Full wwPDB X-ray Structure Validation Report (i)

Sep 28, 2023 – 10:14 AM EDT

PDB ID	:	2E0Z
Title	:	Crystal structure of virus-like particle from Pyrococcus furiosus
Authors	:	Akita, F.; Chong, K.T.; Tanaka, H.; Yamashita, E.; Miyazaki, N.; Nakaishi, Y.; Namba, K.; Ono, Y.; Suzuki, M.; Tsukihara, T.; Nakagawa, A.
Deposited on	:	2006-10-16
Resolution	:	3.60 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 (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:

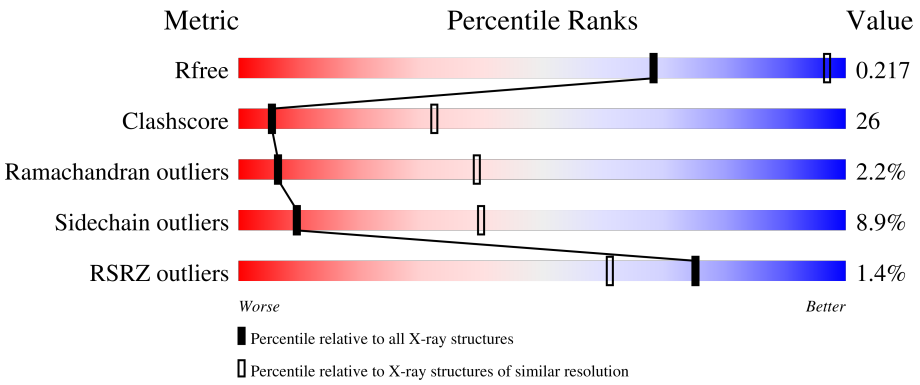
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 3.60 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	1257 (3.70-3.50)
Clashscore	141614	1353 (3.70-3.50)
Ramachandran outliers	138981	1307 (3.70-3.50)
Sidechain outliers	138945	1307 (3.70-3.50)
RSRZ outliers	127900	1161 (3.70-3.50)

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	A	345	37% 28% • 32%
1	B	345	% 39% 25% • • 32%
1	C	345	% 37% 24% • 34%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 5488 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 Virus-like particle.

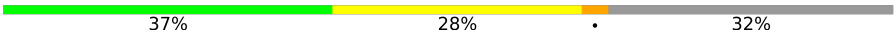
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	236	1851	1191	307	350	3	0	0	0
			Total	C	N	O	S			
1	B	236	1851	1191	307	350	3	0	0	0
			Total	C	N	O	S			
1	C	228	1786	1149	297	338	2	0	0	0

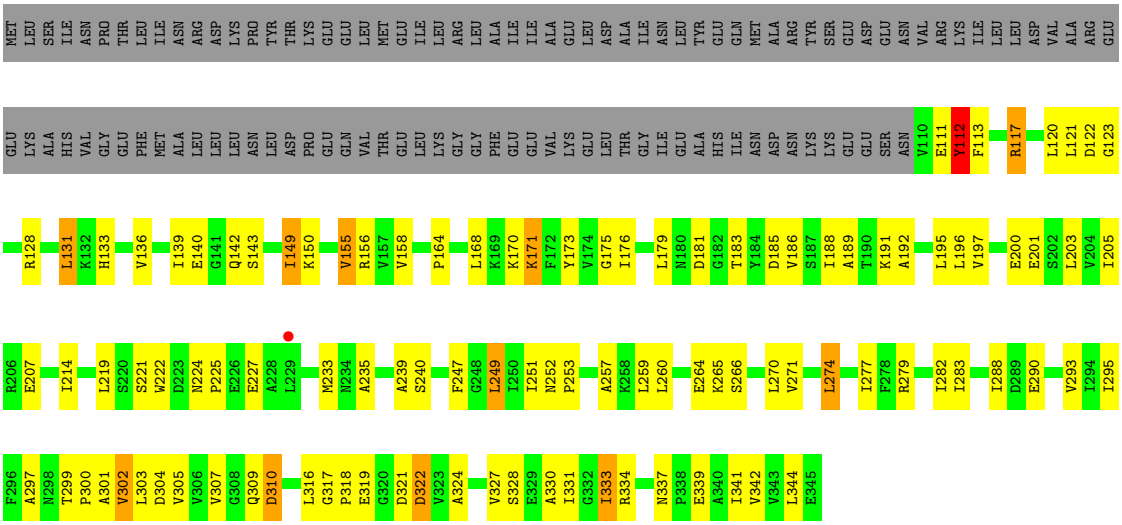
3 Residue-property plots (i)

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: Virus-like particle

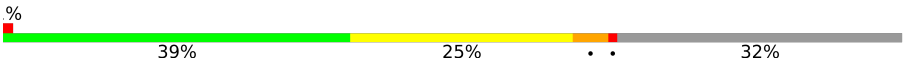
Chain A:

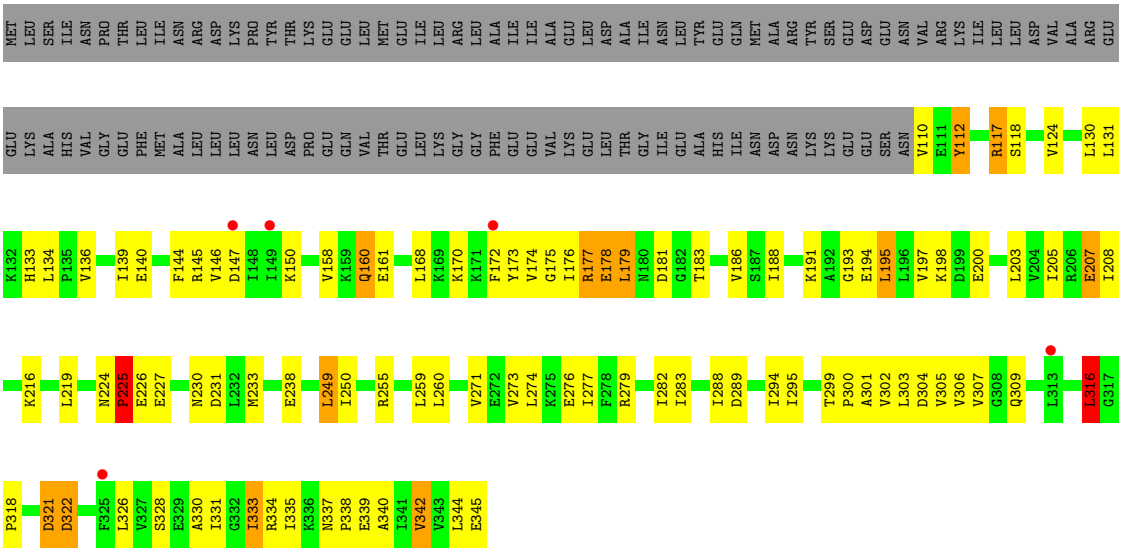




• Molecule 1: Virus-like particle

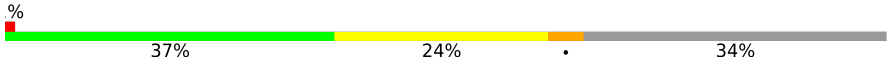
Chain B:

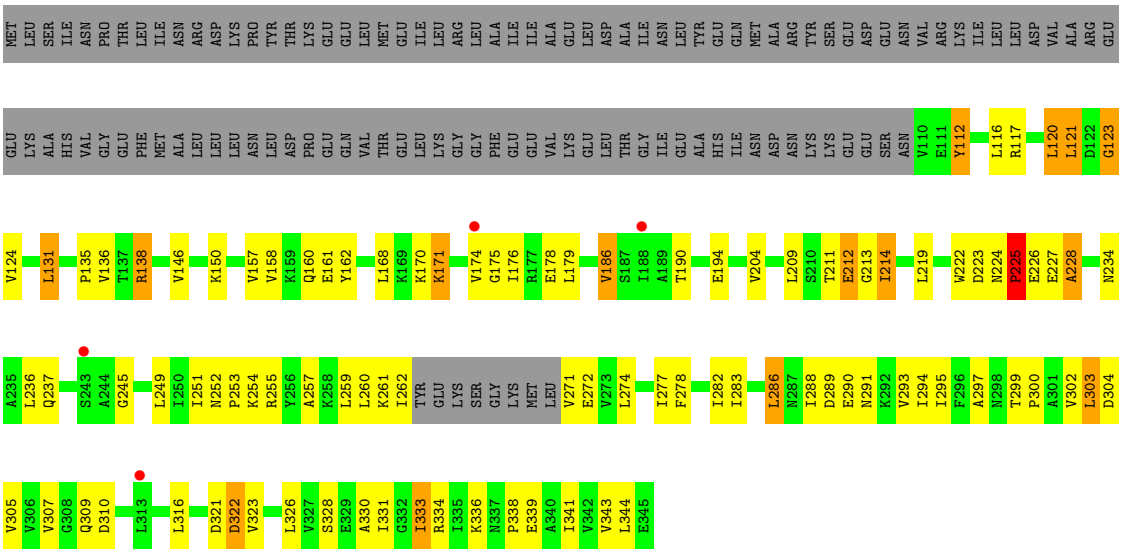




• Molecule 1: Virus-like particle

Chain C:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	631.50Å 631.50Å 351.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.60 79.61 – 3.61	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-3.60) 96.8 (79.61-3.61)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.85 (at 3.58Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.268 , 0.267 0.215 , 0.217	Depositor DCC
R_{free} test set	38570 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	138.0	Xtriage
Anisotropy	0.051	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 60.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	5488	wwPDB-VP
Average B, all atoms (Å^2)	99.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.29% 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)

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	0.54	0/1876	0.67	0/2530
1	B	0.55	0/1876	0.69	0/2530
1	C	0.49	0/1809	0.66	0/2441
All	All	0.53	0/5561	0.67	0/7501

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	1851	0	1940	100	0
1	B	1851	0	1940	99	0
1	C	1786	0	1870	99	0
All	All	5488	0	5750	292	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 26.

All (292) 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:C:171:LYS:H	1:C:171:LYS:HE2	1.00	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:181:ASP:HB2	1:A:183:THR:HG22	1.27	1.06
1:A:333:ILE:HD13	1:A:333:ILE:H	1.23	1.02
1:B:117:ARG:HH11	1:B:117:ARG:HB2	1.26	0.99
1:C:333:ILE:HD12	1:C:333:ILE:H	1.25	0.98
1:A:175:GLY:HA2	1:A:322:ASP:HB3	1.47	0.95
1:B:333:ILE:H	1:B:333:ILE:HD12	1.31	0.95
1:B:175:GLY:HA2	1:B:322:ASP:HB3	1.50	0.93
1:C:112:TYR:HD2	1:C:179:LEU:HD22	1.31	0.92
1:C:171:LYS:HE2	1:C:171:LYS:N	1.86	0.91
1:A:112:TYR:HD2	1:A:179:LEU:HD22	1.35	0.90
1:B:146:VAL:HG12	1:B:334:ARG:HG3	1.54	0.90
1:A:136:VAL:HG12	1:A:305:VAL:HB	1.54	0.89
1:C:176:ILE:HG12	1:C:321:ASP:O	1.74	0.88
1:C:249:LEU:HB2	1:C:278:PHE:CD2	2.11	0.86
1:C:261:LYS:HE2	1:C:261:LYS:HA	1.59	0.85
1:C:112:TYR:CD2	1:C:179:LEU:HD22	2.12	0.84
1:C:277:ILE:HG23	1:C:278:PHE:HD1	1.40	0.84
1:C:171:LYS:H	1:C:171:LYS:CE	1.88	0.83
1:B:233:MET:HE3	1:B:277:ILE:HG13	1.59	0.83
1:B:176:ILE:HG13	1:B:322:ASP:HA	1.61	0.83
1:A:149:ILE:HD13	1:A:149:ILE:H	1.43	0.83
1:B:299:THR:HG22	1:B:301:ALA:H	1.43	0.81
1:A:176:ILE:HG12	1:A:321:ASP:O	1.81	0.80
1:A:112:TYR:CD2	1:A:179:LEU:HD22	2.17	0.79
1:A:181:ASP:HB2	1:A:183:THR:CG2	2.11	0.79
1:C:219:LEU:HB2	1:C:344:LEU:HB3	1.65	0.78
1:A:214:ILE:HG22	1:A:341:ILE:HB	1.64	0.78
1:C:260:LEU:HD12	1:C:260:LEU:O	1.83	0.77
1:A:155:VAL:HG13	1:B:172:PHE:HB3	1.66	0.77
1:C:251:ILE:HG22	1:C:293:VAL:HG22	1.66	0.76
1:A:214:ILE:O	1:A:214:ILE:HD12	1.86	0.76
1:A:150:LYS:HB2	1:A:158:VAL:HG21	1.68	0.76
1:A:251:ILE:HG22	1:A:293:VAL:HG13	1.68	0.75
1:A:170:LYS:HA	1:A:171:LYS:HE3	1.68	0.75
1:A:309:GLN:N	1:A:330:ALA:HB3	2.02	0.75
1:C:333:ILE:HD12	1:C:333:ILE:N	2.01	0.74
1:A:120:LEU:HD21	1:A:327:VAL:HG13	1.70	0.73
1:A:333:ILE:HD13	1:A:333:ILE:N	2.00	0.72
1:B:304:ASP:HB3	1:B:334:ARG:HB3	1.72	0.71
1:A:309:GLN:H	1:A:330:ALA:HB3	1.55	0.71
1:B:302:VAL:HG13	1:B:337:ASN:HB3	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:138:ARG:HG2	1:C:138:ARG:HH11	1.54	0.70
1:C:146:VAL:CG1	1:C:161:GLU:HB3	2.22	0.69
1:B:136:VAL:HG12	1:B:305:VAL:HB	1.75	0.69
1:B:150:LYS:HB3	1:B:158:VAL:HG21	1.72	0.69
1:B:309:GLN:N	1:B:330:ALA:HB3	2.08	0.69
1:C:257:ALA:O	1:C:260:LEU:HG	1.93	0.68
1:A:333:ILE:H	1:A:333:ILE:CD1	2.02	0.68
1:A:173:TYR:HD2	1:A:324:ALA:HA	1.59	0.67
1:A:176:ILE:HG12	1:A:321:ASP:C	2.14	0.67
1:B:139:ILE:HG13	1:B:140:GLU:H	1.59	0.66
1:C:282:ILE:HD12	1:C:282:ILE:N	2.10	0.66
1:C:283:ILE:N	1:C:283:ILE:HD12	2.11	0.66
1:A:128:ARG:NH1	1:A:200:GLU:OE1	2.28	0.65
1:C:146:VAL:HG12	1:C:161:GLU:HB3	1.78	0.65
1:B:259:LEU:O	1:B:271:VAL:HG23	1.96	0.65
1:C:222:TRP:CD1	1:C:228:ALA:HA	2.32	0.64
1:C:286:LEU:H	1:C:286:LEU:HD12	1.62	0.64
1:C:176:ILE:HG12	1:C:321:ASP:C	2.18	0.64
1:C:304:ASP:OD1	1:C:334:ARG:HD3	1.97	0.64
1:A:219:LEU:HB2	1:A:344:LEU:HB3	1.79	0.64
1:A:155:VAL:HG13	1:B:172:PHE:CB	2.26	0.64
1:B:224:ASN:O	1:B:226:GLU:N	2.31	0.63
1:C:249:LEU:HB2	1:C:278:PHE:CE2	2.33	0.63
1:B:144:PHE:CD2	1:B:306:VAL:HG21	2.33	0.63
1:B:130:LEU:HD22	1:B:134:LEU:HD11	1.80	0.63
1:B:130:LEU:HD11	1:B:205:ILE:HD11	1.79	0.63
1:B:309:GLN:H	1:B:330:ALA:HB3	1.63	0.62
1:B:146:VAL:CG2	1:B:161:GLU:HB3	2.29	0.62
1:A:299:THR:HG22	1:A:301:ALA:H	1.64	0.62
1:B:117:ARG:HH11	1:B:117:ARG:CB	2.09	0.62
1:B:197:VAL:HA	1:B:200:GLU:HB3	1.83	0.61
1:C:224:ASN:O	1:C:226:GLU:N	2.34	0.60
1:C:297:ALA:HB3	1:C:302:VAL:HG21	1.83	0.60
1:C:174:VAL:HG11	1:C:179:LEU:HD21	1.84	0.60
1:A:149:ILE:HG21	1:B:188:ILE:HG12	1.84	0.60
1:B:150:LYS:HB3	1:B:158:VAL:CG2	2.32	0.59
1:A:171:LYS:CD	1:A:171:LYS:H	2.14	0.59
1:A:333:ILE:N	1:A:333:ILE:CD1	2.65	0.59
1:C:260:LEU:O	1:C:261:LYS:HG2	2.02	0.59
1:B:207:GLU:HB3	1:B:333:ILE:HD11	1.83	0.59
1:A:197:VAL:HA	1:A:200:GLU:HB3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:150:LYS:HB2	1:A:158:VAL:CG2	2.34	0.58
1:A:171:LYS:HE3	1:A:171:LYS:H	1.69	0.58
1:B:307:VAL:HG23	1:B:307:VAL:O	2.02	0.58
1:A:249:LEU:CD1	1:A:282:ILE:HG23	2.34	0.58
1:B:219:LEU:HB2	1:B:344:LEU:HB3	1.85	0.57
1:C:219:LEU:HD11	1:C:255:ARG:CZ	2.35	0.56
1:B:207:GLU:CB	1:B:333:ILE:HD11	2.35	0.56
1:A:304:ASP:HB3	1:A:334:ARG:HG2	1.87	0.56
1:C:219:LEU:HD11	1:C:255:ARG:NH2	2.21	0.56
1:B:259:LEU:HB3	1:B:271:VAL:HG22	1.86	0.56
1:B:333:ILE:H	1:B:333:ILE:CD1	2.08	0.56
1:A:304:ASP:HB3	1:A:334:ARG:CG	2.35	0.56
1:C:252:ASN:CB	1:C:290:GLU:HA	2.36	0.56
1:A:297:ALA:HB3	1:A:302:VAL:HG11	1.88	0.55
1:C:112:TYR:H	1:C:112:TYR:HD1	1.54	0.55
1:A:257:ALA:HA	1:A:260:LEU:HD12	1.89	0.55
1:C:209:LEU:HD23	1:C:343:VAL:HG11	1.89	0.55
1:A:155:VAL:CG1	1:B:172:PHE:HB3	2.36	0.54
1:A:305:VAL:HG22	1:A:333:ILE:HG22	1.88	0.54
1:A:317:GLY:O	1:A:319:GLU:HG3	2.08	0.54
1:A:173:TYR:CD2	1:A:324:ALA:HA	2.42	0.54
1:A:249:LEU:HD11	1:A:282:ILE:HG12	1.90	0.53
1:C:261:LYS:HA	1:C:261:LYS:CE	2.36	0.53
1:A:171:LYS:H	1:A:171:LYS:CE	2.22	0.53
1:A:224:ASN:O	1:A:225:PRO:C	2.43	0.53
1:C:252:ASN:CG	1:C:253:PRO:HD2	2.29	0.53
1:A:224:ASN:O	1:A:227:GLU:N	2.42	0.53
1:C:136:VAL:HG22	1:C:305:VAL:HB	1.89	0.53
1:A:142:GLN:HG2	1:C:162:TYR:OH	2.09	0.53
1:A:117:ARG:O	1:A:120:LEU:HB3	2.09	0.53
1:A:171:LYS:HE3	1:A:171:LYS:N	2.24	0.53
1:B:130:LEU:HD11	1:B:205:ILE:CD1	2.38	0.53
1:C:277:ILE:HG23	1:C:278:PHE:CD1	2.32	0.53
1:C:309:GLN:N	1:C:330:ALA:HB3	2.24	0.53
1:A:205:ILE:HD13	1:A:288:ILE:HB	1.91	0.53
1:B:176:ILE:HG13	1:B:322:ASP:CA	2.37	0.53
1:A:259:LEU:O	1:A:271:VAL:HG23	2.09	0.52
1:B:174:VAL:HG11	1:B:179:LEU:HD13	1.90	0.52
1:B:333:ILE:HD12	1:B:333:ILE:N	2.06	0.52
1:C:251:ILE:HG22	1:C:293:VAL:HG13	1.92	0.52
1:C:138:ARG:HG2	1:C:138:ARG:NH1	2.23	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:160:GLN:O	1:C:161:GLU:HB2	2.10	0.52
1:C:249:LEU:HB2	1:C:278:PHE:HD2	1.69	0.52
1:A:175:GLY:CA	1:A:322:ASP:HB3	2.30	0.52
1:A:207:GLU:HB2	1:A:333:ILE:HD11	1.90	0.52
1:A:249:LEU:HD12	1:A:282:ILE:HA	1.91	0.52
1:A:176:ILE:HG12	1:A:322:ASP:HA	1.92	0.52
1:A:121:LEU:C	1:A:123:GLY:H	2.13	0.52
1:A:207:GLU:CB	1:A:333:ILE:HD11	2.40	0.51
1:B:194:GLU:O	1:B:197:VAL:HG22	2.10	0.51
1:C:131:LEU:HD21	1:C:204:VAL:HG21	1.90	0.51
1:C:224:ASN:O	1:C:227:GLU:HG2	2.11	0.51
1:C:262:ILE:HB	1:C:271:VAL:HG11	1.92	0.51
1:C:175:GLY:HA2	1:C:322:ASP:HB3	1.92	0.51
1:B:133:HIS:HB2	1:B:283:ILE:HD12	1.92	0.51
1:B:249:LEU:HD12	1:B:282:ILE:HA	1.92	0.51
1:C:300:PRO:O	1:C:336:LYS:HD2	2.11	0.51
1:A:221:SER:O	1:A:222:TRP:HB2	2.10	0.51
1:B:146:VAL:HG23	1:B:161:GLU:HB3	1.92	0.51
1:B:112:TYR:HD2	1:B:179:LEU:HD11	1.76	0.51
1:C:252:ASN:OD1	1:C:253:PRO:HD2	2.11	0.51
1:A:133:HIS:CD2	1:A:283:ILE:HD12	2.46	0.51
1:B:197:VAL:HG23	1:B:198:LYS:N	2.26	0.51
1:B:295:ILE:N	1:B:295:ILE:HD12	2.27	0.50
1:B:224:ASN:O	1:B:227:GLU:N	2.43	0.50
1:B:219:LEU:HD11	1:B:255:ARG:HH12	1.76	0.50
1:C:288:ILE:HG23	1:C:288:ILE:O	2.12	0.50
1:B:175:GLY:CA	1:B:322:ASP:HB3	2.34	0.50
1:C:236:LEU:O	1:C:236:LEU:HD23	2.12	0.50
1:A:299:THR:CG2	1:A:300:PRO:HD2	2.43	0.49
1:B:230:ASN:O	1:B:231:ASP:C	2.50	0.49
1:C:307:VAL:O	1:C:307:VAL:HG23	2.11	0.49
1:A:171:LYS:CD	1:A:171:LYS:N	2.75	0.49
1:A:189:ALA:O	1:A:192:ALA:HB3	2.13	0.48
1:B:145:ARG:HD2	1:B:160:GLN:HG2	1.95	0.48
1:B:302:VAL:HG11	1:B:340:ALA:HB3	1.95	0.48
1:C:121:LEU:C	1:C:123:GLY:H	2.14	0.48
1:C:254:LYS:O	1:C:257:ALA:HB3	2.13	0.48
1:A:279:ARG:HH11	1:A:279:ARG:HG3	1.78	0.48
1:B:175:GLY:O	1:B:179:LEU:HB2	2.13	0.48
1:A:170:LYS:CA	1:A:171:LYS:HE3	2.41	0.48
1:C:112:TYR:CD1	1:C:112:TYR:N	2.82	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:121:LEU:O	1:C:123:GLY:N	2.38	0.48
1:A:233:MET:HE1	1:A:277:ILE:HG21	1.95	0.48
1:B:168:LEU:O	1:B:328:SER:HA	2.13	0.48
1:B:288:ILE:O	1:B:289:ASP:C	2.52	0.48
1:C:294:ILE:C	1:C:295:ILE:HD12	2.34	0.47
1:A:171:LYS:H	1:A:171:LYS:HD2	1.78	0.47
1:A:260:LEU:HD23	1:A:271:VAL:HG21	1.96	0.47
1:A:191:LYS:O	1:A:195:LEU:HB2	2.14	0.47
1:B:178:GLU:H	1:B:178:GLU:CD	2.18	0.47
1:C:219:LEU:HD11	1:C:255:ARG:NH1	2.29	0.47
1:C:259:LEU:HD21	1:C:274:LEU:HD11	1.97	0.47
1:A:111:GLU:O	1:A:113:PHE:N	2.47	0.47
1:C:213:GLY:O	1:C:214:ILE:C	2.52	0.47
1:C:282:ILE:HD12	1:C:282:ILE:H	1.80	0.47
1:A:235:ALA:CB	1:A:295:ILE:HG13	2.44	0.47
1:B:117:ARG:HB2	1:B:117:ARG:NH1	2.10	0.47
1:C:251:ILE:HG22	1:C:293:VAL:CG2	2.39	0.47
1:A:233:MET:CE	1:A:277:ILE:HG21	2.43	0.47
1:B:288:ILE:O	1:B:288:ILE:HG23	2.14	0.47
1:B:117:ARG:HG3	1:B:118:SER:N	2.30	0.47
1:C:252:ASN:OD1	1:C:253:PRO:CD	2.63	0.47
1:A:239:ALA:HB2	1:A:342:VAL:HG23	1.97	0.47
1:A:299:THR:HG23	1:A:300:PRO:HD2	1.96	0.47
1:A:307:VAL:HG12	1:A:307:VAL:O	2.14	0.47
1:C:286:LEU:HD12	1:C:286:LEU:N	2.30	0.47
1:B:249:LEU:CD1	1:B:282:ILE:HG23	2.45	0.46
1:C:168:LEU:O	1:C:328:SER:HA	2.15	0.46
1:B:216:LYS:HD3	1:B:345:GLU:OE1	2.15	0.46
1:C:295:ILE:HD12	1:C:295:ILE:N	2.31	0.46
1:B:131:LEU:HD11	1:B:331:ILE:HD11	1.97	0.46
1:B:303:LEU:HA	1:B:303:LEU:HD12	1.49	0.46
1:B:208:ILE:HG12	1:B:335:ILE:HD11	1.98	0.46
1:C:112:TYR:HD1	1:C:112:TYR:N	2.14	0.46
1:C:150:LYS:HB2	1:C:158:VAL:HG21	1.97	0.46
1:B:224:ASN:O	1:B:225:PRO:C	2.53	0.46
1:B:295:ILE:HB	1:B:342:VAL:HG13	1.98	0.46
1:C:223:ASP:O	1:C:225:PRO:HD3	2.15	0.46
1:A:235:ALA:HB1	1:A:295:ILE:HG13	1.98	0.46
1:A:143:SER:HB3	1:A:164:PRO:HA	1.97	0.45
1:B:316:LEU:HD13	1:B:326:LEU:HB2	1.98	0.45
1:A:185:ASP:O	1:A:188:ILE:HG13	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:133:HIS:CB	1:B:283:ILE:HD12	2.47	0.45
1:B:146:VAL:HG23	1:B:146:VAL:O	2.16	0.45
1:C:117:ARG:O	1:C:120:LEU:HB3	2.17	0.45
1:B:302:VAL:CG1	1:B:340:ALA:HB3	2.47	0.45
1:C:214:ILE:HG22	1:C:341:ILE:HB	1.97	0.44
1:B:170:LYS:HD3	1:B:170:LYS:HA	1.82	0.44
1:B:181:ASP:OD1	1:B:183:THR:HG23	2.18	0.44
1:B:274:LEU:O	1:B:277:ILE:O	2.35	0.44
1:C:176:ILE:HD13	1:C:323:VAL:HG23	1.99	0.44
1:B:197:VAL:CG2	1:B:198:LYS:N	2.80	0.44
1:B:279:ARG:NH1	1:B:279:ARG:HG3	2.32	0.44
1:A:249:LEU:HD11	1:A:282:ILE:HG23	2.00	0.44
1:A:264:GLU:O	1:A:266:SER:N	2.50	0.43
1:B:139:ILE:HG23	1:B:140:GLU:N	2.32	0.43
1:A:300:PRO:HA	1:A:303:LEU:O	2.19	0.43
1:A:303:LEU:HD12	1:A:303:LEU:HA	1.61	0.43
1:B:139:ILE:HD12	1:B:139:ILE:HA	1.90	0.43
1:B:176:ILE:HG13	1:B:321:ASP:O	2.18	0.43
1:C:223:ASP:C	1:C:225:PRO:HD3	2.39	0.43
1:B:233:MET:CE	1:B:277:ILE:HG21	2.49	0.43
1:B:260:LEU:HD23	1:B:271:VAL:HG21	2.00	0.43
1:B:273:VAL:O	1:B:276:GLU:HB2	2.18	0.43
1:C:283:ILE:N	1:C:283:ILE:CD1	2.78	0.43
1:A:168:LEU:O	1:A:328:SER:HA	2.18	0.43
1:A:264:GLU:C	1:A:266:SER:H	2.22	0.43
1:A:339:GLU:H	1:A:339:GLU:HG2	1.66	0.43
1:B:249:LEU:HD11	1:B:282:ILE:HG23	2.00	0.43
1:C:135:PRO:HG2	1:C:304:ASP:HA	2.00	0.43
1:C:303:LEU:HA	1:C:334:ARG:O	2.18	0.43
1:A:252:ASN:CG	1:A:253:PRO:HD2	2.39	0.43
1:C:146:VAL:HG13	1:C:146:VAL:O	2.18	0.43
1:B:177:ARG:NH1	1:B:177:ARG:HG3	2.34	0.43
1:B:249:LEU:HD12	1:B:249:LEU:O	2.19	0.43
1:C:271:VAL:HG13	1:C:272:GLU:HG3	2.01	0.43
1:A:121:LEU:CD1	1:A:121:LEU:N	2.82	0.42
1:A:233:MET:HE3	1:A:277:ILE:HD13	2.01	0.42
1:A:149:ILE:HD13	1:A:149:ILE:N	2.22	0.42
1:A:264:GLU:C	1:A:266:SER:N	2.71	0.42
1:C:170:LYS:HD3	1:C:170:LYS:HA	1.90	0.42
1:A:240:SER:HA	1:A:247:PHE:CZ	2.54	0.42
1:B:207:GLU:HB3	1:B:333:ILE:CD1	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:130:LEU:HD21	1:B:250:ILE:HD12	2.02	0.42
1:C:211:THR:HG22	1:C:212:GLU:N	2.34	0.42
1:C:214:ILE:O	1:C:214:ILE:HG13	2.20	0.42
1:C:288:ILE:O	1:C:289:ASP:C	2.58	0.42
1:C:168:LEU:HD23	1:C:168:LEU:HA	1.78	0.42
1:A:170:LYS:HA	1:A:170:LYS:HD3	1.90	0.41
1:B:130:LEU:HD23	1:B:283:ILE:HG21	2.02	0.41
1:B:299:THR:HG23	1:B:300:PRO:HD2	2.02	0.41
1:B:110:VAL:HG22	1:B:110:VAL:O	2.19	0.41
1:B:112:TYR:HD2	1:B:179:LEU:CD1	2.32	0.41
1:B:337:ASN:O	1:B:339:GLU:N	2.53	0.41
1:A:120:LEU:HD11	1:A:327:VAL:HG11	2.02	0.41
1:A:270:LEU:HG	1:A:274:LEU:HD22	2.03	0.41
1:B:191:LYS:HG3	1:B:195:LEU:HD12	2.02	0.41
1:A:139:ILE:HG13	1:A:140:GLU:N	2.36	0.41
1:C:257:ALA:C	1:C:259:LEU:N	2.73	0.41
1:C:316:LEU:HA	1:C:316:LEU:HD12	1.85	0.41
1:B:279:ARG:HG3	1:B:279:ARG:HH11	1.85	0.41
1:C:175:GLY:O	1:C:179:LEU:HG	2.20	0.41
1:A:259:LEU:CB	1:A:271:VAL:HG22	2.51	0.41
1:C:213:GLY:HA3	1:C:338:PRO:HB2	2.03	0.41
1:C:255:ARG:HH21	1:C:291:ASN:ND2	2.18	0.41
1:A:121:LEU:C	1:A:123:GLY:N	2.74	0.41
1:A:252:ASN:HB3	1:A:290:GLU:HA	2.03	0.41
1:B:147:ASP:OD1	1:B:160:GLN:HG3	2.21	0.41
1:B:177:ARG:HG3	1:B:177:ARG:HH11	1.86	0.41
1:A:156:ARG:CZ	1:B:173:TYR:CE1	3.04	0.41
1:B:124:VAL:HG23	1:B:193:GLY:HA3	2.02	0.41
1:C:121:LEU:C	1:C:123:GLY:N	2.75	0.41
1:C:307:VAL:HG12	1:C:331:ILE:HG13	2.03	0.41
1:B:133:HIS:CD2	1:B:283:ILE:HD12	2.56	0.40
1:B:238:GLU:HA	1:B:238:GLU:OE1	2.20	0.40
1:C:116:LEU:HD23	1:C:186:VAL:CG1	2.51	0.40
1:C:121:LEU:O	1:C:124:VAL:N	2.51	0.40
1:C:234:ASN:HD22	1:C:234:ASN:HA	1.64	0.40
1:C:249:LEU:HD11	1:C:251:ILE:HG23	2.03	0.40
1:C:339:GLU:OE2	1:C:339:GLU:N	2.51	0.40
1:C:251:ILE:CG2	1:C:293:VAL:HG13	2.50	0.40
1:A:131:LEU:HD11	1:A:305:VAL:HG11	2.03	0.40
1:A:224:ASN:HB2	1:A:227:GLU:HB2	2.03	0.40
1:B:255:ARG:HD3	1:B:255:ARG:HA	1.83	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:190:THR:O	1:C:194:GLU:HG3	2.21	0.40
1:A:191:LYS:HE2	1:A:195:LEU:HD13	2.02	0.40
1:B:249:LEU:HA	1:B:294:ILE:O	2.22	0.40
1:C:174:VAL:CG1	1:C:179:LEU:HD21	2.51	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	234/345 (68%)	205 (88%)	24 (10%)	5 (2%)	7	40
1	B	234/345 (68%)	197 (84%)	33 (14%)	4 (2%)	9	45
1	C	224/345 (65%)	192 (86%)	26 (12%)	6 (3%)	5	35
All	All	692/1035 (67%)	594 (86%)	83 (12%)	15 (2%)	6	39

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	225	PRO
1	A	112	TYR
1	A	316	LEU
1	A	318	PRO
1	B	225	PRO
1	B	316	LEU
1	C	212	GLU
1	C	245	GLY
1	C	214	ILE
1	A	265	LYS
1	A	310	ASP
1	C	123	GLY
1	C	228	ALA

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Mol	Chain	Res	Type
1	B	318	PRO
1	B	338	PRO

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	205/302 (68%)	186 (91%)	19 (9%)	9 38
1	B	205/302 (68%)	188 (92%)	17 (8%)	11 42
1	C	198/302 (66%)	180 (91%)	18 (9%)	9 39
All	All	608/906 (67%)	554 (91%)	54 (9%)	9 40

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	112	TYR
1	A	117	ARG
1	A	122	ASP
1	A	131	LEU
1	A	149	ILE
1	A	155	VAL
1	A	171	LYS
1	A	186	VAL
1	A	196	LEU
1	A	201	GLU
1	A	203	LEU
1	A	249	LEU
1	A	274	LEU
1	A	302	VAL
1	A	310	ASP
1	A	322	ASP
1	A	331	ILE
1	A	333	ILE
1	A	337	ASN
1	B	112	TYR

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Mol	Chain	Res	Type
1	B	117	ARG
1	B	160	GLN
1	B	177	ARG
1	B	178	GLU
1	B	179	LEU
1	B	186	VAL
1	B	195	LEU
1	B	203	LEU
1	B	207	GLU
1	B	225	PRO
1	B	249	LEU
1	B	316	LEU
1	B	321	ASP
1	B	322	ASP
1	B	333	ILE
1	B	342	VAL
1	C	112	TYR
1	C	120	LEU
1	C	121	LEU
1	C	131	LEU
1	C	138	ARG
1	C	157	VAL
1	C	171	LYS
1	C	178	GLU
1	C	186	VAL
1	C	225	PRO
1	C	237	GLN
1	C	286	LEU
1	C	299	THR
1	C	303	LEU
1	C	310	ASP
1	C	322	ASP
1	C	326	LEU
1	C	333	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	133	HIS
1	A	142	GLN
1	A	160	GLN
1	A	291	ASN

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Mol	Chain	Res	Type
1	A	337	ASN
1	B	133	HIS
1	B	291	ASN
1	C	133	HIS
1	C	234	ASN
1	C	287	ASN
1	C	291	ASN

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)

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 (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	236/345 (68%)	0.10	1 (0%)	92	86	63, 92, 121, 160	0
1	B	236/345 (68%)	0.12	5 (2%)	63	48	64, 90, 120, 155	0
1	C	228/345 (66%)	0.11	4 (1%)	68	53	72, 102, 181, 195	0
All	All	700/1035 (67%)	0.11	10 (1%)	75	61	63, 95, 145, 195	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	243	SER	2.8
1	C	313	LEU	2.6
1	B	313	LEU	2.5
1	A	229	LEU	2.5
1	B	172	PHE	2.2
1	B	147	ASP	2.2
1	B	325	PHE	2.2
1	C	188	ILE	2.2
1	C	174	VAL	2.1
1	B	149	ILE	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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.