



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2018 – 02:26 am GMT

PDB ID : 2D0I  
Title : Crystal Structure PH0520 protein from *Pyrococcus horikoshii* OT3  
Authors : Lokanath, N.K.; Terao, Y.; Kunishima, N.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)  
Deposited on : 2005-08-02  
Resolution : 1.95 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](mailto: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.

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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	:	trunk30967
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac	:	5.8.0158
CCP4	:	7.0 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk30967

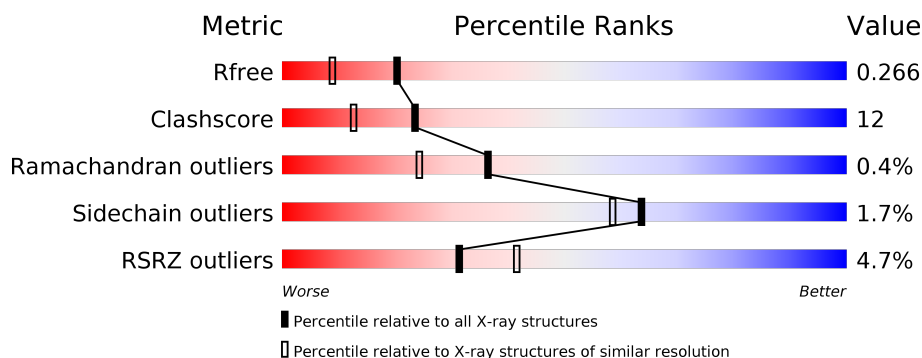
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.95 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))
$R_{free}$	111664	2220 (1.96-1.96)
Clashscore	122126	2333 (1.96-1.96)
Ramachandran outliers	120053	2314 (1.96-1.96)
Sidechain outliers	120020	2314 (1.96-1.96)
RSRZ outliers	108989	2174 (1.96-1.96)

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  $\geq 3$ , 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	333	<div> <div>5%</div> <div> <div></div> <div>76%</div> <div>23%</div> <div>.</div> </div> </div>
1	B	333	<div> <div>3%</div> <div> <div></div> <div>87%</div> <div>12%</div> <div>.</div> </div> </div>
1	C	333	<div> <div>8%</div> <div> <div></div> <div>68%</div> <div>32%</div> <div>.</div> </div> </div>
1	D	333	<div> <div>3%</div> <div> <div></div> <div>75%</div> <div>23%</div> <div>.</div> </div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11762 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 dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	333	Total	C	N	O	S	0	0	0
			2683	1728	462	486	7			
1	B	333	Total	C	N	O	S	0	0	0
			2683	1728	462	486	7			
1	C	333	Total	C	N	O	S	0	0	0
			2683	1728	462	486	7			
1	D	333	Total	C	N	O	S	0	0	0
			2683	1728	462	486	7			

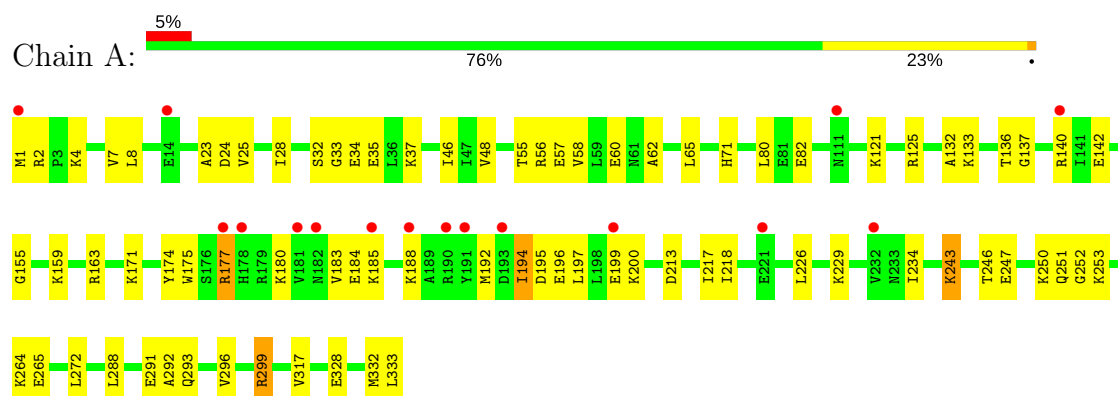
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	254	Total	O	0	0
			254	254		
2	B	299	Total	O	0	0
			299	299		
2	C	218	Total	O	0	0
			218	218		
2	D	259	Total	O	0	0
			259	259		

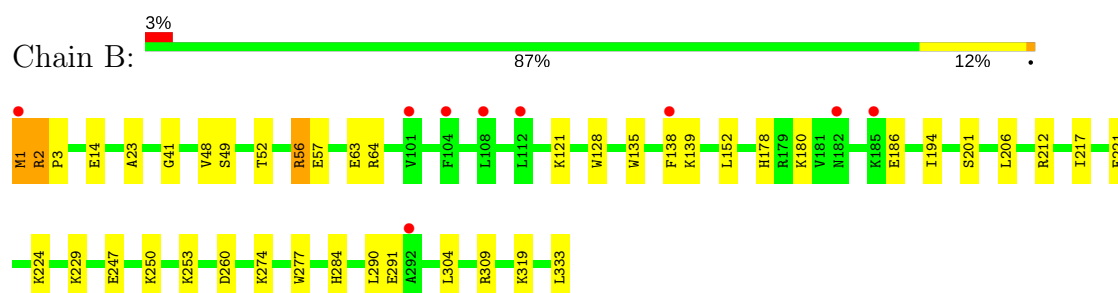
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

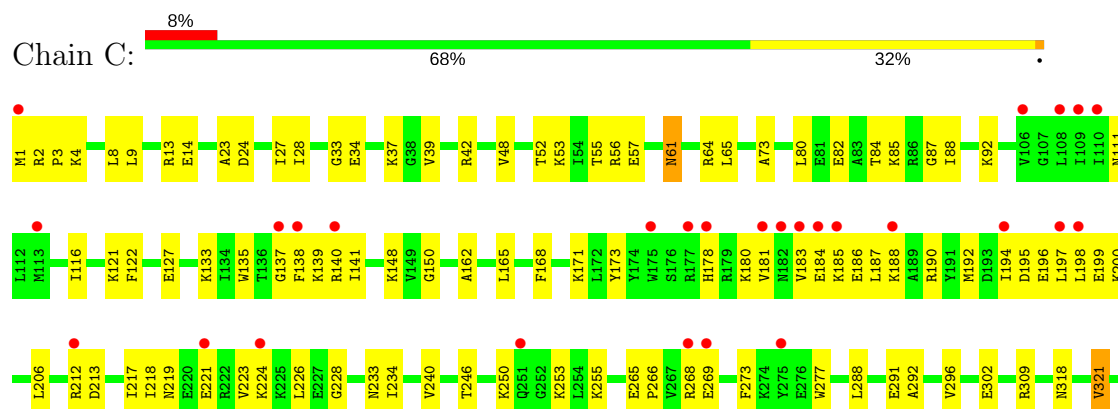
#### • Molecule 1: dehydrogenase

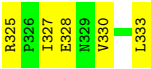


#### • Molecule 1: dehydrogenase

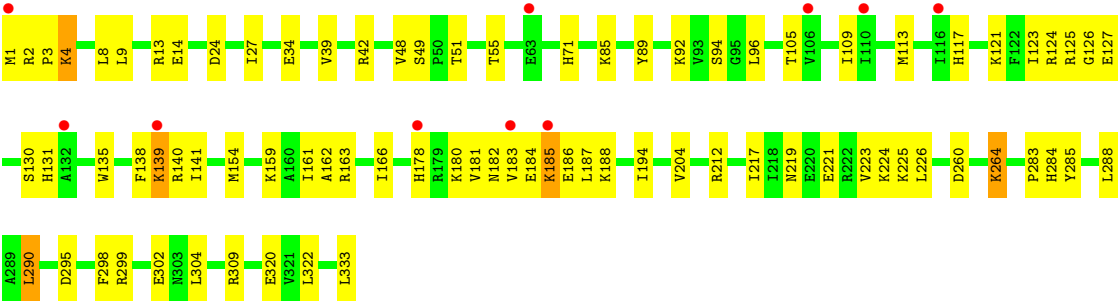
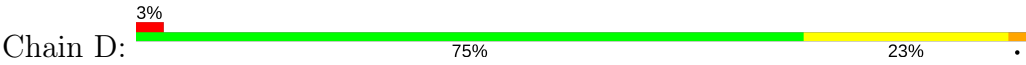


#### • Molecule 1: dehydrogenase





● Molecule 1: dehydrogenase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	91.76Å 63.74Å 131.98Å 90.00° 103.14° 90.00°	Depositor
Resolution (Å)	34.69 – 1.95 34.69 – 1.92	Depositor EDS
% Data completeness (in resolution range)	97.0 (34.69-1.95) 92.1 (34.69-1.92)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.76 (at 1.92Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.235 , 0.265 0.234 , 0.266	Depositor DCC
$R_{free}$ test set	5320 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	25.6	Xtriage
Anisotropy	0.480	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 48.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	11762	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 45.15 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.3782e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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	0.36	0/2728	0.62	1/3669 (0.0%)
1	B	0.34	0/2728	0.62	0/3669
1	C	0.34	0/2728	0.64	0/3669
1	D	0.36	0/2728	0.63	1/3669 (0.0%)
All	All	0.35	0/10912	0.63	2/14676 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	71	HIS	N-CA-CB	-6.72	98.50	110.60
1	D	264	LYS	CD-CE-NZ	5.91	125.29	111.70

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	2683	0	2804	73	0
1	B	2683	0	2804	43	0
1	C	2683	0	2804	99	0
1	D	2683	0	2804	65	0
2	A	254	0	0	13	0
2	B	299	0	0	10	0
2	C	218	0	0	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	259	0	0	18	0
All	All	11762	0	11216	265	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 12.

All (265) 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:8:LEU:HD12	1:A:48:VAL:HG12	1.49	0.93
1:C:246:THR:O	1:C:250:LYS:HG3	1.72	0.90
1:C:121:LYS:HZ2	1:D:121:LYS:HZ2	0.91	0.89
1:C:221:GLU:O	1:C:224:LYS:HG2	1.72	0.89
1:B:56:ARG:HB3	1:B:56:ARG:HH11	1.39	0.86
1:D:125:ARG:HG3	1:D:127:GLU:HG3	1.58	0.86
1:B:121:LYS:HE3	2:B:387:HOH:O	1.74	0.85
1:C:253:LYS:HE3	2:C:433:HOH:O	1.77	0.84
1:B:221:GLU:O	1:B:224:LYS:HG2	1.78	0.84
1:C:121:LYS:NZ	1:D:121:LYS:HZ2	1.76	0.84
1:C:186:GLU:HG3	2:C:530:HOH:O	1.77	0.83
1:C:218:ILE:HB	1:C:240:VAL:HG12	1.59	0.83
1:A:243:LYS:HE3	1:A:243:LYS:HA	1.59	0.83
1:A:247:GLU:OE2	1:A:250:LYS:HD2	1.82	0.80
1:C:195:ASP:O	1:C:199:GLU:HG2	1.83	0.79
1:A:34:GLU:HA	1:A:37:LYS:HE2	1.65	0.78
1:A:175:TRP:HH2	1:A:177:ARG:HE	1.31	0.78
1:C:194:ILE:HD13	1:C:217:ILE:HD11	1.66	0.77
1:C:212:ARG:HG3	2:C:352:HOH:O	1.85	0.76
1:A:121:LYS:HE3	2:A:422:HOH:O	1.85	0.76
1:A:192:MET:HE3	1:A:196:GLU:HG2	1.67	0.75
1:C:121:LYS:HZ2	1:D:121:LYS:NZ	1.79	0.74
1:B:2:ARG:HB3	1:B:3:PRO:HD3	1.68	0.74
1:B:309:ARG:HG2	1:B:333:LEU:HB2	1.69	0.74
1:C:265:GLU:HG3	2:C:540:HOH:O	1.86	0.74
1:C:34:GLU:HG2	2:C:522:HOH:O	1.86	0.74
1:B:48:VAL:CG2	1:B:52:THR:HB	2.18	0.72
1:C:291:GLU:HB2	2:C:484:HOH:O	1.89	0.72
1:C:181:VAL:HG12	2:C:507:HOH:O	1.88	0.72
1:D:181:VAL:O	1:D:185:LYS:HG2	1.90	0.72
1:D:117:HIS:O	1:D:121:LYS:HD2	1.90	0.71
1:C:55:THR:OG1	1:C:57:GLU:HG2	1.91	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:MET:HB3	1:A:24:ASP:OD1	1.91	0.70
1:A:247:GLU:HG3	1:A:251:GLN:HE21	1.58	0.69
1:D:264:LYS:NZ	2:D:424:HOH:O	2.25	0.69
1:C:148:LYS:HG2	1:C:171:LYS:HD2	1.73	0.69
1:C:33:GLY:O	1:C:37:LYS:HG3	1.93	0.68
1:D:212:ARG:HG2	2:D:591:HOH:O	1.94	0.67
1:C:221:GLU:HG2	1:C:224:LYS:HE3	1.77	0.66
1:C:1:MET:HB3	1:C:24:ASP:N	2.10	0.66
1:D:139:LYS:NZ	2:D:514:HOH:O	2.29	0.66
1:D:2:ARG:HB3	1:D:3:PRO:HD3	1.76	0.66
1:C:268:ARG:HB2	1:C:269:GLU:OE2	1.96	0.65
1:A:226:LEU:HA	1:A:229:LYS:HD2	1.78	0.65
1:A:188:LYS:HE2	1:A:188:LYS:HA	1.78	0.65
1:D:283:PRO:HD2	1:D:285:TYR:CE2	2.32	0.65
1:A:32:SER:OG	1:A:35:GLU:HG3	1.98	0.64
1:C:288:LEU:HD11	1:D:139:LYS:HD3	1.80	0.64
1:B:319:LYS:NZ	2:B:487:HOH:O	2.30	0.64
1:C:198:LEU:HD22	1:C:226:LEU:HD21	1.78	0.64
1:D:283:PRO:HD2	1:D:285:TYR:CD2	2.33	0.64
1:A:56:ARG:O	1:A:60:GLU:HG2	1.98	0.64
1:C:111:ASN:ND2	1:C:116:ILE:HB	2.13	0.63
1:C:309:ARG:HG2	1:C:333:LEU:HB2	1.82	0.61
1:C:121:LYS:NZ	1:D:121:LYS:HG3	2.16	0.61
1:D:49:SER:OG	1:D:51:THR:HG22	2.00	0.61
1:D:219:ASN:O	1:D:223:VAL:HG23	2.01	0.61
1:C:140:ARG:HD3	1:D:290:LEU:HD21	1.82	0.61
1:A:34:GLU:HA	1:A:37:LYS:CE	2.30	0.61
1:C:4:LYS:NZ	2:C:487:HOH:O	2.34	0.61
1:C:192:MET:CE	1:C:200:LYS:HD2	2.32	0.60
1:B:138:PHE:O	1:B:138:PHE:HD1	1.85	0.60
1:B:56:ARG:CB	1:B:56:ARG:HH11	2.11	0.60
1:C:192:MET:HE3	1:C:200:LYS:HD2	1.82	0.60
1:C:219:ASN:O	1:C:223:VAL:HG23	2.02	0.60
1:B:1:MET:N	2:B:363:HOH:O	2.35	0.59
1:D:299:ARG:HD3	2:D:486:HOH:O	2.02	0.59
1:D:135:TRP:O	1:D:139:LYS:HG2	2.02	0.59
1:D:92:LYS:NZ	2:D:573:HOH:O	2.24	0.58
1:A:1:MET:HA	1:A:23:ALA:HA	1.84	0.58
1:A:4:LYS:HD2	2:A:566:HOH:O	2.03	0.58
1:B:178:HIS:O	1:B:180:LYS:HD2	2.03	0.58
1:D:138:PHE:O	1:D:141:ILE:HG13	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:288:LEU:HD13	1:B:135:TRP:CE3	2.39	0.58
1:A:33:GLY:O	1:A:37:LYS:HG3	2.03	0.58
1:A:293:GLN:HG3	1:B:139:LYS:HE2	1.86	0.58
1:C:178:HIS:O	1:C:180:LYS:HD2	2.03	0.58
1:C:217:ILE:HG23	1:C:218:ILE:HG12	1.85	0.58
1:A:288:LEU:HD11	1:B:139:LYS:HG3	1.86	0.57
1:C:139:LYS:O	1:C:139:LYS:HG2	2.04	0.56
1:C:192:MET:HE3	1:C:196:GLU:HG2	1.86	0.56
1:C:87:GLY:HA2	1:C:321:VAL:HG12	1.86	0.56
1:A:333:LEU:OXT	2:A:562:HOH:O	2.17	0.56
1:C:318:ASN:O	1:C:321:VAL:HG22	2.05	0.56
1:C:57:GLU:HG3	2:C:345:HOH:O	2.06	0.56
1:C:48:VAL:CG2	1:C:52:THR:HB	2.36	0.56
1:D:34:GLU:HG3	2:D:390:HOH:O	2.05	0.56
1:A:177:ARG:HH22	1:A:213:ASP:HB3	1.71	0.55
1:D:4:LYS:HD3	2:D:570:HOH:O	2.05	0.55
1:A:292:ALA:O	1:A:296:VAL:HG23	2.05	0.55
1:D:14:GLU:HG3	2:D:547:HOH:O	2.07	0.55
1:C:48:VAL:HG23	1:C:52:THR:HB	1.89	0.55
1:A:192:MET:HE3	1:A:200:LYS:HD2	1.88	0.55
1:C:309:ARG:HD3	2:C:335:HOH:O	2.07	0.55
1:B:138:PHE:HB2	1:B:277:TRP:CH2	2.42	0.54
1:C:228:GLY:HA2	1:C:255:LYS:HG3	1.89	0.54
1:B:247:GLU:HA	1:B:250:LYS:HG2	1.90	0.54
1:D:298:PHE:O	1:D:302:GLU:HG3	2.07	0.54
1:C:133:LYS:O	1:C:137:GLY:HA3	2.05	0.54
1:C:64:ARG:NH1	2:C:421:HOH:O	2.40	0.54
1:A:247:GLU:HG3	1:A:251:GLN:NE2	2.23	0.53
1:B:1:MET:SD	1:B:23:ALA:C	2.86	0.53
1:A:291:GLU:HB2	2:A:420:HOH:O	2.09	0.53
1:C:188:LYS:HG2	1:C:188:LYS:O	2.08	0.53
1:D:85:LYS:NZ	2:D:410:HOH:O	2.41	0.53
1:C:266:PRO:HG2	1:D:130:SER:HA	1.91	0.53
1:A:56:ARG:HG2	1:A:56:ARG:HH11	1.73	0.53
1:C:87:GLY:O	1:C:325:ARG:HD2	2.09	0.53
1:A:1:MET:HA	1:A:23:ALA:CA	2.38	0.52
1:A:57:GLU:HG3	2:A:417:HOH:O	2.09	0.52
1:D:194:ILE:HD13	1:D:217:ILE:HD11	1.91	0.52
1:B:212:ARG:NH1	2:B:545:HOH:O	2.42	0.52
1:C:138:PHE:HB3	2:C:501:HOH:O	2.09	0.52
1:D:309:ARG:HG3	1:D:333:LEU:HD12	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:41:GLY:O	1:B:64:ARG:HD3	2.11	0.51
1:D:139:LYS:HG3	2:D:435:HOH:O	2.09	0.51
1:B:274:LYS:NZ	2:B:592:HOH:O	2.21	0.51
1:C:194:ILE:CD1	1:C:217:ILE:HD11	2.40	0.51
1:C:121:LYS:HZ1	1:D:121:LYS:HG3	1.74	0.51
1:C:141:ILE:HD11	1:C:277:TRP:CH2	2.46	0.51
1:C:84:THR:HA	1:C:321:VAL:HG13	1.92	0.51
1:D:178:HIS:HB3	1:D:180:LYS:NZ	2.25	0.51
1:C:65:LEU:HD23	1:C:88:ILE:HD13	1.93	0.50
1:A:80:LEU:HD11	1:A:317:VAL:CG1	2.42	0.50
1:C:14:GLU:H	1:C:14:GLU:CD	2.15	0.50
1:D:224:LYS:HG2	1:D:225:LYS:N	2.25	0.50
1:A:192:MET:CE	1:A:196:GLU:HG2	2.38	0.50
1:D:180:LYS:HB3	1:D:182:ASN:OD1	2.12	0.50
1:A:177:ARG:HH22	1:A:213:ASP:CB	2.25	0.50
1:B:138:PHE:O	1:B:138:PHE:CD1	2.64	0.50
1:B:14:GLU:CD	1:B:14:GLU:H	2.15	0.50
1:B:48:VAL:HG23	1:B:52:THR:HB	1.91	0.50
1:D:27:ILE:N	1:D:27:ILE:HD12	2.27	0.49
1:A:121:LYS:O	1:A:125:ARG:HG3	2.12	0.49
1:A:171:LYS:NZ	2:A:580:HOH:O	2.24	0.49
1:C:268:ARG:HH11	1:C:268:ARG:HG2	1.77	0.49
1:C:8:LEU:HA	1:C:28:ILE:O	2.11	0.49
1:D:126:GLY:HA2	2:D:371:HOH:O	2.12	0.49
1:A:194:ILE:HD13	1:A:217:ILE:HD11	1.94	0.49
1:C:61:ASN:N	1:C:61:ASN:HD22	2.11	0.49
1:C:190:ARG:HB2	2:C:452:HOH:O	2.13	0.49
1:A:183:VAL:HG22	2:A:489:HOH:O	2.13	0.49
1:A:142:GLU:HG2	1:B:290:LEU:HD12	1.94	0.48
1:D:163:ARG:HG2	1:D:187:LEU:HD21	1.95	0.48
1:C:265:GLU:N	2:C:540:HOH:O	2.33	0.48
1:C:2:ARG:NH1	1:C:2:ARG:HG3	2.28	0.48
1:C:2:ARG:HG3	1:C:2:ARG:HH11	1.79	0.48
1:A:197:LEU:C	1:A:197:LEU:HD23	2.34	0.48
1:D:221:GLU:O	1:D:224:LYS:HG2	2.13	0.48
1:C:273:PHE:CD2	1:D:124:ARG:HA	2.49	0.48
1:D:1:MET:N	2:D:360:HOH:O	2.40	0.48
1:D:8:LEU:HD12	1:D:48:VAL:HG12	1.95	0.48
1:C:4:LYS:NZ	1:C:4:LYS:HB2	2.29	0.47
1:D:320:GLU:CD	1:D:320:GLU:H	2.17	0.47
1:D:131:HIS:HA	2:D:552:HOH:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:327:ILE:O	1:C:330:VAL:HG22	2.14	0.47
1:D:184:GLU:O	1:D:188:LYS:HA	2.14	0.47
1:A:175:TRP:HH2	1:A:177:ARG:NE	2.08	0.47
1:D:1:MET:HG3	1:D:24:ASP:OD1	2.14	0.47
1:A:56:ARG:HG3	1:A:82:GLU:HG2	1.97	0.47
1:B:63:GLU:HG3	2:B:479:HOH:O	2.15	0.47
1:B:309:ARG:HG2	1:B:333:LEU:CB	2.43	0.47
1:B:247:GLU:OE1	1:B:250:LYS:HD2	2.14	0.47
1:C:122:PHE:CZ	1:C:127:GLU:HB3	2.50	0.47
1:C:218:ILE:CB	1:C:240:VAL:HG12	2.38	0.47
1:A:132:ALA:O	1:A:136:THR:HB	2.15	0.46
1:C:292:ALA:O	1:C:296:VAL:HG23	2.15	0.46
1:D:123:ILE:HG23	1:D:124:ARG:N	2.31	0.46
1:A:195:ASP:O	1:A:199:GLU:HG3	2.15	0.46
1:A:247:GLU:HA	1:A:250:LYS:HG2	1.97	0.46
1:C:2:ARG:N	1:C:3:PRO:HD2	2.31	0.46
1:D:13:ARG:HD2	2:D:469:HOH:O	2.15	0.46
1:C:165:LEU:O	1:C:168:PHE:HB2	2.16	0.46
1:C:73:ALA:O	1:C:92:LYS:HD2	2.15	0.46
1:D:204:VAL:HG21	1:D:226:LEU:HD21	1.98	0.46
1:A:177:ARG:HD3	2:A:537:HOH:O	2.15	0.46
1:C:39:VAL:O	1:C:42:ARG:HG2	2.15	0.46
1:C:135:TRP:HA	1:D:288:LEU:HD22	1.98	0.46
1:B:48:VAL:HG22	1:B:49:SER:N	2.31	0.46
1:A:177:ARG:HG2	1:A:177:ARG:HH11	1.81	0.46
1:C:325:ARG:HD3	1:C:330:VAL:CG1	2.46	0.45
1:D:39:VAL:HG12	1:D:42:ARG:NH2	2.31	0.45
1:A:55:THR:OG1	1:A:58:VAL:HG23	2.15	0.45
1:B:253:LYS:HD3	2:B:585:HOH:O	2.17	0.45
1:C:192:MET:CE	1:C:197:LEU:HA	2.47	0.45
1:B:1:MET:SD	1:B:23:ALA:O	2.75	0.45
1:A:159:LYS:O	1:A:163:ARG:HG3	2.16	0.45
1:B:291:GLU:H	1:B:291:GLU:CD	2.21	0.44
1:C:27:ILE:HD13	2:C:338:HOH:O	2.18	0.44
1:A:171:LYS:HB3	1:A:171:LYS:NZ	2.32	0.44
1:C:234:ILE:HD12	1:C:234:ILE:C	2.38	0.44
1:C:291:GLU:CD	1:C:291:GLU:H	2.21	0.44
1:A:8:LEU:HA	1:A:28:ILE:O	2.17	0.44
1:C:206:LEU:HB2	1:C:233:ASN:HA	1.99	0.44
1:C:3:PRO:HG2	1:C:23:ALA:HB2	2.00	0.44
1:A:46:ILE:HD12	1:A:48:VAL:CG1	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:80:LEU:HD11	1:A:317:VAL:HG12	1.98	0.44
1:C:2:ARG:HB3	1:C:3:PRO:HD3	2.00	0.44
1:D:109:ILE:O	1:D:113:MET:HG2	2.17	0.44
1:C:185:LYS:HB3	2:C:530:HOH:O	2.18	0.44
1:D:2:ARG:HG2	2:D:407:HOH:O	2.18	0.44
1:A:2:ARG:NH1	1:A:2:ARG:HG3	2.33	0.44
1:B:319:LYS:CE	2:B:487:HOH:O	2.66	0.44
1:C:162:ALA:HB1	1:C:187:LEU:HD13	1.99	0.43
1:C:206:LEU:HD11	1:C:240:VAL:CG1	2.49	0.43
1:B:152:LEU:HD12	1:B:206:LEU:CD2	2.48	0.43
1:D:121:LYS:O	1:D:125:ARG:HG2	2.18	0.43
1:D:159:LYS:O	1:D:163:ARG:HG3	2.17	0.43
1:C:13:ARG:NH2	1:C:14:GLU:OE2	2.52	0.43
1:B:304:LEU:C	1:B:304:LEU:HD23	2.38	0.43
1:A:174:TYR:HE2	1:A:184:GLU:HG2	1.83	0.43
1:B:138:PHE:HA	2:B:367:HOH:O	2.17	0.43
1:B:260:ASP:O	1:B:284:HIS:HA	2.19	0.43
1:C:228:GLY:C	1:C:255:LYS:HG3	2.39	0.43
1:D:105:THR:HG21	1:D:161:ILE:HD13	2.01	0.43
1:D:89:TYR:OH	1:D:322:LEU:HD23	2.19	0.43
1:A:188:LYS:CE	1:A:188:LYS:HA	2.45	0.43
1:B:56:ARG:NH1	1:B:57:GLU:N	2.67	0.42
1:C:82:GLU:OE2	1:C:85:LYS:HE3	2.18	0.42
1:B:319:LYS:HE2	2:B:487:HOH:O	2.19	0.42
1:C:180:LYS:O	1:C:184:GLU:HG3	2.20	0.42
1:A:177:ARG:NH1	2:A:462:HOH:O	2.49	0.42
1:C:228:GLY:CA	1:C:255:LYS:HG3	2.50	0.42
1:A:37:LYS:HD3	1:A:57:GLU:HG2	2.01	0.42
1:A:253:LYS:HD2	2:A:446:HOH:O	2.19	0.42
1:A:175:TRP:CH2	1:A:177:ARG:NE	2.84	0.42
1:A:192:MET:CE	1:A:200:LYS:HD2	2.48	0.42
1:C:2:ARG:HB3	1:C:3:PRO:CD	2.50	0.42
1:B:138:PHE:HB2	1:B:277:TRP:HH2	1.84	0.42
1:C:150:GLY:HA2	1:C:173:TYR:O	2.19	0.42
1:D:154:MET:HG2	1:D:183:VAL:HG11	2.01	0.42
1:A:140:ARG:NH2	2:A:464:HOH:O	2.52	0.41
1:A:217:ILE:HG23	1:A:218:ILE:HG12	2.02	0.41
1:A:246:THR:HA	1:A:272:LEU:HD21	2.02	0.41
1:B:194:ILE:HD13	1:B:217:ILE:HD11	2.02	0.41
1:D:260:ASP:CG	1:D:284:HIS:HA	2.41	0.41
1:A:265:GLU:HG2	1:B:128:TRP:CH2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:96:LEU:HD12	1:D:295:ASP:HB2	2.02	0.41
1:A:155:GLY:O	1:A:159:LYS:HG3	2.20	0.41
1:A:7:VAL:HG23	1:A:25:VAL:HG13	2.02	0.41
1:D:4:LYS:NZ	2:D:570:HOH:O	2.36	0.41
1:C:56:ARG:HG2	1:C:56:ARG:HH11	1.86	0.41
1:D:9:LEU:HD11	1:D:71:HIS:CG	2.55	0.41
1:A:133:LYS:O	1:A:137:GLY:HA3	2.21	0.41
1:C:162:ALA:CB	1:C:187:LEU:HD13	2.51	0.41
1:C:61:ASN:ND2	1:C:61:ASN:N	2.68	0.41
1:A:180:LYS:O	1:A:184:GLU:HG3	2.21	0.41
1:A:264:LYS:HE2	2:A:468:HOH:O	2.19	0.41
1:B:260:ASP:CG	1:B:284:HIS:HA	2.42	0.41
1:C:291:GLU:HB2	2:D:382:HOH:O	2.20	0.41
1:C:53:LYS:HE3	2:C:431:HOH:O	2.20	0.41
1:A:234:ILE:HD12	1:A:234:ILE:C	2.41	0.41
1:A:2:ARG:NH2	1:A:332:MET:O	2.49	0.41
1:D:304:LEU:C	1:D:304:LEU:HD23	2.41	0.41
1:B:201:SER:O	1:B:229:LYS:HD3	2.20	0.40
1:C:187:LEU:O	1:C:188:LYS:HB3	2.21	0.40
1:C:192:MET:HE2	1:C:197:LEU:N	2.36	0.40
1:C:111:ASN:HD22	1:C:116:ILE:HB	1.84	0.40
1:A:299:ARG:HA	1:A:299:ARG:HD3	1.82	0.40
1:D:162:ALA:O	1:D:166:ILE:HG13	2.22	0.40
1:A:252:GLY:HA2	2:A:467:HOH:O	2.21	0.40
1:A:62:ALA:HB1	1:A:65:LEU:CB	2.52	0.40
1:C:1:MET:HB3	1:C:23:ALA:C	2.42	0.40
1:D:135:TRP:N	1:D:135:TRP:CD1	2.90	0.40
1:D:55:THR:HB	2:D:354:HOH:O	2.21	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	331/333 (99%)	314 (95%)	16 (5%)	1 (0%)	43	32
1	B	331/333 (99%)	315 (95%)	15 (4%)	1 (0%)	43	32
1	C	331/333 (99%)	311 (94%)	19 (6%)	1 (0%)	43	32
1	D	331/333 (99%)	317 (96%)	12 (4%)	2 (1%)	27	15
All	All	1324/1332 (99%)	1257 (95%)	62 (5%)	5 (0%)	36	24

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	290	LEU
1	D	140	ARG
1	A	194	ILE
1	B	2	ARG
1	C	183	VAL

### 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	286/286 (100%)	281 (98%)	5 (2%)	63	58
1	B	286/286 (100%)	283 (99%)	3 (1%)	78	76
1	C	286/286 (100%)	279 (98%)	7 (2%)	52	43
1	D	286/286 (100%)	281 (98%)	5 (2%)	63	58
All	All	1144/1144 (100%)	1124 (98%)	20 (2%)	63	58

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	177	ARG
1	A	185	LYS
1	A	243	LYS
1	A	299	ARG
1	A	328	GLU
1	B	1	MET

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Mol	Chain	Res	Type
1	B	56	ARG
1	B	186	GLU
1	C	9	LEU
1	C	61	ASN
1	C	80	LEU
1	C	213	ASP
1	C	302	GLU
1	C	321	VAL
1	C	328	GLU
1	D	4	LYS
1	D	94	SER
1	D	139	LYS
1	D	185	LYS
1	D	186	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	251	GLN
1	C	61	ASN
1	C	111	ASN
1	C	329	ASN
1	D	111	ASN
1	D	131	HIS

### 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

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	333/333 (100%)	0.25	16 (4%) 30 41	15, 27, 47, 71	0
1	B	333/333 (100%)	0.12	9 (2%) 54 64	16, 25, 41, 56	0
1	C	333/333 (100%)	0.56	28 (8%) 11 18	20, 34, 58, 73	0
1	D	333/333 (100%)	0.18	10 (3%) 50 59	19, 28, 44, 54	0
All	All	1332/1332 (100%)	0.28	63 (4%) 31 41	15, 29, 50, 73	0

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1	MET	5.2
1	B	138	PHE	4.8
1	A	181	VAL	4.8
1	A	185	LYS	4.2
1	C	182	ASN	4.2
1	C	140	ARG	4.1
1	C	1	MET	4.0
1	A	182	ASN	3.9
1	D	110	ILE	3.8
1	A	1	MET	3.7
1	A	178	HIS	3.7
1	C	109	ILE	3.6
1	C	212	ARG	3.5
1	D	183	VAL	3.5
1	C	188	LYS	3.4
1	A	188	LYS	3.3
1	C	183	VAL	3.2
1	D	116	ILE	3.1
1	C	178	HIS	3.0
1	A	140	ARG	2.9
1	C	198	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	110	ILE	2.9
1	C	224	LYS	2.8
1	B	108	LEU	2.8
1	C	138	PHE	2.8
1	A	191	TYR	2.6
1	C	275	TYR	2.6
1	C	251	GLN	2.6
1	C	197	LEU	2.6
1	C	181	VAL	2.6
1	D	178	HIS	2.5
1	C	268	ARG	2.5
1	D	185	LYS	2.5
1	C	137	GLY	2.5
1	C	177	ARG	2.5
1	A	193	ASP	2.4
1	A	177	ARG	2.4
1	C	194	ILE	2.4
1	A	14	GLU	2.4
1	C	184	GLU	2.4
1	A	190	ARG	2.3
1	C	106	VAL	2.3
1	C	175	TRP	2.3
1	B	112	LEU	2.3
1	D	106	VAL	2.3
1	D	139	LYS	2.2
1	C	221	GLU	2.2
1	C	185	LYS	2.2
1	D	63	GLU	2.1
1	B	292	ALA	2.1
1	C	269	GLU	2.1
1	B	182	ASN	2.1
1	B	104	PHE	2.1
1	A	232	VAL	2.1
1	A	199	GLU	2.1
1	B	101	VAL	2.1
1	D	132	ALA	2.1
1	C	108	LEU	2.1
1	C	113	MET	2.0
1	A	111	ASN	2.0
1	D	1	MET	2.0
1	B	185	LYS	2.0
1	A	221	GLU	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 [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.