



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:33 AM GMT

PDB ID : 2R89
Title : Crystal structure of the long-chain fatty acid transporter FadL mutant delta N3
Authors : Hearn, E.M.; Patel, D.R.; Lepore, B.W.; Indic, M.; van den Berg, B.
Deposited on : 2007-09-10
Resolution : 3.40 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

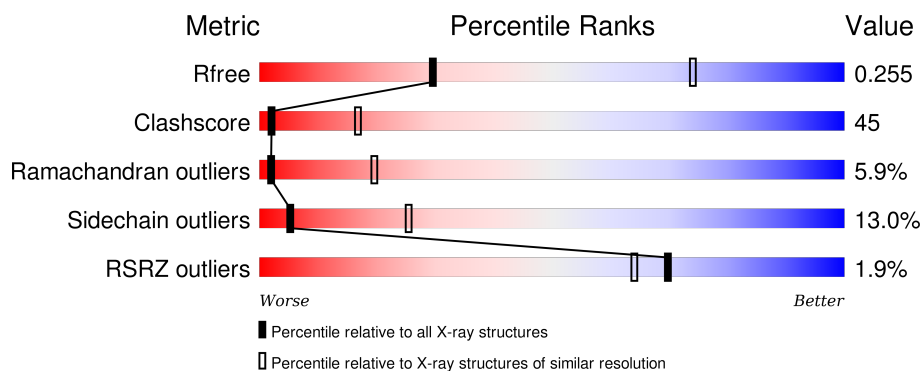
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

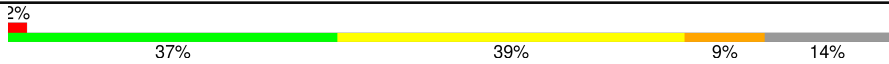
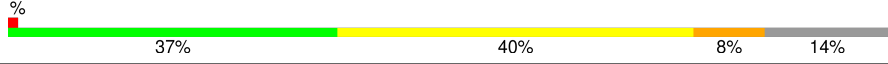
The reported resolution of this entry is 3.40 Å.

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}	91344	1476 (3.50-3.30)
Clashscore	102246	1611 (3.50-3.30)
Ramachandran outliers	100387	1571 (3.50-3.30)
Sidechain outliers	100360	1571 (3.50-3.30)
RSRZ outliers	91569	1485 (3.50-3.30)

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	424	 2% 37% 39% 9% 14%
1	B	424	 2% 37% 40% 8% 14%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 5608 atoms, of which 0 are hydrogens and 0 are deuteriums.

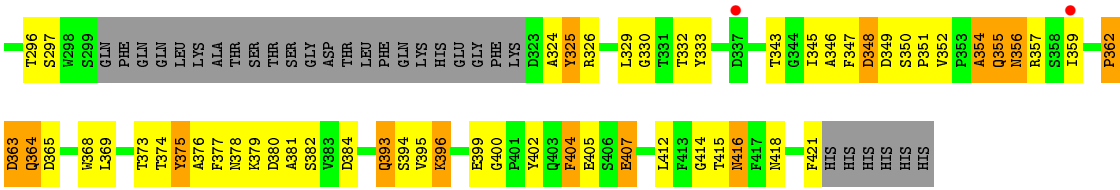
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Long-chain fatty acid transport protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	363	Total	C	N	O	S	0	0	0
			2804	1774	475	549	6			
1	B	363	Total	C	N	O	S	0	0	0
			2804	1774	475	549	6			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	PHE	DELETION	UNP P10384
A	?	-	GLN	DELETION	UNP P10384
A	?	-	LEU	DELETION	UNP P10384
A	197	THR	ILE	CONFLICT	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
A	427	HIS	-	EXPRESSION TAG	UNP P10384
B	?	-	PHE	DELETION	UNP P10384
B	?	-	GLN	DELETION	UNP P10384
B	?	-	LEU	DELETION	UNP P10384
B	197	THR	ILE	CONFLICT	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
B	427	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	92.02Å 91.91Å 289.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 3.40 38.81 – 3.40	Depositor EDS
% Data completeness (in resolution range)	97.7 (10.00-3.40) 98.6 (38.81-3.40)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.48 (at 3.40Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.252 , 0.302 0.257 , 0.255	Depositor DCC
R_{free} test set	1269 reflections (7.76%)	DCC
Wilson B-factor (Å ²)	78.5	Xtriage
Anisotropy	0.444	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , -1.2	EDS
Estimated twinning fraction	0.459 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 17064 reflections	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	5608	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.40% 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	0.50	0/2880	0.73	0/3924
1	B	0.50	0/2880	0.73	0/3924
All	All	0.50	0/5760	0.73	0/7848

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

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	2804	0	2598	243	0
1	B	2804	0	2598	252	0
All	All	5608	0	5196	491	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 45.

All (491) 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:A:137:ASN:HD22	1:A:138:ASN:N	1.55	1.04
1:B:137:ASN:HD22	1:B:138:ASN:N	1.54	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:352:VAL:HG11	1:A:357:ARG:HA	1.47	0.97
1:B:52:ILE:HG12	1:B:412:LEU:HD22	1.48	0.96
1:B:352:VAL:HG11	1:B:357:ARG:HA	1.47	0.96
1:A:52:ILE:HG12	1:A:412:LEU:HD22	1.48	0.95
1:B:109:ASN:HD22	1:B:109:ASN:H	1.00	0.94
1:A:48:GLY:HA3	1:A:416:ASN:HD22	1.32	0.93
1:B:57:ASN:ND2	1:B:72:ASN:H	1.68	0.92
1:A:57:ASN:ND2	1:A:72:ASN:H	1.67	0.92
1:A:109:ASN:H	1:A:109:ASN:HD22	0.99	0.92
1:B:48:GLY:HA3	1:B:416:ASN:HD22	1.32	0.91
1:A:109:ASN:H	1:A:109:ASN:ND2	1.69	0.89
1:A:378:ASN:O	1:A:380:ASP:N	2.06	0.89
1:B:378:ASN:O	1:B:380:ASP:N	2.06	0.88
1:B:89:ASN:ND2	1:B:90:ASP:H	1.71	0.88
1:A:89:ASN:ND2	1:A:90:ASP:H	1.72	0.87
1:B:66:ARG:HH11	1:B:164:GLN:NE2	1.72	0.87
1:B:109:ASN:ND2	1:B:109:ASN:H	1.70	0.87
1:B:66:ARG:HH11	1:B:164:GLN:HE22	0.89	0.87
1:A:66:ARG:HH11	1:A:164:GLN:NE2	1.72	0.87
1:A:66:ARG:NH1	1:A:164:GLN:HE22	1.73	0.87
1:A:33:ASN:HB3	1:A:36:LEU:HD13	1.55	0.86
1:A:66:ARG:HH11	1:A:164:GLN:HE22	0.90	0.86
1:B:33:ASN:HB3	1:B:36:LEU:HD13	1.55	0.86
1:B:66:ARG:NH1	1:B:164:GLN:HE22	1.73	0.83
1:B:7:GLU:HB3	1:B:50:VAL:HG21	1.60	0.83
1:B:137:ASN:HD22	1:B:138:ASN:H	1.27	0.83
1:A:402:TYR:HB2	1:A:404:PHE:CE1	2.14	0.82
1:B:402:TYR:HB2	1:B:404:PHE:CE1	2.14	0.82
1:A:137:ASN:HD22	1:A:138:ASN:H	1.28	0.82
1:B:48:GLY:HA3	1:B:416:ASN:ND2	1.94	0.81
1:B:186:ALA:C	1:B:188:ALA:H	1.82	0.81
1:A:186:ALA:C	1:A:188:ALA:H	1.81	0.81
1:A:48:GLY:HA3	1:A:416:ASN:ND2	1.94	0.81
1:A:213:ILE:O	1:A:213:ILE:HG22	1.81	0.80
1:B:213:ILE:O	1:B:213:ILE:HG22	1.79	0.80
1:B:136:LEU:O	1:B:136:LEU:HG	1.83	0.78
1:B:178:THR:HG22	1:B:180:GLN:H	1.48	0.78
1:A:136:LEU:HG	1:A:136:LEU:O	1.82	0.77
1:B:73:ILE:HD12	1:B:108:PHE:CE2	2.19	0.77
1:B:158:PHE:HE2	1:B:196:LYS:HG3	1.50	0.77
1:A:73:ILE:HD12	1:A:108:PHE:CE2	2.19	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:89:ASN:CG	1:B:90:ASP:H	1.88	0.76
1:A:178:THR:HG22	1:A:180:GLN:H	1.48	0.76
1:B:49:ALA:HB2	1:B:80:PRO:HA	1.67	0.76
1:A:49:ALA:HB2	1:A:80:PRO:HA	1.67	0.76
1:A:158:PHE:HE2	1:A:196:LYS:HG3	1.50	0.76
1:A:109:ASN:N	1:A:109:ASN:HD22	1.80	0.75
1:A:137:ASN:ND2	1:A:138:ASN:N	2.34	0.75
1:A:363:ASP:C	1:A:364:GLN:HG3	2.06	0.75
1:A:52:ILE:HG12	1:A:412:LEU:CD2	2.17	0.75
1:A:89:ASN:CG	1:A:90:ASP:H	1.89	0.75
1:A:101:ASN:HB3	1:A:102:TYR:CE1	2.22	0.75
1:B:101:ASN:HB3	1:B:102:TYR:CE1	2.22	0.74
1:B:52:ILE:HG12	1:B:412:LEU:CD2	2.17	0.74
1:A:382:SER:OG	1:A:418:ASN:HB2	1.87	0.74
1:B:363:ASP:C	1:B:364:GLN:HG3	2.06	0.74
1:B:382:SER:OG	1:B:418:ASN:HB2	1.88	0.74
1:B:137:ASN:ND2	1:B:138:ASN:N	2.33	0.73
1:B:56:VAL:HG12	1:B:73:ILE:HG23	1.71	0.73
1:A:41:ASP:O	1:A:87:PRO:HG3	1.88	0.73
1:B:41:ASP:O	1:B:87:PRO:HG3	1.88	0.72
1:B:7:GLU:CB	1:B:50:VAL:HG21	2.19	0.72
1:B:326:ARG:HG3	1:B:348:ASP:HB3	1.71	0.72
1:A:56:VAL:HG12	1:A:73:ILE:HG23	1.70	0.72
1:A:186:ALA:O	1:A:188:ALA:N	2.21	0.72
1:B:109:ASN:N	1:B:109:ASN:HD22	1.81	0.71
1:A:109:ASN:ND2	1:A:109:ASN:N	2.36	0.71
1:A:326:ARG:HG3	1:A:348:ASP:HB3	1.72	0.71
1:B:186:ALA:O	1:B:188:ALA:N	2.22	0.70
1:A:89:ASN:ND2	1:A:90:ASP:N	2.40	0.70
1:A:125:THR:HG23	1:A:149:VAL:HG13	1.73	0.70
1:B:394:SER:HB2	1:B:407:GLU:HB2	1.74	0.70
1:B:117:VAL:HG23	1:B:359:ILE:HD11	1.73	0.70
1:A:106:THR:HG21	1:A:362:PRO:CD	2.22	0.70
1:B:158:PHE:CE2	1:B:196:LYS:HG3	2.27	0.70
1:A:34:PRO:HB2	1:A:143:GLY:HA3	1.74	0.69
1:B:89:ASN:ND2	1:B:90:ASP:N	2.39	0.69
1:A:117:VAL:HG23	1:A:359:ILE:HD11	1.73	0.69
1:B:125:THR:HG23	1:B:149:VAL:HG13	1.73	0.69
1:B:34:PRO:HB2	1:B:143:GLY:HA3	1.75	0.69
1:A:158:PHE:CE2	1:A:196:LYS:HG3	2.27	0.69
1:A:394:SER:HB2	1:A:407:GLU:HB2	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:106:THR:HG21	1:B:362:PRO:CD	2.22	0.68
1:A:24:ALA:HB2	1:A:36:LEU:HD23	1.75	0.68
1:B:109:ASN:N	1:B:109:ASN:ND2	2.37	0.68
1:A:50:VAL:HG12	1:A:414:GLY:HA3	1.77	0.67
1:B:381:ALA:HA	1:B:418:ASN:O	1.93	0.67
1:B:24:ALA:HB2	1:B:36:LEU:HD23	1.75	0.67
1:A:381:ALA:HA	1:A:418:ASN:O	1.94	0.67
1:B:131:SER:HB3	1:B:145:GLY:HA3	1.77	0.67
1:A:131:SER:HB3	1:A:145:GLY:HA3	1.77	0.67
1:B:50:VAL:HG12	1:B:414:GLY:HA3	1.77	0.66
1:A:8:PHE:CE2	1:A:32:ARG:HD2	2.30	0.66
1:A:82:MET:O	1:A:97:SER:HA	1.96	0.66
1:A:43:PRO:HG2	1:A:421:PHE:HB2	1.78	0.66
1:B:82:MET:O	1:B:97:SER:HA	1.96	0.66
1:B:7:GLU:HA	1:B:17:TYR:OH	1.96	0.65
1:B:49:ALA:CB	1:B:80:PRO:HA	2.26	0.65
1:B:157:ARG:HB2	1:B:198:ALA:HB3	1.78	0.65
1:B:20:GLU:HB2	1:B:32:ARG:HD3	1.79	0.65
1:A:20:GLU:HB2	1:A:32:ARG:HD3	1.79	0.64
1:A:157:ARG:HB2	1:A:198:ALA:HB3	1.78	0.64
1:A:407:GLU:HG3	1:A:407:GLU:O	1.98	0.64
1:B:43:PRO:HG2	1:B:421:PHE:HB2	1.79	0.64
1:B:186:ALA:C	1:B:188:ALA:N	2.51	0.64
1:A:49:ALA:CB	1:A:80:PRO:HA	2.27	0.64
1:A:32:ARG:HH11	1:A:32:ARG:HG3	1.63	0.64
1:A:378:ASN:C	1:A:380:ASP:H	2.02	0.64
1:B:378:ASN:C	1:B:380:ASP:H	2.01	0.64
1:B:73:ILE:HG12	1:B:73:ILE:O	1.97	0.64
1:B:32:ARG:HH11	1:B:32:ARG:HG3	1.63	0.63
1:A:73:ILE:HG12	1:A:73:ILE:O	1.97	0.63
1:B:347:PHE:CG	1:B:348:ASP:N	2.67	0.63
1:A:347:PHE:CG	1:A:348:ASP:N	2.66	0.63
1:A:232:LYS:HG2	1:A:270:ASN:HD21	1.63	0.63
1:B:232:LYS:HG2	1:B:270:ASN:HD21	1.63	0.63
1:B:64:SER:HB3	1:B:165:LEU:HD21	1.81	0.63
1:B:108:PHE:HB2	1:B:118:GLY:O	1.99	0.63
1:A:108:PHE:HB2	1:A:118:GLY:O	1.99	0.63
1:B:407:GLU:O	1:B:407:GLU:HG3	1.97	0.62
1:A:144:LEU:HD21	1:A:146:PHE:CE1	2.35	0.62
1:A:106:THR:HG21	1:A:362:PRO:HD3	1.80	0.62
1:B:144:LEU:HD21	1:B:146:PHE:CE1	2.35	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:81:ASN:C	1:A:81:ASN:HD22	2.01	0.62
1:B:106:THR:HG21	1:B:362:PRO:HD3	1.80	0.62
1:B:6:ASN:ND2	1:B:101:ASN:O	2.33	0.61
1:A:284:ASP:CG	1:A:285:PRO:HD2	2.21	0.61
1:B:284:ASP:CG	1:B:285:PRO:HD2	2.20	0.61
1:A:52:ILE:HG23	1:A:412:LEU:HD21	1.84	0.60
1:A:64:SER:HB3	1:A:165:LEU:HD21	1.81	0.60
1:B:52:ILE:HG23	1:B:412:LEU:HD21	1.83	0.60
1:A:48:GLY:CA	1:A:416:ASN:ND2	2.64	0.60
1:B:19:GLY:HA3	1:B:290:HIS:HB2	1.84	0.60
1:B:136:LEU:CG	1:B:136:LEU:O	2.50	0.60
1:A:19:GLY:HA3	1:A:290:HIS:HB2	1.84	0.59
1:B:48:GLY:CA	1:B:416:ASN:ND2	2.64	0.59
1:B:8:PHE:CE2	1:B:32:ARG:HD2	2.38	0.59
1:A:5:GLY:HA2	1:A:17:TYR:CB	2.32	0.59
1:B:213:ILE:CG2	1:B:213:ILE:O	2.51	0.59
1:A:75:PRO:HD2	1:A:105:ALA:O	2.03	0.59
1:A:57:ASN:ND2	1:A:72:ASN:N	2.46	0.59
1:B:89:ASN:CG	1:B:90:ASP:N	2.57	0.58
1:A:16:ALA:O	1:A:326:ARG:NH2	2.36	0.58
1:A:136:LEU:O	1:A:137:ASN:HB2	2.03	0.58
1:A:15:ARG:HD2	1:A:20:GLU:OE1	2.02	0.58
1:B:136:LEU:O	1:B:137:ASN:HB2	2.04	0.58
1:B:163:GLY:HA3	1:B:188:ALA:O	2.04	0.58
1:B:15:ARG:HD2	1:B:20:GLU:OE1	2.02	0.58
1:A:142:PHE:CD1	1:A:142:PHE:N	2.70	0.58
1:B:75:PRO:HD2	1:B:105:ALA:O	2.03	0.58
1:B:16:ALA:O	1:B:326:ARG:NH2	2.37	0.58
1:A:217:LEU:O	1:A:218:ASP:HB3	2.03	0.58
1:A:186:ALA:C	1:A:188:ALA:N	2.51	0.57
1:A:213:ILE:O	1:A:213:ILE:CG2	2.52	0.57
1:B:421:PHE:CD2	1:B:421:PHE:N	2.71	0.57
1:B:217:LEU:O	1:B:218:ASP:HB3	2.03	0.57
1:B:142:PHE:N	1:B:142:PHE:CD1	2.70	0.57
1:A:136:LEU:CG	1:A:136:LEU:O	2.49	0.57
1:A:89:ASN:CG	1:A:90:ASP:N	2.57	0.57
1:B:81:ASN:HD22	1:B:81:ASN:C	2.01	0.57
1:B:105:ALA:HA	1:B:121:THR:O	2.04	0.57
1:A:105:ALA:HA	1:A:121:THR:O	2.04	0.57
1:A:163:GLY:HA3	1:A:188:ALA:O	2.04	0.57
1:A:119:GLY:HA3	1:A:156:GLU:O	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:166:VAL:O	1:A:170:ILE:HG13	2.05	0.57
1:A:6:ASN:OD1	1:A:101:ASN:O	2.22	0.57
1:B:166:VAL:O	1:B:170:ILE:HG13	2.05	0.57
1:A:421:PHE:CD2	1:A:421:PHE:N	2.71	0.56
1:B:119:GLY:HA3	1:B:156:GLU:O	2.05	0.56
1:B:57:ASN:ND2	1:B:72:ASN:N	2.47	0.56
1:A:19:GLY:O	1:A:20:GLU:C	2.44	0.56
1:A:57:ASN:HD22	1:A:72:ASN:H	1.50	0.56
1:A:26:ASP:O	1:A:28:GLY:N	2.40	0.55
1:A:73:ILE:HD12	1:A:108:PHE:HE2	1.71	0.55
1:B:81:ASN:HD21	1:B:416:ASN:HD21	1.55	0.55
1:B:49:ALA:HB2	1:B:80:PRO:CA	2.35	0.55
1:B:375:TYR:C	1:B:375:TYR:HD2	2.10	0.55
1:B:26:ASP:O	1:B:28:GLY:N	2.40	0.55
1:B:19:GLY:O	1:B:20:GLU:C	2.44	0.54
1:A:49:ALA:HB2	1:A:80:PRO:CA	2.36	0.54
1:B:73:ILE:HD12	1:B:108:PHE:HE2	1.71	0.54
1:B:329:LEU:HD23	1:B:330:GLY:N	2.22	0.54
1:B:357:ARG:NH1	1:B:395:VAL:HB	2.23	0.54
1:B:182:GLN:O	1:B:185:ALA:HB3	2.07	0.54
1:A:375:TYR:HD2	1:A:375:TYR:C	2.11	0.54
1:A:84:PHE:HZ	1:B:325:TYR:CE1	2.25	0.54
1:A:182:GLN:O	1:A:185:ALA:HB3	2.07	0.54
1:B:144:LEU:C	1:B:144:LEU:HD23	2.28	0.54
1:A:352:VAL:HG11	1:A:357:ARG:CA	2.30	0.54
1:A:357:ARG:NH1	1:A:395:VAL:HB	2.23	0.54
1:B:33:ASN:CB	1:B:36:LEU:HD13	2.34	0.54
1:A:375:TYR:CD2	1:A:375:TYR:C	2.82	0.54
1:A:8:PHE:C	1:A:8:PHE:CD1	2.82	0.53
1:A:81:ASN:HD21	1:A:416:ASN:HD21	1.57	0.53
1:B:27:ALA:HB1	1:B:85:VAL:HG23	1.90	0.53
1:B:178:THR:HG22	1:B:180:GLN:N	2.21	0.53
1:A:144:LEU:C	1:A:144:LEU:HD23	2.28	0.53
1:B:125:THR:HG23	1:B:149:VAL:CG1	2.39	0.53
1:A:125:THR:HG23	1:A:149:VAL:CG1	2.39	0.53
1:A:20:GLU:HA	1:A:29:ASN:ND2	2.24	0.53
1:B:17:TYR:HA	1:B:20:GLU:OE1	2.10	0.52
1:B:7:GLU:CD	1:B:7:GLU:H	2.11	0.52
1:A:62:SER:C	1:A:64:SER:H	2.13	0.52
1:A:178:THR:HG22	1:A:180:GLN:N	2.20	0.52
1:A:329:LEU:HD23	1:A:330:GLY:N	2.23	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:374:THR:HG23	1:B:384:ASP:OD2	2.09	0.52
1:B:144:LEU:O	1:B:144:LEU:HD23	2.10	0.52
1:A:374:THR:HG23	1:A:384:ASP:OD2	2.09	0.52
1:A:214:LEU:HD11	1:A:222:ARG:HB2	1.92	0.52
1:A:27:ALA:HB1	1:A:85:VAL:HG23	1.90	0.52
1:B:214:LEU:HD11	1:B:222:ARG:HB2	1.92	0.52
1:A:174:PRO:C	1:A:176:GLY:H	2.13	0.52
1:A:33:ASN:CB	1:A:36:LEU:HD13	2.34	0.52
1:A:144:LEU:O	1:A:144:LEU:HD23	2.10	0.52
1:B:57:ASN:HD22	1:B:72:ASN:H	1.51	0.52
1:A:158:PHE:HD2	1:A:196:LYS:HA	1.75	0.52
1:B:73:ILE:HD12	1:B:108:PHE:CZ	2.44	0.52
1:B:20:GLU:HA	1:B:29:ASN:ND2	2.24	0.51
1:A:421:PHE:N	1:A:421:PHE:HD2	2.07	0.51
1:A:81:ASN:ND2	1:A:81:ASN:O	2.32	0.51
1:A:104:LEU:HD12	1:A:105:ALA:N	2.25	0.51
1:B:158:PHE:HD2	1:B:196:LYS:HA	1.75	0.51
1:B:18:SER:OG	1:B:290:HIS:HD2	1.94	0.51
1:A:404:PHE:CD1	1:A:404:PHE:N	2.79	0.51
1:B:174:PRO:C	1:B:176:GLY:H	2.13	0.51
1:A:73:ILE:HD12	1:A:108:PHE:CZ	2.45	0.51
1:B:34:PRO:HB2	1:B:143:GLY:CA	2.41	0.51
1:B:8:PHE:CD1	1:B:8:PHE:C	2.84	0.51
1:A:131:SER:HB3	1:A:145:GLY:CA	2.41	0.51
1:A:5:GLY:N	1:A:326:ARG:NE	2.58	0.51
1:B:421:PHE:N	1:B:421:PHE:HD2	2.08	0.51
1:B:52:ILE:HG23	1:B:412:LEU:CD2	2.41	0.51
1:B:21:GLY:HA2	1:B:33:ASN:HB2	1.93	0.51
1:B:79:VAL:CG1	1:B:100:SER:HB3	2.41	0.51
1:B:404:PHE:N	1:B:404:PHE:CD1	2.79	0.51
1:B:81:ASN:O	1:B:81:ASN:ND2	2.32	0.50
1:A:17:TYR:HA	1:A:20:GLU:OE1	2.10	0.50
1:A:79:VAL:CG1	1:A:100:SER:HB3	2.42	0.50
1:B:62:SER:C	1:B:64:SER:H	2.13	0.50
1:A:332:THR:HG22	1:A:333:TYR:N	2.26	0.50
1:A:284:ASP:CG	1:A:285:PRO:CD	2.80	0.50
1:B:375:TYR:C	1:B:375:TYR:CD2	2.81	0.50
1:B:104:LEU:HD12	1:B:105:ALA:N	2.26	0.50
1:B:332:THR:HG22	1:B:333:TYR:N	2.25	0.50
1:A:52:ILE:HG23	1:A:412:LEU:CD2	2.41	0.50
1:A:18:SER:OG	1:A:290:HIS:HD2	1.95	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:34:PRO:HB2	1:A:143:GLY:CA	2.40	0.50
1:B:402:TYR:HB2	1:B:404:PHE:CZ	2.47	0.50
1:A:280:TYR:HA	1:A:289:ILE:O	2.12	0.50
1:B:280:TYR:HA	1:B:289:ILE:O	2.12	0.50
1:A:101:ASN:HB3	1:A:102:TYR:CD1	2.46	0.50
1:A:21:GLY:HA2	1:A:33:ASN:HB2	1.94	0.49
1:B:12:GLY:O	1:B:13:LEU:C	2.51	0.49
1:A:12:GLY:O	1:A:13:LEU:C	2.50	0.49
1:B:131:SER:HB3	1:B:145:GLY:CA	2.41	0.49
1:A:84:PHE:HZ	1:B:325:TYR:HE1	1.60	0.49
1:B:284:ASP:CG	1:B:285:PRO:CD	2.80	0.49
1:A:402:TYR:HB2	1:A:404:PHE:CZ	2.47	0.49
1:B:167:ALA:O	1:B:169:GLN:N	2.46	0.49
1:B:7:GLU:N	1:B:7:GLU:CD	2.65	0.49
1:A:396:LYS:HA	1:A:405:GLU:HA	1.94	0.49
1:A:133:ALA:HA	1:A:143:GLY:HA2	1.94	0.49
1:B:133:ALA:HA	1:B:143:GLY:HA2	1.95	0.49
1:A:350:SER:HB2	1:A:365:ASP:N	2.28	0.49
1:B:101:ASN:HB3	1:B:102:TYR:CD1	2.47	0.49
1:B:350:SER:HB2	1:B:365:ASP:N	2.28	0.49
1:B:167:ALA:O	1:B:170:ILE:N	2.46	0.49
1:B:26:ASP:C	1:B:28:GLY:N	2.66	0.49
1:A:167:ALA:O	1:A:170:ILE:N	2.46	0.48
1:B:396:LYS:HA	1:B:405:GLU:HA	1.94	0.48
1:A:279:GLY:O	1:A:290:HIS:HA	2.13	0.48
1:A:382:SER:HG	1:A:418:ASN:HB2	1.78	0.48
1:B:279:GLY:O	1:B:290:HIS:HA	2.13	0.48
1:A:194:ASN:C	1:A:194:ASN:OD1	2.52	0.48
1:A:13:LEU:HA	1:A:17:TYR:CE1	2.49	0.48
1:A:167:ALA:O	1:A:169:GLN:N	2.46	0.48
1:B:394:SER:HB2	1:B:407:GLU:CB	2.43	0.48
1:B:407:GLU:O	1:B:407:GLU:CG	2.62	0.48
1:A:43:PRO:CG	1:A:421:PHE:HB2	2.43	0.48
1:B:214:LEU:HD12	1:B:215:TYR:N	2.29	0.48
1:B:194:ASN:C	1:B:194:ASN:OD1	2.52	0.48
1:B:108:PHE:HD1	1:B:118:GLY:O	1.97	0.48
1:B:50:VAL:CG1	1:B:414:GLY:HA3	2.43	0.48
1:B:158:PHE:CD2	1:B:196:LYS:HA	2.49	0.48
1:B:325:TYR:HE2	1:B:349:ASP:HB2	1.79	0.48
1:B:329:LEU:C	1:B:329:LEU:HD23	2.34	0.48
1:A:394:SER:HB2	1:A:407:GLU:CB	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:13:LEU:HA	1:B:17:TYR:CE1	2.48	0.47
1:B:232:LYS:HA	1:B:270:ASN:ND2	2.30	0.47
1:B:204:GLN:OE1	1:B:204:GLN:HA	2.14	0.47
1:A:73:ILE:O	1:A:73:ILE:CG1	2.62	0.47
1:B:64:SER:HB3	1:B:165:LEU:CD2	2.44	0.47
1:A:173:SER:HB2	1:A:174:PRO:HD2	1.96	0.47
1:B:151:ALA:HB2	1:B:233:ILE:CD1	2.44	0.47
1:A:50:VAL:CG1	1:A:414:GLY:HA3	2.42	0.47
1:A:64:SER:HB3	1:A:165:LEU:CD2	2.44	0.47
1:A:15:ARG:HD3	1:A:290:HIS:CD2	2.49	0.47
1:B:26:ASP:OD2	1:B:28:GLY:HA3	2.15	0.47
1:B:173:SER:HB2	1:B:174:PRO:HD2	1.97	0.47
1:B:33:ASN:ND2	1:B:36:LEU:CD1	2.78	0.47
1:B:15:ARG:HD3	1:B:290:HIS:CD2	2.49	0.47
1:A:26:ASP:C	1:A:28:GLY:N	2.66	0.47
1:A:329:LEU:HD23	1:A:329:LEU:C	2.35	0.47
1:A:151:ALA:HB2	1:A:233:ILE:CD1	2.44	0.47
1:B:354:ALA:O	1:B:357:ARG:HG3	2.15	0.47
1:B:108:PHE:CD1	1:B:118:GLY:O	2.67	0.47
1:A:33:ASN:ND2	1:A:36:LEU:CD1	2.78	0.47
1:B:214:LEU:HD12	1:B:215:TYR:H	1.80	0.47
1:A:325:TYR:HE2	1:A:349:ASP:HB2	1.80	0.47
1:A:232:LYS:HA	1:A:270:ASN:ND2	2.30	0.47
1:A:108:PHE:CD1	1:A:118:GLY:HA3	2.50	0.47
1:B:346:ALA:HB3	1:B:368:TRP:HB2	1.97	0.47
1:A:108:PHE:CD1	1:A:118:GLY:O	2.68	0.46
1:A:407:GLU:CG	1:A:407:GLU:O	2.62	0.46
1:B:43:PRO:CG	1:B:421:PHE:HB2	2.43	0.46
1:B:129:ASN:HB2	1:B:147:ASN:ND2	2.30	0.46
1:A:26:ASP:OD2	1:A:28:GLY:HA3	2.15	0.46
1:B:22:ALA:O	1:B:280:TYR:HB3	2.16	0.46
1:A:108:PHE:HD1	1:A:118:GLY:O	1.98	0.46
1:A:364:GLN:O	1:A:365:ASP:C	2.54	0.46
1:A:204:GLN:HA	1:A:204:GLN:OE1	2.14	0.46
1:A:376:ALA:HA	1:A:382:SER:HA	1.97	0.46
1:B:7:GLU:HA	1:B:17:TYR:CZ	2.51	0.46
1:B:137:ASN:HD22	1:B:137:ASN:C	2.06	0.46
1:B:364:GLN:O	1:B:365:ASP:C	2.53	0.46
1:A:22:ALA:O	1:A:280:TYR:HB3	2.15	0.46
1:A:136:LEU:O	1:A:137:ASN:CB	2.63	0.46
1:A:158:PHE:CD2	1:A:196:LYS:HA	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:26:ASP:C	1:A:28:GLY:H	2.19	0.46
1:A:102:TYR:O	1:A:125:THR:HB	2.15	0.46
1:B:351:PRO:HD2	1:B:363:ASP:OD1	2.16	0.46
1:A:217:LEU:HD23	1:A:217:LEU:H	1.80	0.46
1:A:217:LEU:O	1:A:218:ASP:CB	2.63	0.46
1:A:214:LEU:HD12	1:A:215:TYR:N	2.30	0.46
1:B:137:ASN:ND2	1:B:137:ASN:C	2.67	0.46
1:A:354:ALA:HA	1:A:357:ARG:HE	1.81	0.46
1:A:354:ALA:O	1:A:357:ARG:HG3	2.15	0.46
1:B:108:PHE:CD1	1:B:118:GLY:HA3	2.51	0.46
1:B:37:ILE:HB	1:B:133:ALA:HB3	1.98	0.46
1:B:217:LEU:O	1:B:218:ASP:CB	2.63	0.46
1:B:102:TYR:O	1:B:125:THR:HB	2.15	0.46
1:A:23:ILE:O	1:A:23:ILE:HG23	2.16	0.46
1:B:376:ALA:HA	1:B:382:SER:HA	1.97	0.45
1:B:377:PHE:N	1:B:381:ALA:O	2.49	0.45
1:A:346:ALA:HB3	1:A:368:TRP:HB2	1.97	0.45
1:B:20:GLU:CB	1:B:32:ARG:HD3	2.46	0.45
1:A:351:PRO:HD2	1:A:363:ASP:OD1	2.16	0.45
1:A:20:GLU:CB	1:A:32:ARG:HD3	2.46	0.45
1:A:117:VAL:HG11	1:A:399:GLU:HG2	1.99	0.45
1:A:129:ASN:HB2	1:A:147:ASN:ND2	2.31	0.45
1:B:18:SER:O	1:B:290:HIS:CD2	2.70	0.45
1:B:50:VAL:HG23	1:B:79:VAL:HB	1.98	0.45
1:A:137:ASN:C	1:A:137:ASN:ND2	2.67	0.45
1:A:32:ARG:HG3	1:A:32:ARG:NH1	2.31	0.45
1:B:217:LEU:H	1:B:217:LEU:HD23	1.80	0.45
1:A:37:ILE:HB	1:A:133:ALA:HB3	1.98	0.45
1:A:377:PHE:N	1:A:381:ALA:O	2.49	0.45
1:A:157:ARG:HA	1:A:157:ARG:HD3	1.74	0.45
1:A:50:VAL:HG23	1:A:79:VAL:HB	1.98	0.45
1:B:167:ALA:C	1:B:169:GLN:N	2.70	0.45
1:B:112:TYR:HD2	1:B:114:GLY:C	2.20	0.45
1:A:421:PHE:HE1	1:B:325:TYR:CD1	2.34	0.45
1:B:354:ALA:HA	1:B:357:ARG:HE	1.81	0.45
1:A:127:ASN:ND2	1:A:149:VAL:CG2	2.80	0.45
1:A:112:TYR:HD2	1:A:114:GLY:C	2.20	0.45
1:B:159:ALA:O	1:B:160:GLY:C	2.55	0.45
1:B:73:ILE:CG1	1:B:73:ILE:O	2.63	0.45
1:A:18:SER:O	1:A:290:HIS:CD2	2.70	0.45
1:B:82:MET:O	1:B:97:SER:CA	2.63	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:26:ASP:C	1:B:28:GLY:H	2.20	0.45
1:A:375:TYR:HD2	1:A:376:ALA:N	2.15	0.45
1:A:214:LEU:HD12	1:A:215:TYR:H	1.82	0.44
1:B:273:GLU:O	1:B:296:THR:HA	2.17	0.44
1:B:219:LYS:HA	1:B:219:LYS:HD3	1.73	0.44
1:B:352:VAL:HG11	1:B:357:ARG:CA	2.31	0.44
1:B:161:ASP:OD1	1:B:161:ASP:C	2.56	0.44
1:A:273:GLU:O	1:A:296:THR:HA	2.17	0.44
1:B:216:GLU:HB3	1:B:222:ARG:HB3	1.99	0.44
1:A:161:ASP:OD1	1:A:161:ASP:C	2.55	0.44
1:B:23:ILE:O	1:B:23:ILE:HG23	2.17	0.44
1:A:324:ALA:HB2	1:A:351:PRO:HA	1.99	0.44
1:B:117:VAL:HG11	1:B:399:GLU:HG2	1.99	0.44
1:B:134:TYR:CE2	1:B:135:ARG:O	2.70	0.44
1:A:159:ALA:O	1:A:160:GLY:C	2.56	0.44
1:B:127:ASN:ND2	1:B:149:VAL:CG2	2.80	0.44
1:A:72:ASN:C	1:A:72:ASN:HD22	2.21	0.44
1:A:219:LYS:HD3	1:A:219:LYS:HA	1.72	0.44
1:B:72:ASN:C	1:B:72:ASN:HD22	2.21	0.44
1:B:324:ALA:HB2	1:B:351:PRO:HA	1.99	0.44
1:A:216:GLU:HB3	1:A:222:ARG:HB3	1.99	0.44
1:A:73:ILE:HD11	1:A:106:THR:HB	2.00	0.44
1:A:82:MET:O	1:A:97:SER:CA	2.63	0.44
1:B:325:TYR:CE2	1:B:349:ASP:HB2	2.52	0.44
1:B:284:ASP:OD2	1:B:286:GLN:N	2.32	0.44
1:B:81:ASN:ND2	1:B:81:ASN:C	2.69	0.44
1:A:167:ALA:C	1:A:169:GLN:N	2.70	0.44
1:B:58:ILE:HB	1:B:70:ALA:HB3	1.99	0.44
1:A:134:TYR:CE2	1:A:135:ARG:O	2.71	0.44
1:B:356:ASN:HA	1:B:356:ASN:HD22	1.62	0.44
1:A:81:ASN:ND2	1:A:81:ASN:C	2.69	0.43
1:A:382:SER:O	1:A:418:ASN:N	2.48	0.43
1:B:375:TYR:HD2	1:B:376:ALA:N	2.15	0.43
1:A:13:LEU:HD22	1:A:50:VAL:HG11	2.00	0.43
1:A:121:THR:OG1	1:A:157:ARG:NH2	2.49	0.43
1:A:33:ASN:O	1:A:34:PRO:C	2.57	0.43
1:B:127:ASN:ND2	1:B:149:VAL:HG22	2.33	0.43
1:B:325:TYR:CD2	1:B:325:TYR:C	2.91	0.43
1:A:284:ASP:OD1	1:A:285:PRO:HD2	2.18	0.43
1:A:325:TYR:CE2	1:A:349:ASP:HB2	2.53	0.43
1:A:13:LEU:HD22	1:A:50:VAL:CG1	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:127:ASN:ND2	1:A:149:VAL:HG22	2.33	0.43
1:B:382:SER:O	1:B:418:ASN:N	2.47	0.43
1:B:117:VAL:HG23	1:B:117:VAL:O	2.18	0.43
1:A:58:ILE:HB	1:A:70:ALA:HB3	2.00	0.43
1:B:284:ASP:OD1	1:B:285:PRO:HD2	2.18	0.43
1:B:33:ASN:O	1:B:34:PRO:C	2.57	0.43
1:B:350:SER:HA	1:B:351:PRO:HD3	1.80	0.43
1:A:399:GLU:O	1:A:400:GLY:C	2.56	0.43
1:A:378:ASN:CG	1:A:378:ASN:O	2.57	0.43
1:A:50:VAL:HG12	1:A:414:GLY:CA	2.47	0.43
1:A:117:VAL:HG23	1:A:117:VAL:O	2.18	0.43
1:A:325:TYR:C	1:A:325:TYR:CD2	2.91	0.43
1:B:73:ILE:HD11	1:B:106:THR:HB	1.99	0.42
1:B:399:GLU:O	1:B:400:GLY:C	2.56	0.42
1:B:13:LEU:HD22	1:B:50:VAL:CG1	2.50	0.42
1:B:81:ASN:HD21	1:B:416:ASN:ND2	2.17	0.42
1:B:8:PHE:O	1:B:83:HIS:HE1	2.02	0.42
1:A:364:GLN:HE21	1:A:364:GLN:HB2	1.59	0.42
1:B:393:GLN:NE2	1:B:394:SER:N	2.67	0.42
1:B:192:ASP:O	1:B:194:ASN:N	2.50	0.42
1:A:6:ASN:O	1:A:8:PHE:N	2.52	0.42
1:A:179:GLN:HA	1:A:182:GLN:HB3	2.02	0.42
1:B:121:THR:OG1	1:B:157:ARG:NH2	2.50	0.42
1:B:13:LEU:HD22	1:B:50:VAL:HG11	2.01	0.42
1:B:157:ARG:HA	1:B:157:ARG:HD3	1.74	0.42
1:B:355:GLN:NE2	1:B:356:ASN:N	2.67	0.42
1:B:378:ASN:CG	1:B:378:ASN:O	2.57	0.42
1:B:32:ARG:HG3	1:B:32:ARG:NH1	2.31	0.42
1:A:421:PHE:CE1	1:B:325:TYR:CD1	3.07	0.42
1:A:356:ASN:HA	1:A:356:ASN:HD22	1.62	0.42
1:B:137:ASN:C	1:B:139:ALA:N	2.73	0.42
1:A:81:ASN:HD21	1:A:416:ASN:ND2	2.18	0.42
1:B:15:ARG:HG3	1:B:18:SER:H	1.84	0.42
1:B:179:GLN:HA	1:B:182:GLN:HB3	2.02	0.42
1:B:7:GLU:OE2	1:B:7:GLU:N	2.36	0.42
1:A:15:ARG:HG3	1:A:18:SER:H	1.83	0.42
1:A:137:ASN:C	1:A:139:ALA:N	2.72	0.41
1:B:232:LYS:HG2	1:B:270:ASN:ND2	2.32	0.41
1:B:137:ASN:ND2	1:B:139:ALA:H	2.17	0.41
1:A:393:GLN:NE2	1:A:394:SER:N	2.68	0.41
1:B:56:VAL:C	1:B:57:ASN:HD22	2.23	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:21:GLY:HA2	1:B:33:ASN:CB	2.50	0.41
1:A:16:ALA:O	1:A:17:TYR:C	2.59	0.41
1:A:232:LYS:HG2	1:A:270:ASN:ND2	2.33	0.41
1:A:192:ASP:O	1:A:194:ASN:N	2.50	0.41
1:A:34:PRO:HB2	1:A:143:GLY:C	2.41	0.41
1:B:325:TYR:CE2	1:B:349:ASP:CB	3.03	0.41
1:A:8:PHE:O	1:A:83:HIS:HE1	2.03	0.41
1:B:126:MET:O	1:B:149:VAL:HA	2.21	0.41
1:A:355:GLN:NE2	1:A:356:ASN:N	2.68	0.41
1:B:73:ILE:CD1	1:B:108:PHE:CE2	2.97	0.41
1:A:56:VAL:C	1:A:57:ASN:HD22	2.24	0.41
1:A:182:GLN:HG3	1:A:183:ALA:N	2.36	0.41
1:A:325:TYR:CE2	1:A:349:ASP:CB	3.04	0.41
1:A:21:GLY:HA2	1:A:33:ASN:CB	2.51	0.41
1:B:34:PRO:HB2	1:B:143:GLY:C	2.41	0.41
1:B:11:SER:OG	1:B:15:ARG:NH2	2.52	0.41
1:B:16:ALA:O	1:B:17:TYR:C	2.58	0.41
1:A:13:LEU:HD12	1:A:13:LEU:HA	1.94	0.41
1:B:134:TYR:CD2	1:B:135:ARG:N	2.89	0.41
1:B:151:ALA:CB	1:B:233:ILE:HD13	2.51	0.41
1:B:50:VAL:HG12	1:B:414:GLY:CA	2.47	0.40
1:A:170:ILE:HD13	1:A:184:LEU:HB3	2.03	0.40
1:B:8:PHE:CD1	1:B:9:SER:HB2	2.56	0.40
1:A:11:SER:OG	1:A:15:ARG:NH2	2.53	0.40
1:A:126:MET:O	1:A:149:VAL:HA	2.20	0.40
1:B:170:ILE:HD13	1:B:184:LEU:HB3	2.03	0.40
1:B:26:ASP:OD2	1:B:28:GLY:N	2.54	0.40
1:A:357:ARG:HB2	1:A:397:ILE:HG23	2.04	0.40
1:A:73:ILE:CD1	1:A:108:PHE:CE2	2.98	0.40
1:B:348:ASP:OD2	1:B:348:ASP:N	2.53	0.40
1:B:7:GLU:HB2	1:B:50:VAL:HG21	1.99	0.40
1:B:197:THR:O	1:B:198:ALA:HB2	2.21	0.40
1:A:134:TYR:CD2	1:A:135:ARG:N	2.89	0.40
1:B:182:GLN:CG	1:B:183:ALA:N	2.85	0.40
1:A:182:GLN:CG	1:A:183:ALA:N	2.85	0.40
1:B:209:TRP:N	1:B:209:TRP:CD1	2.88	0.40
1:A:230:GLU:OE1	1:A:232:LYS:HE3	2.22	0.40
1:B:230:GLU:OE1	1:B:232:LYS:HE3	2.21	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	357/424 (84%)	295 (83%)	41 (12%)	21 (6%)	2	19
1	B	357/424 (84%)	297 (83%)	39 (11%)	21 (6%)	2	19
All	All	714/848 (84%)	592 (83%)	80 (11%)	42 (6%)	2	19

All (42) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	7	GLU
1	A	194	ASN
1	A	354	ALA
1	A	379	LYS
1	B	194	ASN
1	B	354	ALA
1	B	379	LYS
1	A	27	ALA
1	B	27	ALA
1	A	137	ASN
1	A	187	THR
1	A	193	SER
1	A	218	ASP
1	A	348	ASP
1	B	137	ASN
1	B	187	THR
1	B	193	SER
1	B	218	ASP
1	B	348	ASP
1	A	20	GLU
1	A	118	GLY
1	A	168	GLY
1	A	198	ALA
1	B	20	GLU
1	B	118	GLY

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Mol	Chain	Res	Type
1	B	168	GLY
1	B	198	ALA
1	A	89	ASN
1	A	167	ALA
1	A	229	SER
1	B	6	ASN
1	B	89	ASN
1	B	167	ALA
1	B	229	SER
1	A	172	GLN
1	A	210	ASN
1	B	172	GLN
1	B	210	ASN
1	A	213	ILE
1	A	362	PRO
1	B	213	ILE
1	B	362	PRO

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	284/334 (85%)	246 (87%)	38 (13%)	5	24
1	B	284/334 (85%)	248 (87%)	36 (13%)	5	26
All	All	568/668 (85%)	494 (87%)	74 (13%)	5	25

All (74) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	ASN
1	A	7	GLU
1	A	50	VAL
1	A	72	ASN
1	A	73	ILE
1	A	80	PRO

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Mol	Chain	Res	Type
1	A	81	ASN
1	A	82	MET
1	A	107	GLU
1	A	109	ASN
1	A	122	ASP
1	A	123	LEU
1	A	136	LEU
1	A	137	ASN
1	A	142	PHE
1	A	144	LEU
1	A	180	GLN
1	A	217	LEU
1	A	226	THR
1	A	267	LEU
1	A	275	TRP
1	A	297	SER
1	A	325	TYR
1	A	343	THR
1	A	345	ILE
1	A	355	GLN
1	A	356	ASN
1	A	363	ASP
1	A	364	GLN
1	A	369	LEU
1	A	373	THR
1	A	375	TYR
1	A	393	GLN
1	A	396	LYS
1	A	404	PHE
1	A	407	GLU
1	A	415	THR
1	A	416	ASN
1	B	50	VAL
1	B	72	ASN
1	B	73	ILE
1	B	80	PRO
1	B	81	ASN
1	B	82	MET
1	B	107	GLU
1	B	109	ASN
1	B	122	ASP
1	B	123	LEU

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Mol	Chain	Res	Type
1	B	136	LEU
1	B	137	ASN
1	B	142	PHE
1	B	144	LEU
1	B	180	GLN
1	B	217	LEU
1	B	226	THR
1	B	267	LEU
1	B	275	TRP
1	B	297	SER
1	B	325	TYR
1	B	343	THR
1	B	345	ILE
1	B	355	GLN
1	B	356	ASN
1	B	363	ASP
1	B	364	GLN
1	B	369	LEU
1	B	373	THR
1	B	375	TYR
1	B	393	GLN
1	B	396	LYS
1	B	404	PHE
1	B	407	GLU
1	B	415	THR
1	B	416	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	ASN
1	A	57	ASN
1	A	72	ASN
1	A	83	HIS
1	A	89	ASN
1	A	109	ASN
1	A	137	ASN
1	A	164	GLN
1	A	169	GLN
1	A	182	GLN
1	A	270	ASN
1	A	281	ASN

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Mol	Chain	Res	Type
1	A	290	HIS
1	A	355	GLN
1	A	356	ASN
1	A	364	GLN
1	A	391	HIS
1	A	393	GLN
1	A	416	ASN
1	A	418	ASN
1	B	6	ASN
1	B	57	ASN
1	B	72	ASN
1	B	83	HIS
1	B	89	ASN
1	B	101	ASN
1	B	109	ASN
1	B	137	ASN
1	B	164	GLN
1	B	169	GLN
1	B	182	GLN
1	B	270	ASN
1	B	281	ASN
1	B	290	HIS
1	B	355	GLN
1	B	356	ASN
1	B	364	GLN
1	B	391	HIS
1	B	393	GLN
1	B	416	ASN
1	B	418	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	363/424 (85%)	0.06	8 (2%) 65 60	24, 49, 83, 108	0
1	B	363/424 (85%)	0.05	6 (1%) 73 67	20, 50, 82, 106	0
All	All	726/848 (85%)	0.05	14 (1%) 70 64	20, 49, 83, 108	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	123	LEU	3.7
1	A	123	LEU	3.4
1	A	298	TRP	3.3
1	A	337	ASP	2.9
1	A	232	LYS	2.8
1	B	337	ASP	2.8
1	A	362	PRO	2.7
1	B	232	LYS	2.5
1	B	359	ILE	2.3
1	B	102	TYR	2.2
1	A	359	ILE	2.1
1	A	233	ILE	2.1
1	B	233	ILE	2.1
1	A	102	TYR	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.