Full wwPDB X-ray Structure Validation Report (i)

Aug 6, 2023 – 02:20 AM EDT

PDB ID	:	1L3F
Title	:	Thermolysin in the Absence of Substrate has an Open Conformation
Authors	:	Hausrath, A.C.; Matthews, B.W.
Deposited on	:	2002-02-26
Resolution	:	2.30 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

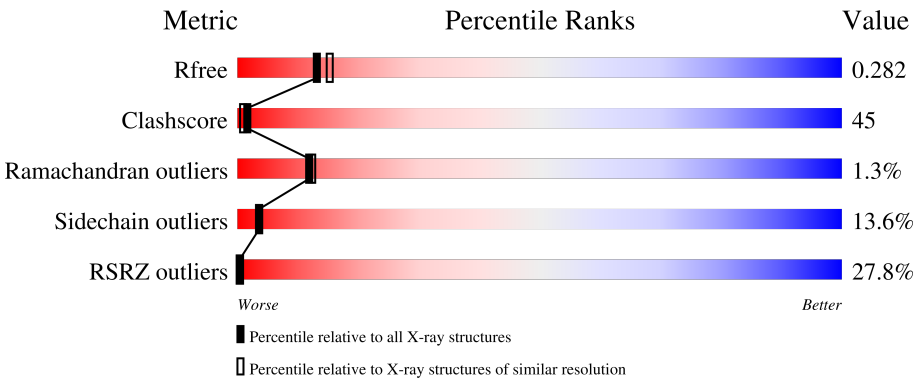
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 of 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 <=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	E	316	28% 34% 46% 16% •

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2561 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 Thermolysin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	E	316	2427	1525	406	494	2	0	0	0

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
2	E	4	4	4	0	0

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
3	E	3	3	3	0	0

- Molecule 4 is water.

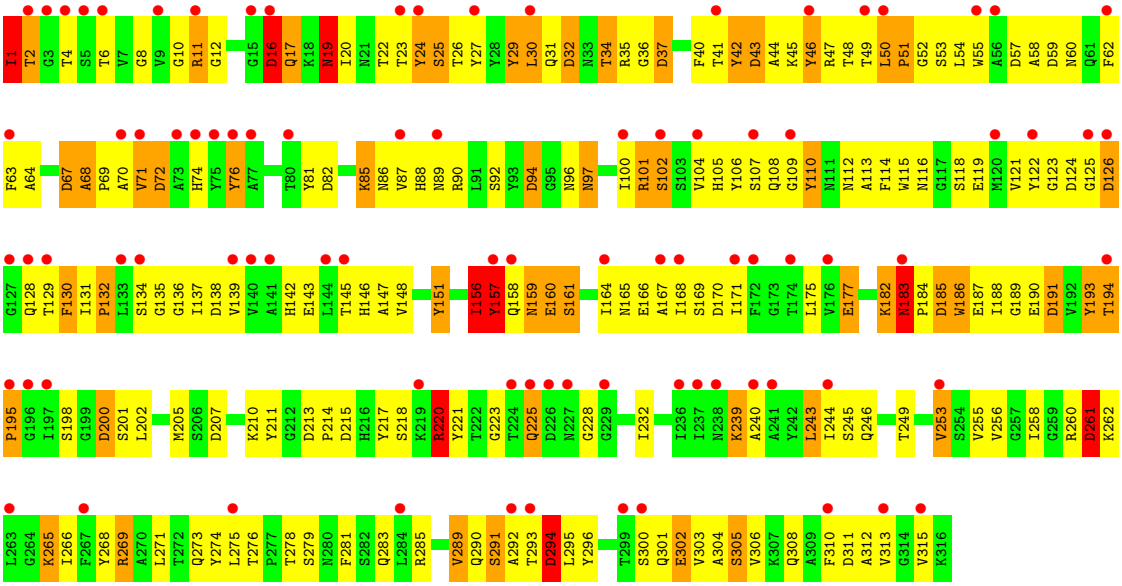
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	E	127	127	127	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Thermolysin

Chain E:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	97.05Å 97.05Å 106.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 2.30 24.84 – 2.30	Depositor EDS
% Data completeness (in resolution range)	96.7 (25.00-2.30) 96.8 (24.84-2.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$< I/\sigma(I) >$ [1]	1.79 (at 2.31Å)	Xtriage
Refinement program		Depositor
R, R_{free}	0.202 , 0.302 0.190 , 0.282	Depositor DCC
R_{free} test set	1138 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	55.9	Xtriage
Anisotropy	0.093	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.24 , 105.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	2561	wwPDB-VP
Average B, all atoms (Å^2)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.41% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, CA

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	E	1.13	5/2486 (0.2%)	1.91	70/3386 (2.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	302	GLU	CD-OE2	9.02	1.35	1.25
1	E	187	GLU	CD-OE2	8.22	1.34	1.25
1	E	143	GLU	CD-OE2	5.26	1.31	1.25
1	E	177	GLU	CD-OE2	5.20	1.31	1.25
1	E	160	GLU	CD-OE2	5.15	1.31	1.25

All (70) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	94	ASP	CB-CG-OD2	-12.50	107.05	118.30
1	E	274	TYR	CB-CG-CD1	-10.20	114.88	121.00
1	E	32	ASP	CB-CG-OD1	9.97	127.28	118.30
1	E	94	ASP	CB-CG-OD1	9.78	127.10	118.30
1	E	16	ASP	CB-CG-OD2	-9.19	110.03	118.30
1	E	126	ASP	CB-CG-OD1	8.90	126.31	118.30
1	E	43	ASP	CB-CG-OD2	-8.85	110.34	118.30
1	E	261	ASP	CB-CG-OD2	-8.84	110.35	118.30
1	E	32	ASP	CB-CG-OD2	-8.68	110.49	118.30
1	E	185	ASP	CB-CG-OD2	-8.48	110.66	118.30
1	E	200	ASP	CB-CG-OD2	-8.48	110.67	118.30
1	E	126	ASP	CB-CG-OD2	-8.43	110.71	118.30
1	E	170	ASP	CB-CG-OD1	8.20	125.68	118.30
1	E	200	ASP	CB-CG-OD1	8.14	125.63	118.30
1	E	29	TYR	CB-CG-CD2	-8.08	116.15	121.00
1	E	220	ARG	NE-CZ-NH1	7.97	124.29	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	37	ASP	CB-CG-OD1	7.94	125.44	118.30
1	E	59	ASP	CB-CG-OD2	-7.91	111.19	118.30
1	E	82	ASP	CB-CG-OD2	-7.88	111.21	118.30
1	E	274	TYR	CB-CG-CD2	7.49	125.49	121.00
1	E	157	TYR	CB-CG-CD1	7.39	125.43	121.00
1	E	16	ASP	CB-CG-OD1	7.17	124.75	118.30
1	E	101	ARG	NE-CZ-NH2	-6.95	116.83	120.30
1	E	37	ASP	CB-CG-OD2	-6.92	112.08	118.30
1	E	170	ASP	CB-CG-OD2	-6.80	112.18	118.30
1	E	76	TYR	CB-CG-CD1	-6.63	117.02	121.00
1	E	285	ARG	NE-CZ-NH1	6.61	123.61	120.30
1	E	42	TYR	CB-CA-C	-6.53	97.34	110.40
1	E	191	ASP	CB-CG-OD2	-6.52	112.43	118.30
1	E	42	TYR	CB-CG-CD1	-6.48	117.11	121.00
1	E	269	ARG	NE-CZ-NH1	6.47	123.54	120.30
1	E	194	THR	CA-CB-CG2	-6.29	103.60	112.40
1	E	124	ASP	CB-CG-OD1	6.28	123.95	118.30
1	E	294	ASP	CB-CG-OD2	-6.21	112.71	118.30
1	E	293	THR	CA-CB-CG2	-6.12	103.83	112.40
1	E	213	ASP	CB-CG-OD1	6.09	123.78	118.30
1	E	67	ASP	CB-CG-OD1	6.05	123.74	118.30
1	E	43	ASP	CB-CG-OD1	6.01	123.71	118.30
1	E	124	ASP	CB-CG-OD2	-5.94	112.96	118.30
1	E	185	ASP	CB-CG-OD1	5.92	123.62	118.30
1	E	24	TYR	CA-CB-CG	-5.91	102.18	113.40
1	E	110	TYR	CB-CG-CD1	-5.78	117.53	121.00
1	E	193	TYR	CA-CB-CG	-5.70	102.58	113.40
1	E	193	TYR	N-CA-CB	-5.68	100.38	110.60
1	E	30	LEU	CB-CG-CD2	-5.64	101.42	111.00
1	E	268	TYR	CA-CB-CG	-5.62	102.72	113.40
1	E	29	TYR	CB-CA-C	-5.62	99.17	110.40
1	E	239	LYS	N-CA-CB	5.60	120.69	110.60
1	E	24	TYR	N-CA-CB	-5.48	100.73	110.60
1	E	101	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	E	51	PRO	CB-CA-C	-5.42	98.46	112.00
1	E	72	ASP	CB-CG-OD2	-5.41	113.43	118.30
1	E	19	ASN	N-CA-CB	5.40	120.32	110.60
1	E	191	ASP	CB-CG-OD1	5.39	123.16	118.30
1	E	303	VAL	CA-CB-CG1	-5.39	102.81	110.90
1	E	276	THR	CA-CB-CG2	-5.35	104.91	112.40
1	E	151	TYR	CB-CG-CD2	-5.34	117.80	121.00
1	E	130	PHE	CB-CA-C	-5.30	99.79	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	215	ASP	CB-CG-OD2	-5.26	113.56	118.30
1	E	194	THR	CB-CA-C	-5.14	97.71	111.60
1	E	122	TYR	CB-CG-CD2	-5.13	117.92	121.00
1	E	1	ILE	CA-CB-CG2	-5.11	100.68	110.90
1	E	289	VAL	C-N-CA	-5.09	108.96	121.70
1	E	195	PRO	CA-N-CD	5.09	118.82	111.70
1	E	156	ILE	N-CA-CB	-5.07	99.13	110.80
1	E	186	TRP	N-CA-CB	5.07	119.72	110.60
1	E	239	LYS	CB-CG-CD	5.07	124.77	111.60
1	E	220	ARG	NE-CZ-NH2	-5.06	117.77	120.30
1	E	46	TYR	CB-CA-C	-5.05	100.29	110.40
1	E	225	GLN	N-CA-CB	5.04	119.67	110.60

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	E	2427	0	2251	207	0
2	E	4	0	0	0	0
3	E	3	0	0	0	0
4	E	127	0	0	10	1
All	All	2561	0	2251	207	1

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 (207) 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:E:11:ARG:HD2	1:E:63:PHE:CD1	2.03	0.93
1:E:68:ALA:HB3	1:E:69:PRO:HD3	1.48	0.93
1:E:245:SER:HB3	1:E:246:GLN:HG2	1.52	0.89
1:E:11:ARG:HD2	1:E:63:PHE:HD1	1.45	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:262:LYS:O	1:E:266:ILE:HG12	1.81	0.81
1:E:271:LEU:HA	1:E:275:LEU:HD12	1.63	0.79
1:E:1:ILE:HG13	1:E:2:THR:N	2.00	0.77
1:E:57:ASP:HA	4:E:477:HOH:O	1.86	0.76
1:E:1:ILE:HG23	1:E:31:GLN:HE22	1.52	0.74
1:E:30:LEU:HB3	1:E:41:THR:HB	1.70	0.74
1:E:30:LEU:CD1	1:E:70:ALA:HB1	2.18	0.74
1:E:30:LEU:HG	1:E:55:TRP:HB3	1.71	0.73
1:E:240:ALA:O	1:E:244:ILE:HG13	1.89	0.72
1:E:265:LYS:HE3	4:E:403:HOH:O	1.88	0.72
1:E:128:GLN:O	1:E:195:PRO:HD2	1.89	0.71
1:E:42:TYR:CG	1:E:51:PRO:HB2	2.25	0.71
1:E:253:VAL:HG22	1:E:312:ALA:HB2	1.71	0.70
1:E:158:GLN:HG3	1:E:159:ASN:ND2	2.05	0.70
1:E:1:ILE:HG23	1:E:31:GLN:NE2	2.06	0.70
1:E:72:ASP:OD2	1:E:135:GLY:HA2	1.91	0.70
1:E:126:ASP:OD1	1:E:128:GLN:N	2.23	0.70
1:E:167:ALA:O	1:E:171:ILE:HG13	1.92	0.69
1:E:44:ALA:O	1:E:47:ARG:HB2	1.93	0.69
1:E:142:HIS:CG	1:E:169:SER:HB3	2.29	0.68
1:E:35:ARG:HD3	1:E:81:TYR:CD1	2.28	0.68
1:E:183:ASN:ND2	4:E:353:HOH:O	2.27	0.68
1:E:164:ILE:O	1:E:168:ILE:HG12	1.94	0.68
1:E:129:THR:HG22	1:E:130:PHE:CD2	2.29	0.67
1:E:30:LEU:HD12	1:E:70:ALA:HB1	1.76	0.67
1:E:301:GLN:O	1:E:304:ALA:HB3	1.94	0.67
1:E:221:TYR:CZ	1:E:223:GLY:HA3	2.30	0.66
1:E:177:GLU:HG2	1:E:184:PRO:HA	1.77	0.65
1:E:37:ASP:HB2	1:E:97:ASN:O	1.96	0.64
1:E:108:GLN:HA	4:E:820:HOH:O	1.97	0.64
1:E:202:LEU:HD22	1:E:202:LEU:N	2.11	0.64
1:E:290:GLN:NE2	1:E:294:ASP:OD1	2.29	0.64
1:E:116:ASN:OD1	1:E:119:GLU:N	2.29	0.64
1:E:94:ASP:HA	1:E:151:TYR:CD1	2.33	0.64
1:E:68:ALA:CB	1:E:69:PRO:HD3	2.24	0.63
1:E:36:GLY:HA3	1:E:97:ASN:ND2	2.14	0.63
1:E:183:ASN:N	1:E:184:PRO:HD3	2.14	0.63
1:E:182:LYS:O	1:E:183:ASN:ND2	2.33	0.61
1:E:217:TYR:O	1:E:220:ARG:HB3	1.99	0.61
1:E:214:PRO:HD2	1:E:232:ILE:CG2	2.31	0.61
1:E:30:LEU:HD23	1:E:30:LEU:N	2.09	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:190:GLU:HG2	1:E:191:ASP:OD1	2.00	0.60
1:E:182:LYS:C	1:E:184:PRO:HD3	2.21	0.60
1:E:4:THR:O	1:E:6:THR:HG23	2.02	0.60
1:E:295:LEU:HB2	1:E:296:TYR:CD2	2.35	0.60
1:E:115:TRP:CZ3	1:E:119:GLU:HA	2.36	0.60
1:E:253:VAL:CG2	1:E:312:ALA:HB2	2.31	0.59
1:E:296:TYR:O	1:E:300:SER:HB3	2.02	0.59
1:E:294:ASP:OD1	1:E:294:ASP:N	2.34	0.59
1:E:279:SER:HA	1:E:283:GLN:OE1	2.02	0.59
1:E:188:ILE:O	1:E:201:SER:HB2	2.03	0.59
1:E:40:PHE:CD1	1:E:40:PHE:N	2.69	0.59
1:E:147:ALA:O	1:E:148:VAL:C	2.41	0.58
1:E:189:GLY:HA3	1:E:202:LEU:HD23	1.85	0.58
1:E:136:GLY:O	1:E:139:VAL:HB	2.03	0.58
1:E:8:GLY:O	1:E:19:ASN:HB3	2.03	0.57
1:E:85:LYS:HE2	1:E:86:ASN:OD1	2.03	0.57
1:E:186:TRP:HB3	1:E:205:MET:HB2	1.86	0.57
1:E:6:THR:HG1	1:E:22:THR:HG1	1.51	0.57
1:E:232:ILE:HD12	1:E:232:ILE:N	2.19	0.57
1:E:110:TYR:CE2	1:E:112:ASN:HB3	2.40	0.57
1:E:42:TYR:HD1	1:E:102:SER:O	1.87	0.57
1:E:10:GLY:HA2	1:E:63:PHE:CE2	2.40	0.56
1:E:188:ILE:O	1:E:202:LEU:HD23	2.05	0.56
1:E:1:ILE:HG23	1:E:1:ILE:O	2.06	0.56
1:E:255:VAL:HG22	1:E:308:GLN:HB2	1.86	0.56
1:E:304:ALA:O	1:E:308:GLN:HG3	2.05	0.56
1:E:271:LEU:HD12	1:E:271:LEU:O	2.06	0.56
1:E:131:ILE:HB	1:E:132:PRO:CD	2.36	0.55
1:E:30:LEU:CG	1:E:55:TRP:HB3	2.35	0.55
1:E:64:ALA:HB3	1:E:67:ASP:CG	2.26	0.55
1:E:85:LYS:HA	1:E:90:ARG:O	2.06	0.55
1:E:255:VAL:HG13	1:E:308:GLN:OE1	2.06	0.55
1:E:32:ASP:OD2	1:E:35:ARG:NH1	2.38	0.55
1:E:158:GLN:HG3	1:E:159:ASN:HD21	1.72	0.54
1:E:249:THR:HA	1:E:253:VAL:O	2.08	0.54
1:E:190:GLU:HG2	1:E:191:ASP:N	2.22	0.54
1:E:295:LEU:HB2	1:E:296:TYR:CE2	2.43	0.54
1:E:207:ASP:O	1:E:210:LYS:HB3	2.09	0.53
1:E:239:LYS:NZ	4:E:524:HOH:O	2.23	0.53
1:E:29:TYR:N	1:E:29:TYR:CD1	2.76	0.53
1:E:183:ASN:C	1:E:183:ASN:HD22	2.12	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:70:ALA:O	1:E:74:HIS:HB2	2.08	0.53
1:E:260:ARG:NH1	4:E:513:HOH:O	2.27	0.53
1:E:255:VAL:HA	1:E:308:GLN:OE1	2.08	0.53
1:E:194:THR:OG1	1:E:200:ASP:OD2	2.27	0.53
1:E:19:ASN:O	1:E:20:ILE:HG23	2.09	0.52
1:E:87:VAL:HG12	1:E:88:HIS:CE1	2.44	0.52
1:E:114:PHE:CD1	1:E:114:PHE:N	2.78	0.52
1:E:131:ILE:HB	1:E:132:PRO:HD2	1.91	0.52
1:E:11:ARG:HA	1:E:16:ASP:O	2.09	0.52
1:E:110:TYR:HD2	1:E:123:GLY:HA3	1.75	0.51
1:E:145:THR:O	1:E:148:VAL:HB	2.11	0.51
1:E:290:GLN:O	1:E:294:ASP:OD1	2.28	0.51
1:E:42:TYR:CD1	1:E:42:TYR:N	2.75	0.50
1:E:50:LEU:HD21	1:E:121:VAL:HG22	1.94	0.50
1:E:244:ILE:O	1:E:258:ILE:HG12	2.12	0.50
1:E:1:ILE:HG21	1:E:54:LEU:CD2	2.42	0.50
1:E:68:ALA:HB3	1:E:69:PRO:CD	2.33	0.50
1:E:131:ILE:O	1:E:132:PRO:C	2.47	0.50
1:E:151:TYR:N	1:E:151:TYR:CD2	2.79	0.50
1:E:6:THR:HG21	1:E:24:TYR:HB2	1.94	0.49
1:E:19:ASN:C	1:E:20:ILE:HG23	2.33	0.49
1:E:29:TYR:HA	1:E:55:TRP:O	2.12	0.49
1:E:92:SER:HB2	1:E:97:ASN:HA	1.94	0.49
1:E:240:ALA:HB2	1:E:313:VAL:HG21	1.95	0.48
1:E:261:ASP:O	1:E:265:LYS:HG2	2.14	0.48
1:E:46:TYR:N	1:E:105:HIS:O	2.44	0.48
1:E:68:ALA:CB	1:E:69:PRO:CD	2.90	0.48
1:E:262:LYS:HG3	4:E:528:HOH:O	2.12	0.48
1:E:184:PRO:O	1:E:185:ASP:HB3	2.14	0.48
1:E:151:TYR:N	1:E:151:TYR:HD2	2.12	0.48
1:E:156:ILE:HG22	1:E:156:ILE:O	2.14	0.47
1:E:137:ILE:HG23	1:E:138:ASP:N	2.27	0.47
1:E:253:VAL:HG11	1:E:312:ALA:HA	1.95	0.47
1:E:4:THR:O	1:E:23:THR:HA	2.14	0.47
1:E:30:LEU:HB2	1:E:55:TRP:HB3	1.97	0.47
1:E:1:ILE:CG2	1:E:31:GLN:NE2	2.78	0.47
1:E:189:GLY:HA3	1:E:202:LEU:CD2	2.45	0.47
1:E:278:THR:O	1:E:279:SER:C	2.53	0.47
1:E:214:PRO:HD2	1:E:232:ILE:HG23	1.97	0.47
1:E:40:PHE:O	1:E:101:ARG:HA	2.16	0.46
1:E:160:GLU:HB3	1:E:281:PHE:CD1	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:253:VAL:HG13	1:E:312:ALA:CB	2.45	0.46
1:E:269:ARG:HD3	1:E:291:SER:HB2	1.97	0.46
1:E:256:VAL:O	1:E:305:SER:HB3	2.15	0.46
1:E:269:ARG:HD3	1:E:291:SER:CB	2.45	0.46
1:E:76:TYR:HD1	1:E:76:TYR:HA	1.49	0.46
1:E:183:ASN:N	1:E:184:PRO:CD	2.78	0.46
1:E:50:LEU:CD2	1:E:121:VAL:HG22	2.45	0.46
1:E:115:TRP:CZ3	1:E:119:GLU:CA	2.99	0.46
1:E:258:ILE:HG21	1:E:302:GLU:HG3	1.97	0.46
1:E:202:LEU:N	1:E:202:LEU:CD2	2.78	0.46
1:E:68:ALA:C	1:E:71:VAL:HG23	2.36	0.45
1:E:100:ILE:HA	4:E:393:HOH:O	2.15	0.45
1:E:159:ASN:OD1	1:E:228:GLY:HA3	2.16	0.45
1:E:194:THR:HA	1:E:195:PRO:HD2	1.36	0.45
1:E:159:ASN:O	1:E:160:GLU:C	2.54	0.45
1:E:214:PRO:HD2	1:E:232:ILE:HG22	1.96	0.45
1:E:202:LEU:HD22	1:E:202:LEU:H	1.80	0.45
1:E:193:TYR:CE1	1:E:194:THR:HG23	2.52	0.45
1:E:185:ASP:OD2	1:E:190:GLU:OE2	2.35	0.45
1:E:310:PHE:O	1:E:311:ASP:C	2.53	0.45
1:E:72:ASP:HB3	1:E:134:SER:O	2.17	0.45
1:E:110:TYR:CZ	1:E:112:ASN:HB3	2.52	0.45
1:E:156:ILE:O	1:E:161:SER:HB3	2.17	0.45
1:E:210:LYS:HG2	1:E:211:TYR:CE2	2.52	0.45
1:E:42:TYR:HB3	1:E:51:PRO:O	2.17	0.44
1:E:188:ILE:HD12	1:E:188:ILE:HG23	1.68	0.44
1:E:10:GLY:HA3	1:E:62:PHE:HB2	2.00	0.44
1:E:305:SER:HA	1:E:308:GLN:CD	2.38	0.44
1:E:116:ASN:N	1:E:119:GLU:O	2.47	0.44
1:E:27:TYR:CD1	1:E:58:ALA:HA	2.52	0.44
1:E:67:ASP:O	1:E:71:VAL:HG23	2.18	0.44
1:E:30:LEU:HD11	1:E:70:ALA:HB1	1.98	0.44
1:E:32:ASP:OD1	1:E:34:THR:HG23	2.17	0.43
1:E:87:VAL:HG12	1:E:88:HIS:CD2	2.53	0.43
1:E:106:TYR:O	1:E:107:SER:HB3	2.18	0.43
1:E:157:TYR:OH	1:E:166:GLU:OE2	2.29	0.43
1:E:182:LYS:HE2	1:E:183:ASN:OD1	2.19	0.43
1:E:202:LEU:HA	1:E:202:LEU:HD13	1.56	0.43
1:E:94:ASP:OD1	1:E:94:ASP:N	2.49	0.43
1:E:1:ILE:HG21	1:E:54:LEU:HD22	2.01	0.43
1:E:177:GLU:OE2	1:E:184:PRO:HA	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:57:ASP:OD2	1:E:60:ASN:N	2.52	0.43
1:E:109:GLY:HA2	1:E:125:GLY:O	2.18	0.43
1:E:131:ILE:CB	1:E:132:PRO:CD	2.95	0.43
1:E:193:TYR:CZ	1:E:194:THR:HG23	2.54	0.43
1:E:239:LYS:HE3	1:E:243:LEU:HD11	2.01	0.43
1:E:12:GLY:N	1:E:16:ASP:O	2.45	0.43
1:E:43:ASP:O	1:E:52:GLY:HA3	2.19	0.43
1:E:104:VAL:O	1:E:105:HIS:HB2	2.19	0.43
1:E:146:HIS:ND1	1:E:165:ASN:OD1	2.52	0.43
1:E:175:LEU:HD23	1:E:175:LEU:HA	1.74	0.43
1:E:269:ARG:HB2	4:E:335:HOH:O	2.18	0.43
1:E:295:LEU:CB	1:E:296:TYR:CE2	3.02	0.43
1:E:85:LYS:O	1:E:89:ASN:HA	2.18	0.42
1:E:110:TYR:HD2	1:E:123:GLY:CA	2.32	0.42
1:E:157:TYR:CE1	1:E:166:GLU:HG2	2.55	0.42
1:E:289:VAL:CG2	1:E:290:GLN:N	2.79	0.42
1:E:289:VAL:HG12	1:E:306:VAL:HG12	2.01	0.42
1:E:62:PHE:N	1:E:62:PHE:CD1	2.86	0.42
1:E:25:SER:O	1:E:27:TYR:N	2.48	0.42
1:E:243:LEU:HD12	1:E:243:LEU:HA	1.70	0.42
1:E:11:ARG:HE	1:E:17:GLN:HG3	1.83	0.42
1:E:112:ASN:CG	1:E:113:ALA:N	2.73	0.42
1:E:217:TYR:HB2	1:E:313:VAL:O	2.20	0.42
1:E:31:GLN:HG3	1:E:40:PHE:CE2	2.55	0.41
1:E:315:VAL:HA	4:E:371:HOH:O	2.20	0.41
1:E:142:HIS:CD2	1:E:142:HIS:C	2.93	0.41
1:E:11:ARG:NE	1:E:17:GLN:HG3	2.36	0.41
1:E:189:GLY:O	1:E:193:TYR:HB2	2.20	0.41
1:E:25:SER:O	1:E:26:THR:HB	2.21	0.41
1:E:194:THR:N	1:E:195:PRO:CD	2.75	0.41
1:E:30:LEU:HD22	1:E:30:LEU:HA	1.75	0.41
1:E:44:ALA:O	1:E:45:LYS:HB2	2.21	0.41
1:E:291:SER:O	1:E:292:ALA:C	2.58	0.41
1:E:146:HIS:CE1	1:E:166:GLU:OE2	2.72	0.40
1:E:11:ARG:HD2	1:E:63:PHE:CE1	2.55	0.40
1:E:11:ARG:HE	1:E:11:ARG:HB3	1.42	0.40
1:E:129:THR:CG2	1:E:130:PHE:CD2	3.03	0.40
1:E:94:ASP:CG	1:E:96:ASN:H	2.24	0.40
1:E:138:ASP:OD2	1:E:188:ILE:HA	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:509:HOH:O	4:E:729:HOH:O[5_545]	2.19	0.01

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	E	314/316 (99%)	286 (91%)	24 (8%)	4 (1%)	12 12

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	68	ALA
1	E	218	SER
1	E	132	PRO
1	E	183	ASN

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	E	250/252 (99%)	216 (86%)	34 (14%)	3 3

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	1	ILE
1	E	2	THR

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Mol	Chain	Res	Type
1	E	11	ARG
1	E	16	ASP
1	E	17	GLN
1	E	19	ASN
1	E	25	SER
1	E	34	THR
1	E	48	THR
1	E	49	THR
1	E	50	LEU
1	E	53	SER
1	E	71	VAL
1	E	85	LYS
1	E	97	ASN
1	E	102	SER
1	E	118	SER
1	E	156	ILE
1	E	157	TYR
1	E	159	ASN
1	E	161	SER
1	E	182	LYS
1	E	183	ASN
1	E	198	SER
1	E	220	ARG
1	E	225	GLN
1	E	243	LEU
1	E	253	VAL
1	E	261	ASP
1	E	265	LYS
1	E	273	GLN
1	E	291	SER
1	E	294	ASP
1	E	305	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	21	ASN
1	E	31	GLN
1	E	33	ASN
1	E	97	ASN
1	E	183	ASN
1	E	227	ASN

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Mol	Chain	Res	Type
1	E	273	GLN

5.3.3 RNA (i)

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 7 ligands modelled in this entry, 7 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (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	E	316/316 (100%)	1.41	88 (27%) 0 0	53, 70, 89, 100	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	30	LEU	6.1
1	E	194	THR	5.0
1	E	55	TRP	4.8
1	E	139	VAL	4.8
1	E	197	ILE	4.5
1	E	144	LEU	4.4
1	E	236	ILE	4.2
1	E	2	THR	4.1
1	E	267	PHE	4.1
1	E	71	VAL	4.0
1	E	171	ILE	4.0
1	E	73	ALA	3.9
1	E	41	THR	3.8
1	E	77	ALA	3.8
1	E	237	ILE	3.8
1	E	241	ALA	3.8
1	E	140	VAL	3.7
1	E	284	LEU	3.6
1	E	310	PHE	3.5
1	E	172	PHE	3.4
1	E	56	ALA	3.4
1	E	227	ASN	3.4
1	E	157	TYR	3.4
1	E	253	VAL	3.3
1	E	183	ASN	3.2
1	E	315	VAL	3.2
1	E	127	GLY	3.2

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Mol	Chain	Res	Type	RSRZ
1	E	62	PHE	3.2
1	E	4	THR	3.2
1	E	299	THR	3.1
1	E	168	ILE	3.1
1	E	87	VAL	3.0
1	E	141	ALA	3.0
1	E	24	TYR	3.0
1	E	100	ILE	2.9
1	E	238	ASN	2.9
1	E	122	TYR	2.9
1	E	195	PRO	2.9
1	E	158	GLN	2.9
1	E	263	LEU	2.9
1	E	240	ALA	2.9
1	E	76	TYR	2.9
1	E	313	VAL	2.8
1	E	3	GLY	2.8
1	E	102	SER	2.8
1	E	244	ILE	2.8
1	E	70	ALA	2.8
1	E	89	ASN	2.7
1	E	11	ARG	2.6
1	E	126	ASP	2.6
1	E	196	GLY	2.6
1	E	225	GLN	2.6
1	E	125	GLY	2.5
1	E	5	SER	2.5
1	E	134	SER	2.5
1	E	80	THR	2.5
1	E	224	THR	2.5
1	E	46	TYR	2.5
1	E	6	THR	2.5
1	E	63	PHE	2.5
1	E	15	GLY	2.5
1	E	292	ALA	2.4
1	E	74	HIS	2.4
1	E	128	GLN	2.4
1	E	176	VAL	2.4
1	E	167	ALA	2.4
1	E	219	LYS	2.3
1	E	275	LEU	2.3
1	E	109	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	E	107	SER	2.3
1	E	293	THR	2.3
1	E	50	LEU	2.2
1	E	104	VAL	2.2
1	E	164	ILE	2.2
1	E	226	ASP	2.2
1	E	300	SER	2.2
1	E	16	ASP	2.2
1	E	120	MET	2.1
1	E	174	THR	2.1
1	E	23	THR	2.1
1	E	49	THR	2.1
1	E	9	VAL	2.1
1	E	75	TYR	2.1
1	E	129	THR	2.1
1	E	27	TYR	2.1
1	E	133	LEU	2.0
1	E	145	THR	2.0
1	E	229	GLY	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 monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	ZN	E	322	1/1	0.87	0.12	64,64,64,64	1
2	CA	E	319	1/1	0.88	0.05	81,81,81,81	0
2	CA	E	317	1/1	0.88	0.07	59,59,59,59	0
2	CA	E	320	1/1	0.91	0.08	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	ZN	E	321	1/1	0.99	0.06	62,62,62,62	0
2	CA	E	318	1/1	0.99	0.08	53,53,53,53	0
3	ZN	E	330	1/1	0.99	0.09	70,70,70,70	0

6.5 Other polymers (i)

There are no such residues in this entry.