



Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 05:40 pm BST

PDB ID : 4EXM
Title : The crystal structure of an engineered phage lysin containing the binding domain of pesticin and the killing domain of T4-lysozyme
Authors : Seddiki, N.; Noinaj, N.; Fairman, J.W.; Lukacik, P.; Barnard, T.J.; Buchanan, S.K.
Deposited on : 2012-04-30
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

<https://www.wwpdb.org/validation/2017/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
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

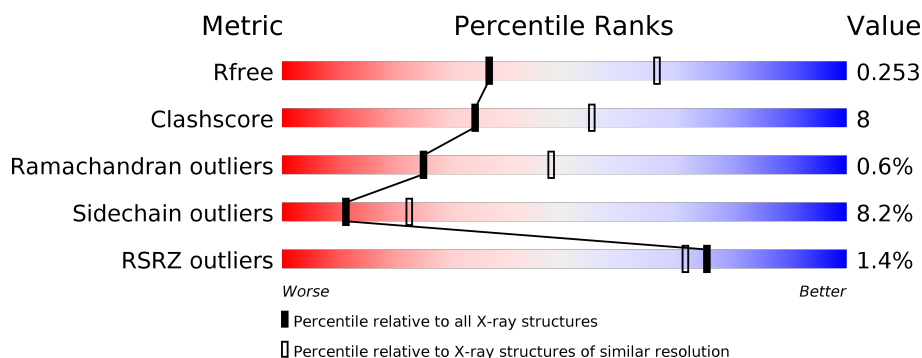
1 Overall quality at a glance

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}	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (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 respectively. 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	347	<div> <div>2%</div> <div> <div></div> <div>63%</div> <div>19%</div> <div>•</div> <div>16%</div> </div> </div>
1	B	347	<div> <div>%</div> <div> <div></div> <div>65%</div> <div>18%</div> <div>•</div> <div>16%</div> </div> </div>
1	C	347	<div> <div>%</div> <div> <div></div> <div>70%</div> <div>22%</div> <div>•</div> <div>5%</div> </div> </div>
1	D	347	<div> <div>2%</div> <div> <div></div> <div>68%</div> <div>25%</div> <div>•</div> <div>5%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9875 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 Pesticin, Lysozyme Chimera.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	291	Total	C	N	O	S	0	0	0
			2269	1429	401	431	8			
1	B	291	Total	C	N	O	S	0	0	0
			2292	1444	401	439	8			
1	C	331	Total	C	N	O	S	0	0	0
			2633	1657	461	505	10			
1	D	331	Total	C	N	O	S	0	0	0
			2606	1640	456	500	10			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-12	MET	-	EXPRESSION TAG	UNP Q57159
A	-11	HIS	-	EXPRESSION TAG	UNP Q57159
A	-10	HIS	-	EXPRESSION TAG	UNP Q57159
A	-9	HIS	-	EXPRESSION TAG	UNP Q57159
A	-8	HIS	-	EXPRESSION TAG	UNP Q57159
A	-7	HIS	-	EXPRESSION TAG	UNP Q57159
A	-6	HIS	-	EXPRESSION TAG	UNP Q57159
A	-5	HIS	-	EXPRESSION TAG	UNP Q57159
A	-4	HIS	-	EXPRESSION TAG	UNP Q57159
A	-3	HIS	-	EXPRESSION TAG	UNP Q57159
A	-2	HIS	-	EXPRESSION TAG	UNP Q57159
A	-1	GLU	-	EXPRESSION TAG	UNP Q57159
A	0	ASN	-	EXPRESSION TAG	UNP Q57159
A	1	LEU	-	EXPRESSION TAG	UNP Q57159
A	2	TYR	-	EXPRESSION TAG	UNP Q57159
A	3	PHE	-	EXPRESSION TAG	UNP Q57159
A	4	GLN	-	EXPRESSION TAG	UNP Q57159
A	5	SER	-	EXPRESSION TAG	UNP Q57159
A	182	ARG	GLY	ENGINEERED MUTATION	UNP P00720
A	224	THR	CYS	ENGINEERED MUTATION	UNP P00720
A	267	ALA	CYS	ENGINEERED MUTATION	UNP P00720

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Chain	Residue	Modelled	Actual	Comment	Reference
A	307	ILE	ARG	ENGINEERED MUTATION	UNP P00720
B	-12	MET	-	EXPRESSION TAG	UNP Q57159
B	-11	HIS	-	EXPRESSION TAG	UNP Q57159
B	-10	HIS	-	EXPRESSION TAG	UNP Q57159
B	-9	HIS	-	EXPRESSION TAG	UNP Q57159
B	-8	HIS	-	EXPRESSION TAG	UNP Q57159
B	-7	HIS	-	EXPRESSION TAG	UNP Q57159
B	-6	HIS	-	EXPRESSION TAG	UNP Q57159
B	-5	HIS	-	EXPRESSION TAG	UNP Q57159
B	-4	HIS	-	EXPRESSION TAG	UNP Q57159
B	-3	HIS	-	EXPRESSION TAG	UNP Q57159
B	-2	HIS	-	EXPRESSION TAG	UNP Q57159
B	-1	GLU	-	EXPRESSION TAG	UNP Q57159
B	0	ASN	-	EXPRESSION TAG	UNP Q57159
B	1	LEU	-	EXPRESSION TAG	UNP Q57159
B	2	TYR	-	EXPRESSION TAG	UNP Q57159
B	3	PHE	-	EXPRESSION TAG	UNP Q57159
B	4	GLN	-	EXPRESSION TAG	UNP Q57159
B	5	SER	-	EXPRESSION TAG	UNP Q57159
B	182	ARG	GLY	ENGINEERED MUTATION	UNP P00720
B	224	THR	CYS	ENGINEERED MUTATION	UNP P00720
B	267	ALA	CYS	ENGINEERED MUTATION	UNP P00720
B	307	ILE	ARG	ENGINEERED MUTATION	UNP P00720
C	-12	MET	-	EXPRESSION TAG	UNP Q57159
C	-11	HIS	-	EXPRESSION TAG	UNP Q57159
C	-10	HIS	-	EXPRESSION TAG	UNP Q57159
C	-9	HIS	-	EXPRESSION TAG	UNP Q57159
C	-8	HIS	-	EXPRESSION TAG	UNP Q57159
C	-7	HIS	-	EXPRESSION TAG	UNP Q57159
C	-6	HIS	-	EXPRESSION TAG	UNP Q57159
C	-5	HIS	-	EXPRESSION TAG	UNP Q57159
C	-4	HIS	-	EXPRESSION TAG	UNP Q57159
C	-3	HIS	-	EXPRESSION TAG	UNP Q57159
C	-2	HIS	-	EXPRESSION TAG	UNP Q57159
C	-1	GLU	-	EXPRESSION TAG	UNP Q57159
C	0	ASN	-	EXPRESSION TAG	UNP Q57159
C	1	LEU	-	EXPRESSION TAG	UNP Q57159
C	2	TYR	-	EXPRESSION TAG	UNP Q57159
C	3	PHE	-	EXPRESSION TAG	UNP Q57159
C	4	GLN	-	EXPRESSION TAG	UNP Q57159
C	5	SER	-	EXPRESSION TAG	UNP Q57159
C	182	ARG	GLY	ENGINEERED MUTATION	UNP P00720

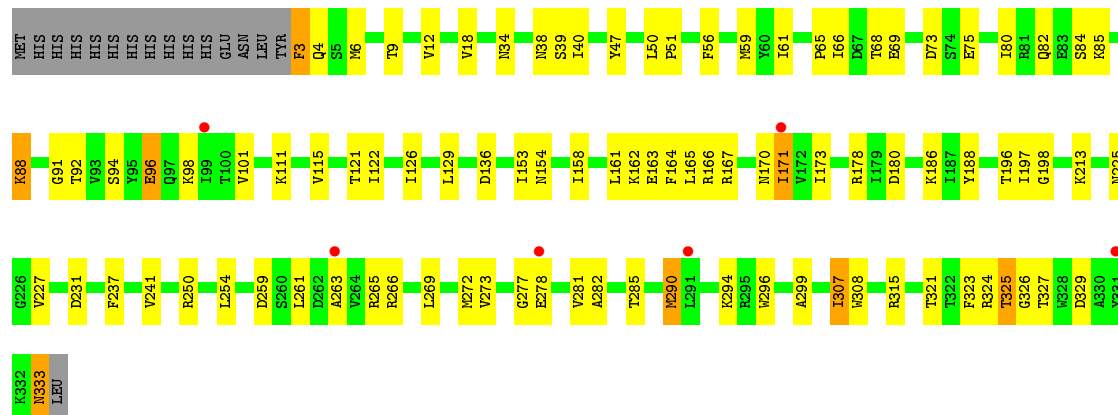
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Chain	Residue	Modelled	Actual	Comment	Reference
C	224	THR	CYS	ENGINEERED MUTATION	UNP P00720
C	267	ALA	CYS	ENGINEERED MUTATION	UNP P00720
C	307	ILE	ARG	ENGINEERED MUTATION	UNP P00720
D	-12	MET	-	EXPRESSION TAG	UNP Q57159
D	-11	HIS	-	EXPRESSION TAG	UNP Q57159
D	-10	HIS	-	EXPRESSION TAG	UNP Q57159
D	-9	HIS	-	EXPRESSION TAG	UNP Q57159
D	-8	HIS	-	EXPRESSION TAG	UNP Q57159
D	-7	HIS	-	EXPRESSION TAG	UNP Q57159
D	-6	HIS	-	EXPRESSION TAG	UNP Q57159
D	-5	HIS	-	EXPRESSION TAG	UNP Q57159
D	-4	HIS	-	EXPRESSION TAG	UNP Q57159
D	-3	HIS	-	EXPRESSION TAG	UNP Q57159
D	-2	HIS	-	EXPRESSION TAG	UNP Q57159
D	-1	GLU	-	EXPRESSION TAG	UNP Q57159
D	0	ASN	-	EXPRESSION TAG	UNP Q57159
D	1	LEU	-	EXPRESSION TAG	UNP Q57159
D	2	TYR	-	EXPRESSION TAG	UNP Q57159
D	3	PHE	-	EXPRESSION TAG	UNP Q57159
D	4	GLN	-	EXPRESSION TAG	UNP Q57159
D	5	SER	-	EXPRESSION TAG	UNP Q57159
D	182	ARG	GLY	ENGINEERED MUTATION	UNP P00720
D	224	THR	CYS	ENGINEERED MUTATION	UNP P00720
D	267	ALA	CYS	ENGINEERED MUTATION	UNP P00720
D	307	ILE	ARG	ENGINEERED MUTATION	UNP P00720

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	28	Total O 28 28	0	0
2	B	27	Total O 27 27	0	0
2	C	9	Total O 9 9	0	0
2	D	11	Total O 11 11	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	108.43Å 108.43Å 109.75Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.80 – 2.60 47.38 – 2.59	Depositor EDS
% Data completeness (in resolution range)	99.9 (29.80-2.60) 99.9 (47.38-2.59)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.88 (at 2.58Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1038)	Depositor
R, R_{free}	0.199 , 0.251 0.202 , 0.253	Depositor DCC
R_{free} test set	2254 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	67.6	Xtriage
Anisotropy	0.109	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 52.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.015 for -h,-k,l 0.479 for h,-h-k,-l 0.017 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9875	wwPDB-VP
Average B, all atoms (Å ²)	88.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.63% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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	0.34	0/2304	0.51	0/3116
1	B	0.34	0/2328	0.51	0/3146
1	C	0.32	0/2674	0.51	0/3606
1	D	0.32	0/2646	0.51	0/3572
All	All	0.33	0/9952	0.51	0/13440

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 [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	2269	0	2212	38	0
1	B	2292	0	2253	34	0
1	C	2633	0	2645	51	0
1	D	2606	0	2604	52	0
2	A	28	0	0	3	0
2	B	27	0	0	4	0
2	C	9	0	0	1	0
2	D	11	0	0	0	0
All	All	9875	0	9714	164	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 8.

All (164) 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:138:LEU:HB3	1:B:158:ILE:HG13	1.53	0.91
1:B:314:ASN:ND2	2:B:425:HOH:O	2.04	0.90
1:B:92:THR:O	2:B:410:HOH:O	1.95	0.84
1:A:138:LEU:HB3	1:A:158:ILE:HG13	1.60	0.83
1:C:265:ARG:NH2	1:C:324:ARG:O	2.15	0.80
1:C:325:THR:O	1:C:327:THR:N	2.15	0.79
1:D:65:PRO:HG2	1:D:115:VAL:HB	1.65	0.78
1:C:65:PRO:HG2	1:C:115:VAL:HB	1.65	0.77
1:D:69:GLU:HB2	1:D:111:LYS:HB2	1.65	0.77
1:A:314:ASN:ND2	2:A:409:HOH:O	2.23	0.71
1:D:186:LYS:HG2	1:D:227:VAL:HG22	1.71	0.71
1:B:274:PHE:O	2:B:419:HOH:O	2.10	0.70
1:C:69:GLU:HB2	1:C:111:LYS:HB2	1.75	0.67
1:A:47:TYR:CE1	1:A:59:MET:HG3	2.30	0.66
1:C:158:ILE:HG13	1:C:162:LYS:HD2	1.79	0.65
1:C:6:MET:HG2	1:D:4:GLN:NE2	2.13	0.64
1:C:186:LYS:HG2	1:C:227:VAL:HG22	1.79	0.63
1:D:122:ILE:HG23	1:D:165:LEU:HG	1.81	0.61
1:B:95:TYR:HA	1:B:122:ILE:HD12	1.82	0.61
1:D:50:LEU:HD12	1:D:51:PRO:HD2	1.82	0.61
1:D:307:ILE:HD12	1:D:308:TRP:H	1.65	0.61
1:D:272:MET:HE3	1:D:323:PHE:HE1	1.66	0.61
1:B:47:TYR:CE1	1:B:59:MET:HG3	2.36	0.60
1:D:170:ASN:HA	1:D:173:ILE:HD12	1.85	0.59
1:A:95:TYR:HA	1:A:122:ILE:HD12	1.84	0.59
1:B:26:SER:HB3	1:C:9:THR:HG22	1.84	0.59
1:D:265:ARG:NH2	1:D:324:ARG:O	2.36	0.58
1:A:180:ASP:OD1	1:A:318:ARG:NH1	2.37	0.58
1:C:292:GLN:HB3	2:C:405:HOH:O	2.04	0.57
1:D:261:LEU:HD22	1:D:265:ARG:HD3	1.87	0.57
1:D:158:ILE:HG13	1:D:162:LYS:HD2	1.85	0.57
1:A:245:VAL:O	1:A:249:LEU:HG	2.04	0.57
1:C:325:THR:O	1:C:325:THR:OG1	2.20	0.57
1:A:32:ARG:HG3	1:B:32:ARG:HD2	1.87	0.57
1:C:307:ILE:HD12	1:C:308:TRP:H	1.70	0.56
1:A:201:HIS:ND1	1:A:240:ASP:OD2	2.31	0.56
1:D:4:GLN:HE22	1:D:6:MET:HG3	1.70	0.56
1:C:91:GLY:N	1:C:167:ARG:HH22	2.05	0.55
1:C:4:GLN:HE22	1:C:6:MET:HG3	1.72	0.55
1:D:92:THR:HG21	1:D:171:ILE:HD11	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:92:THR:HG21	1:C:171:ILE:HD11	1.89	0.55
1:B:201:HIS:ND1	1:B:240:ASP:OD2	2.28	0.55
1:D:325:THR:O	1:D:327:THR:N	2.34	0.55
1:A:201:HIS:CD2	1:A:236:LEU:HD13	2.43	0.54
1:C:261:LEU:HD22	1:C:265:ARG:HD3	1.90	0.54
1:B:65:PRO:HG2	1:B:115:VAL:HB	1.89	0.53
1:B:245:VAL:O	1:B:249:LEU:HG	2.08	0.53
1:A:54:SER:O	1:A:150:ASN:ND2	2.42	0.52
1:D:167:ARG:O	1:D:171:ILE:HG13	2.09	0.52
1:D:47:TYR:HE1	1:D:59:MET:HE2	1.73	0.52
1:D:290:MET:HE3	1:D:299:ALA:HA	1.91	0.52
1:C:167:ARG:O	1:C:171:ILE:HG13	2.10	0.52
1:C:84:SER:HB3	1:C:153:ILE:HG12	1.91	0.52
1:D:277:GLY:O	1:D:281:VAL:HG23	2.10	0.52
1:A:65:PRO:HG2	1:A:115:VAL:HB	1.91	0.52
1:A:124:GLU:OE2	1:D:3:PHE:HZ	1.93	0.52
1:C:296:TRP:HB3	1:C:324:ARG:HA	1.91	0.52
1:D:296:TRP:HB3	1:D:324:ARG:HA	1.92	0.52
1:C:170:ASN:HA	1:C:173:ILE:HD12	1.90	0.52
1:B:166:ARG:HB3	1:B:238:ASN:ND2	2.25	0.51
1:C:290:MET:HB3	1:C:299:ALA:HB2	1.93	0.51
1:D:327:THR:OG1	1:D:329:ASP:OD1	2.29	0.50
1:D:290:MET:HB3	1:D:299:ALA:HB2	1.94	0.50
1:A:172:VAL:HB	1:A:328:TRP:CZ2	2.45	0.50
1:B:172:VAL:HB	1:B:328:TRP:CZ2	2.46	0.50
1:C:59:MET:SD	1:C:66:ILE:HD11	2.52	0.50
1:A:46:HIS:HD2	2:A:402:HOH:O	1.93	0.50
1:C:122:ILE:HG23	1:C:165:LEU:HG	1.93	0.49
1:C:73:ASP:OD1	1:C:73:ASP:N	2.44	0.49
1:A:112:VAL:HG21	1:D:40:ILE:O	2.13	0.49
1:A:74:SER:HB3	1:A:77:SER:HB2	1.94	0.49
1:D:59:MET:SD	1:D:66:ILE:HD11	2.52	0.49
1:C:258:TYR:CE2	1:C:266:ARG:HB3	2.48	0.48
1:A:181:GLU:OE1	1:A:200:GLY:HA3	2.13	0.48
1:B:185:LEU:H	1:B:185:LEU:HD12	1.79	0.48
1:D:91:GLY:N	1:D:167:ARG:HH22	2.12	0.48
1:D:94:SER:OG	1:D:96:GLU:OE1	2.26	0.48
1:D:197:ILE:HG12	1:D:198:GLY:H	1.78	0.47
1:A:32:ARG:CZ	1:B:37:ALA:HB2	2.44	0.47
1:D:321:THR:HG23	1:D:324:ARG:HH12	1.78	0.47
1:D:101:VAL:HG11	1:D:129:LEU:HD21	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:88:LYS:HE3	1:D:154:ASN:O	2.14	0.47
1:B:305:LYS:HG3	1:B:306:SER:N	2.30	0.47
1:C:286:ASN:HA	1:C:289:ARG:NH1	2.30	0.47
1:C:181:GLU:O	1:C:182:ARG:HB2	2.14	0.47
1:C:197:ILE:HG21	1:C:216:LEU:HD13	1.96	0.47
1:C:290:MET:HE3	1:C:299:ALA:HA	1.97	0.47
1:D:254:LEU:HD21	1:D:282:ALA:HA	1.97	0.46
1:B:258:TYR:O	1:B:266:ARG:NH1	2.48	0.46
1:A:163:GLU:OE2	1:A:238:ASN:ND2	2.49	0.46
1:C:94:SER:OG	1:C:96:GLU:OE1	2.31	0.46
1:A:248:ILE:HD11	1:A:273:VAL:HG21	1.98	0.46
1:C:277:GLY:O	1:C:281:VAL:HG23	2.15	0.46
1:C:88:LYS:HE3	1:C:154:ASN:O	2.15	0.46
1:D:269:LEU:O	1:D:273:VAL:HG23	2.15	0.46
1:D:69:GLU:HB3	1:D:80:ILE:HD13	1.97	0.46
1:A:19:PRO:HB2	1:A:22:LEU:HD23	1.98	0.45
1:C:294:LYS:HB3	1:C:296:TRP:CZ2	2.51	0.45
1:C:254:LEU:HD21	1:C:282:ALA:HA	1.98	0.45
1:D:188:TYR:CE2	1:D:196:THR:HB	2.52	0.45
1:D:263:ALA:HA	1:D:266:ARG:HB2	1.99	0.45
1:A:158:ILE:HD13	1:A:162:LYS:HG3	1.98	0.45
1:C:69:GLU:HB3	1:C:80:ILE:HD13	1.98	0.45
1:B:302:ASN:O	1:B:305:LYS:HG2	2.18	0.44
1:C:166:ARG:HH21	1:C:170:ASN:HD21	1.66	0.44
1:B:39:SER:O	1:B:42:ILE:HG12	2.18	0.43
1:C:269:LEU:HA	1:C:269:LEU:HD12	1.86	0.43
1:A:272:MET:O	1:A:276:MET:HG2	2.17	0.43
1:C:42:ILE:O	1:C:62:MET:N	2.43	0.43
1:A:254:LEU:O	1:A:257:VAL:HG12	2.19	0.43
1:A:50:LEU:HA	1:A:51:PRO:HD3	1.85	0.43
1:B:190:ASP:HB3	1:B:196:THR:HG21	2.01	0.43
1:C:284:PHE:O	1:C:286:ASN:N	2.52	0.43
1:C:307:ILE:HD12	1:C:308:TRP:N	2.33	0.43
1:D:325:THR:OG1	1:D:327:THR:OG1	2.31	0.43
1:C:333:ASN:N	1:C:333:ASN:OD1	2.51	0.43
1:B:158:ILE:HD12	1:B:162:LYS:HE3	2.01	0.43
1:B:275:GLN:HB2	1:B:315:ARG:CZ	2.49	0.43
1:C:98:LYS:HE2	1:C:121:THR:HG22	2.01	0.43
1:A:38:ASN:OD1	1:C:3:PHE:HB2	2.18	0.43
1:C:47:TYR:HE1	1:C:59:MET:HE2	1.83	0.43
1:D:307:ILE:HD12	1:D:308:TRP:N	2.31	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:105:GLN:OE1	2:B:423:HOH:O	2.21	0.43
1:D:12:VAL:HG13	1:D:18:VAL:HB	2.01	0.43
1:C:21:PHE:CD2	1:C:136:ASP:HB3	2.54	0.42
1:A:39:SER:O	1:A:42:ILE:HG12	2.20	0.42
1:B:155:PHE:CD2	1:B:161:LEU:HD12	2.55	0.42
1:B:272:MET:O	1:B:276:MET:HG2	2.19	0.42
1:B:257:VAL:HG11	1:B:288:LEU:CD2	2.50	0.42
1:A:241:VAL:O	1:A:245:VAL:HG23	2.19	0.42
1:A:257:VAL:HG11	1:A:288:LEU:CD2	2.48	0.42
1:A:37:ALA:HB2	1:B:32:ARG:CZ	2.49	0.42
1:D:237:PHE:O	1:D:241:VAL:HG23	2.20	0.42
1:D:333:ASN:OD1	1:D:333:ASN:N	2.52	0.42
1:B:38:ASN:OD1	1:D:3:PHE:HB2	2.19	0.42
1:A:177:LEU:HD12	1:A:177:LEU:HA	1.93	0.42
1:A:275:GLN:HB2	1:A:315:ARG:CZ	2.50	0.42
1:A:158:ILE:HD12	1:A:162:LYS:HE3	2.01	0.41
1:B:158:ILE:HD13	1:B:162:LYS:HG3	2.01	0.41
1:C:245:VAL:O	1:C:249:LEU:HG	2.20	0.41
1:C:286:ASN:HA	1:C:289:ARG:HH12	1.85	0.41
1:D:180:ASP:HB3	1:D:315:ARG:NE	2.35	0.41
1:C:126:ILE:HG12	1:C:165:LEU:HB3	2.02	0.41
1:C:180:ASP:HB3	1:C:315:ARG:NE	2.36	0.41
1:A:63:GLY:N	2:A:426:HOH:O	2.24	0.41
1:B:79:LYS:HE3	1:B:79:LYS:HB2	1.94	0.41
1:A:61:ILE:HD12	1:A:61:ILE:HA	1.91	0.41
1:D:98:LYS:HE2	1:D:121:THR:HG22	2.01	0.41
1:D:84:SER:HB3	1:D:153:ILE:HG12	2.03	0.41
1:D:321:THR:HG23	1:D:324:ARG:NH1	2.36	0.41
1:A:26:SER:HB3	1:D:9:THR:HG22	2.01	0.41
1:D:85:LYS:HA	1:D:85:LYS:HD3	1.87	0.41
1:B:158:ILE:O	1:B:158:ILE:HD13	2.21	0.41
1:C:250:ARG:HG2	1:C:250:ARG:H	1.66	0.41
1:A:305:LYS:HG3	1:A:306:SER:N	2.36	0.41
1:D:161:LEU:O	1:D:164:PHE:HB3	2.20	0.41
1:B:75:GLU:HG2	1:B:76:TYR:CG	2.56	0.40
1:C:241:VAL:O	1:C:245:VAL:HG23	2.20	0.40
1:B:106:GLU:HG2	1:B:111:LYS:HG2	2.03	0.40
1:C:6:MET:HG3	1:D:6:MET:HG2	2.04	0.40
1:D:126:ILE:HD13	1:D:166:ARG:HD2	2.03	0.40
1:A:172:VAL:HG23	1:A:173:ILE:HD12	2.03	0.40
1:B:19:PRO:HB2	1:B:22:LEU:HD13	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:273:VAL:HG13	1:D:278:GLU:HG3	2.04	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	287/347 (83%)	269 (94%)	18 (6%)	0	100	100
1	B	287/347 (83%)	270 (94%)	15 (5%)	2 (1%)	22	43
1	C	329/347 (95%)	307 (93%)	19 (6%)	3 (1%)	17	35
1	D	329/347 (95%)	304 (92%)	22 (7%)	3 (1%)	17	35
All	All	1232/1388 (89%)	1150 (93%)	74 (6%)	8 (1%)	25	47

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	326	GLY
1	C	34	ASN
1	C	285	THR
1	D	34	ASN
1	D	285	THR
1	B	250	ARG
1	B	182	ARG
1	D	326	GLY

5.3.2 Protein sidechains [i](#)

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	237/306 (78%)	218 (92%)	19 (8%)	12	24
1	B	244/306 (80%)	227 (93%)	17 (7%)	15	30
1	C	288/306 (94%)	263 (91%)	25 (9%)	10	20
1	D	282/306 (92%)	257 (91%)	25 (9%)	9	19
All	All	1051/1224 (86%)	965 (92%)	86 (8%)	11	22

All (86) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	THR
1	A	44	LEU
1	A	49	ASP
1	A	56	PHE
1	A	73	ASP
1	A	75	GLU
1	A	150	ASN
1	A	158	ILE
1	A	166	ARG
1	A	172	VAL
1	A	177	LEU
1	A	178	ARG
1	A	186	LYS
1	A	202	LEU
1	A	234	GLU
1	A	291	LEU
1	A	295	ARG
1	A	296	TRP
1	A	323	PHE
1	B	41	THR
1	B	49	ASP
1	B	56	PHE
1	B	57	LYS
1	B	73	ASP
1	B	150	ASN
1	B	152	VAL
1	B	158	ILE
1	B	166	ARG
1	B	172	VAL
1	B	177	LEU

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Mol	Chain	Res	Type
1	B	178	ARG
1	B	191	THR
1	B	285	THR
1	B	287	SER
1	B	296	TRP
1	B	323	PHE
1	C	3	PHE
1	C	11	VAL
1	C	38	ASN
1	C	56	PHE
1	C	61	ILE
1	C	68	THR
1	C	73	ASP
1	C	75	GLU
1	C	82	GLN
1	C	88	LYS
1	C	96	GLU
1	C	103	THR
1	C	127	GLU
1	C	136	ASP
1	C	171	ILE
1	C	177	LEU
1	C	178	ARG
1	C	213	LYS
1	C	250	ARG
1	C	259	ASP
1	C	290	MET
1	C	294	LYS
1	C	307	ILE
1	C	317	LYS
1	C	333	ASN
1	D	3	PHE
1	D	38	ASN
1	D	39	SER
1	D	56	PHE
1	D	61	ILE
1	D	68	THR
1	D	73	ASP
1	D	75	GLU
1	D	82	GLN
1	D	88	LYS
1	D	96	GLU

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Mol	Chain	Res	Type
1	D	136	ASP
1	D	163	GLU
1	D	171	ILE
1	D	178	ARG
1	D	213	LYS
1	D	225	ASN
1	D	231	ASP
1	D	250	ARG
1	D	259	ASP
1	D	290	MET
1	D	294	LYS
1	D	307	ILE
1	D	325	THR
1	D	333	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	4	GLN
1	D	4	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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 ⓘ

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	291/347 (83%)	-0.21	6 (2%) 63 58	46, 77, 133, 171	0
1	B	291/347 (83%)	-0.21	4 (1%) 75 71	44, 78, 140, 162	0
1	C	331/347 (95%)	-0.13	2 (0%) 89 88	56, 90, 136, 153	0
1	D	331/347 (95%)	-0.14	6 (1%) 68 64	54, 89, 134, 167	0
All	All	1244/1388 (89%)	-0.17	18 (1%) 75 71	44, 85, 137, 171	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	291	LEU	4.0
1	A	227	VAL	3.8
1	B	328	TRP	3.4
1	D	291	LEU	3.3
1	D	331	TYR	2.9
1	A	328	TRP	2.8
1	D	99	ILE	2.8
1	A	228	ILE	2.8
1	B	228	ILE	2.7
1	C	236	LEU	2.7
1	D	263	ALA	2.6
1	D	171	ILE	2.5
1	A	269	LEU	2.5
1	A	173	ILE	2.4
1	B	199	ILE	2.3
1	D	278	GLU	2.3
1	B	258	TYR	2.2
1	A	197	ILE	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.