1:A:352:PRO:HD2	1:A:355:ASN:HB2	1.95	0.48
1:A:323:ALA:CB	1:A:350:PRO:HG3	2.44	0.48
1:B:322:ASP:O	1:B:323:ALA:HB2	2.14	0.48
1:A:322:ASP:O	1:A:323:ALA:HB2	2.14	0.47
1:B:174:ALA:C	1:B:176:GLN:H	2.18	0.47
1:A:57:ASN:HD22	1:A:71:ASP:HA	1.79	0.47
1:B:342:THR:HG22	1:B:343:GLY:N	2.28	0.47
1:A:342:THR:HG22	1:A:343:GLY:N	2.28	0.47
1:B:349:SER:HA	1:B:350:PRO:HD3	1.69	0.47
1:B:323:ALA:CB	1:B:350:PRO:HG3	2.44	0.47
1:B:396:ILE:HD12	1:B:396:ILE:N	2.29	0.47
1:A:32:ARG:HA	1:A:32:ARG:HD2	1.65	0.47
1:B:321:LYS:HD3	1:B:351:VAL:HA	1.97	0.47
1:A:396:ILE:N	1:A:396:ILE:HD12	2.29	0.47
1:B:57:ASN:HD22	1:B:71:ASP:HA	1.80	0.46
1:B:115:SER:HA	1:B:157:PHE:O	2.16	0.46
1:B:12:GLY:HA2	1:B:15:ARG:HG2	1.98	0.46
1:B:344:ILE:HA	1:B:367:TRP:O	2.16	0.46
1:A:99:THR:OG1	1:A:126:ASN:HB3	2.16	0.46
1:A:115:SER:HA	1:A:157:PHE:O	2.15	0.46
1:A:344:ILE:HA	1:A:367:TRP:O	2.15	0.46
1:B:46:SER:CB	1:B:417:ASN:HD22	2.29	0.45
1:A:321:LYS:HD3	1:A:351:VAL:HA	1.97	0.45
1:A:30:VAL:HG21	1:A:85:VAL:HG22	1.98	0.45
1:A:363:GLN:HG3	1:A:392:GLN:O	2.17	0.45
1:A:156:ARG:C	1:A:196:THR:HG22	2.36	0.45
1:B:156:ARG:HA	1:B:156:ARG:HD3	1.81	0.45
1:A:12:GLY:HA2	1:A:15:ARG:HG2	1.97	0.45
1:A:222:TYR:CE2	1:A:278:GLY:HA3	2.52	0.45
1:A:7:GLU:HG2	1:A:50:VAL:HG11	1.99	0.45
1:A:381:SER:OG	1:A:417:ASN:HB2	2.17	0.45
1:B:222:TYR:CE2	1:B:278:GLY:HA3	2.52	0.45
1:A:116:VAL:HG23	1:A:358:ILE:HD11	1.99	0.45
1:A:324:TYR:HB3	1:B:420:PHE:CE1	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:383:ASP:O	1:B:414:THR:HA	2.16	0.45
1:B:116:VAL:HG23	1:B:358:ILE:HD11	1.99	0.45
1:B:30:VAL:HG21	1:B:85:VAL:HG22	1.98	0.45
1:A:283:ASP:OD1	1:A:284:PRO:HD2	2.17	0.45
1:A:349:SER:HA	1:A:350:PRO:HD3	1.69	0.45
1:B:99:THR:OG1	1:B:126:ASN:HB3	2.17	0.45
1:A:107:PHE:HB2	1:A:118:GLY:O	2.17	0.45
1:A:383:ASP:O	1:A:414:THR:HA	2.16	0.45
1:B:269:ASN:HD22	1:B:269:ASN:HA	1.61	0.45
1:A:46:SER:CB	1:A:417:ASN:HD22	2.29	0.44
1:A:98:ILE:HD12	1:A:127:LEU:HD22	1.98	0.44
1:B:32:ARG:HA	1:B:32:ARG:HD2	1.65	0.44
1:B:7:GLU:HG2	1:B:50:VAL:HG11	1.99	0.44
1:A:122:LEU:HD12	1:A:152:ALA:CB	2.48	0.44
1:B:363:GLN:HG3	1:B:392:GLN:O	2.17	0.44
1:B:156:ARG:C	1:B:196:THR:HG22	2.37	0.44
1:A:46:SER:HA	1:A:416:PHE:O	2.18	0.44
1:B:98:ILE:HD12	1:B:127:LEU:HD22	1.99	0.44
1:A:33:ASN:OD1	1:A:211:GLY:HA3	2.18	0.44
1:A:109:ASP:O	1:A:193:ASN:HA	2.18	0.44
1:B:381:SER:OG	1:B:417:ASN:HB2	2.18	0.44
1:B:122:LEU:HD12	1:B:152:ALA:CB	2.48	0.44
1:B:126:ASN:ND2	1:B:148:VAL:HG22	2.33	0.43
1:B:107:PHE:CZ	1:B:358:ILE:HD13	2.53	0.43
1:B:107:PHE:HB2	1:B:118:GLY:O	2.18	0.43
1:B:33:ASN:OD1	1:B:211:GLY:HA3	2.18	0.43
1:B:283:ASP:OD1	1:B:284:PRO:HD2	2.17	0.43
1:B:57:ASN:ND2	1:B:72:ASN:N	2.47	0.43
1:A:57:ASN:ND2	1:A:72:ASN:N	2.47	0.43
1:A:126:ASN:ND2	1:A:148:VAL:HG22	2.33	0.43
1:B:46:SER:HA	1:B:416:PHE:O	2.18	0.43
1:B:109:ASP:O	1:B:193:ASN:HA	2.19	0.43
1:A:351:VAL:O	1:A:352:PRO:O	2.37	0.43
1:B:81:ASN:HD22	1:B:83:HIS:CE1	2.37	0.43
1:A:206:PHE:O	1:A:231:LYS:HE2	2.19	0.43
1:A:105:THR:CG2	1:A:105:THR:O	2.67	0.43
1:A:19:GLY:HA2	1:A:277:SER:HB2	2.01	0.42
1:B:86:ALA:HA	1:B:87:PRO:HD3	1.88	0.42
1:B:130:SER:HB3	1:B:144:GLY:HA3	2.01	0.42
1:B:351:VAL:O	1:B:352:PRO:O	2.37	0.42
1:A:347:ASP:OD2	1:A:365:ARG:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:270:LEU:HA	1:B:271:PRO:HD3	1.85	0.42
1:A:130:SER:HB3	1:A:144:GLY:HA3	2.01	0.42
1:A:107:PHE:CZ	1:A:358:ILE:HD13	2.54	0.42
1:B:323:ALA:HB2	1:B:350:PRO:HG3	2.02	0.42
1:B:19:GLY:HA2	1:B:277:SER:HB2	2.01	0.42
1:A:75:PRO:HD2	1:A:104:ALA:HB3	2.01	0.42
1:A:17:TYR:HB2	1:A:325:ARG:HH22	1.85	0.42
1:B:347:ASP:OD2	1:B:365:ARG:HB2	2.20	0.42
1:A:52:ILE:HA	1:A:411:LEU:HD22	2.02	0.42
1:A:81:ASN:HD22	1:A:83:HIS:CE1	2.38	0.42
1:B:105:THR:O	1:B:105:THR:CG2	2.67	0.42
1:B:216:LEU:N	1:B:216:LEU:HD23	2.35	0.42
1:B:206:PHE:O	1:B:231:LYS:HE2	2.19	0.41
1:B:354:GLN:OE1	1:B:355:ASN:N	2.53	0.41
1:A:106:GLU:HA	1:A:119:THR:HG22	2.02	0.41
1:B:230:VAL:O	1:B:269:ASN:ND2	2.53	0.41
1:B:105:THR:HG22	1:B:105:THR:O	2.20	0.41
1:A:177:THR:C	1:A:179:GLN:N	2.73	0.41
1:A:105:THR:O	1:A:105:THR:HG22	2.20	0.41
1:A:156:ARG:HD3	1:A:156:ARG:HA	1.81	0.41
1:B:75:PRO:HD2	1:B:104:ALA:HB3	2.02	0.41
1:A:297:TRP:CD1	1:A:297:TRP:N	2.89	0.41
1:B:297:TRP:CD1	1:B:297:TRP:N	2.89	0.41
1:A:116:VAL:O	1:A:358:ILE:HD11	2.21	0.41
1:A:323:ALA:HB2	1:A:350:PRO:HG3	2.02	0.41
1:A:388:TYR:HB2	1:A:410:TRP:CZ3	2.56	0.41
1:B:420:PHE:CD2	1:B:420:PHE:N	2.89	0.41
1:A:420:PHE:N	1:A:420:PHE:CD2	2.89	0.41
1:A:354:GLN:OE1	1:A:355:ASN:N	2.53	0.41
1:A:230:VAL:O	1:A:269:ASN:ND2	2.54	0.41
1:A:15:ARG:HD3	1:A:289:HIS:CD2	2.56	0.40
1:B:15:ARG:HD3	1:B:289:HIS:CD2	2.56	0.40
1:A:178:GLN:HA	1:A:178:GLN:NE2	2.36	0.40
1:B:106:GLU:HA	1:B:119:THR:HG22	2.03	0.40
1:B:52:ILE:HG23	1:B:411:LEU:CD2	2.51	0.40
1:B:396:ILE:HD11	1:B:405:SER:HB3	2.03	0.40
1:A:396:ILE:HD11	1:A:405:SER:HB3	2.03	0.40
1:B:326:ILE:HD13	1:B:327:ALA:N	2.37	0.40
1:B:388:TYR:HB2	1:B:410:TRP:CZ3	2.56	0.40
1:B:52:ILE:HA	1:B:411:LEU:HD22	2.02	0.40
1:B:136:ASN:ND2	1:B:136:ASN:C	2.74	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:174:ALA:O	1:A:180:GLY:HA3	2.21	0.40
1:B:377:ASN:OD1	1:B:378:LYS:N	2.54	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	359/426 (84%)	336 (94%)	15 (4%)	8 (2%)	8	15
1	B	359/426 (84%)	336 (94%)	16 (4%)	7 (2%)	10	19
All	All	718/852 (84%)	672 (94%)	31 (4%)	15 (2%)	9	16

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	231	LYS
1	A	234	PHE
1	A	352	PRO
1	B	231	LYS
1	B	234	PHE
1	B	352	PRO
1	A	159	GLY
1	A	323	ALA
1	B	159	GLY
1	B	323	ALA
1	A	235	LYS
1	B	235	LYS
1	A	377	ASN
1	B	377	ASN
1	A	136	ASN

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	284/336 (84%)	261 (92%)	23 (8%)	15	28
1	B	284/336 (84%)	261 (92%)	23 (8%)	15	28
All	All	568/672 (84%)	522 (92%)	46 (8%)	15	28

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	ASN
1	A	42	ARG
1	A	72	ASN
1	A	89	ASN
1	A	90	ASP
1	A	101	ASN
1	A	105	THR
1	A	109	ASP
1	A	121	ASP
1	A	136	ASN
1	A	216	LEU
1	A	269	ASN
1	A	274	TRP
1	A	277	SER
1	A	281	ARG
1	A	326	ILE
1	A	344	ILE
1	A	354	GLN
1	A	372	THR
1	A	390	HIS
1	A	403	PHE
1	A	406	GLU
1	A	415	ASN
1	B	6	ASN
1	B	42	ARG
1	B	72	ASN
1	B	89	ASN

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Mol	Chain	Res	Type
1	B	90	ASP
1	B	101	ASN
1	B	105	THR
1	B	109	ASP
1	B	121	ASP
1	B	136	ASN
1	B	216	LEU
1	B	269	ASN
1	B	274	TRP
1	B	277	SER
1	B	281	ARG
1	B	326	ILE
1	B	344	ILE
1	B	354	GLN
1	B	372	THR
1	B	390	HIS
1	B	403	PHE
1	B	406	GLU
1	B	415	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	ASN
1	A	57	ASN
1	A	72	ASN
1	A	81	ASN
1	A	83	HIS
1	A	89	ASN
1	A	101	ASN
1	A	108	ASN
1	A	126	ASN
1	A	128	ASN
1	A	136	ASN
1	A	146	ASN
1	A	171	GLN
1	A	178	GLN
1	A	209	ASN
1	A	269	ASN
1	A	280	ASN
1	A	289	HIS
1	A	355	ASN

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Mol	Chain	Res	Type
1	A	390	HIS
1	A	402	GLN
1	A	415	ASN
1	A	417	ASN
1	B	6	ASN
1	B	57	ASN
1	B	72	ASN
1	B	81	ASN
1	B	83	HIS
1	B	89	ASN
1	B	101	ASN
1	B	108	ASN
1	B	126	ASN
1	B	128	ASN
1	B	136	ASN
1	B	146	ASN
1	B	171	GLN
1	B	178	GLN
1	B	209	ASN
1	B	269	ASN
1	B	280	ASN
1	B	289	HIS
1	B	355	ASN
1	B	390	HIS
1	B	402	GLN
1	B	415	ASN
1	B	417	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 carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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 [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	365/426 (85%)	0.07	8 (2%) 65 59	24, 46, 78, 104	0
1	B	365/426 (85%)	0.06	5 (1%) 78 74	23, 46, 78, 98	0
All	All	730/852 (85%)	0.07	13 (1%) 71 66	23, 46, 79, 104	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	351	VAL	5.4
1	B	351	VAL	5.0
1	A	355	ASN	4.4
1	B	355	ASN	4.2
1	B	361	PRO	2.8
1	A	361	PRO	2.4
1	B	196	THR	2.3
1	B	231	LYS	2.3
1	A	196	THR	2.3
1	A	231	LYS	2.2
1	A	233	ASP	2.2
1	A	353	ALA	2.1
1	A	394	VAL	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

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.