WORLDWIDE PDB PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report (i)

Dec 7, 2023 – 09:53 pm GMT

PDB ID	:	2VH2
Title	:	Crystal structure of cell divison protein FtsQ from Yersinia enterecolitica
Authors	:	van den Ent, F.; Vinkenvleugel, T.; Ind, A.; West, P.; Veprintsev, D.; Nanninga, N.; den Blaauwen, T.; Lowe, J.
Deposited on	:	2007-11-16
Resolution	:	3.40 Å(reported)

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

|		
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
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)	:	2.36

1 Overall quality at a glance ⓘ

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

The reported resolution of this entry is 3.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.

Metric	Percentile Ranks	Value
Rfree		0.279
Clashscore		54
Ramachandran outliers		10.1%
Sidechain outliers		11.4%
RSRZ outliers		2.7%

Worse   *Better*

■ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
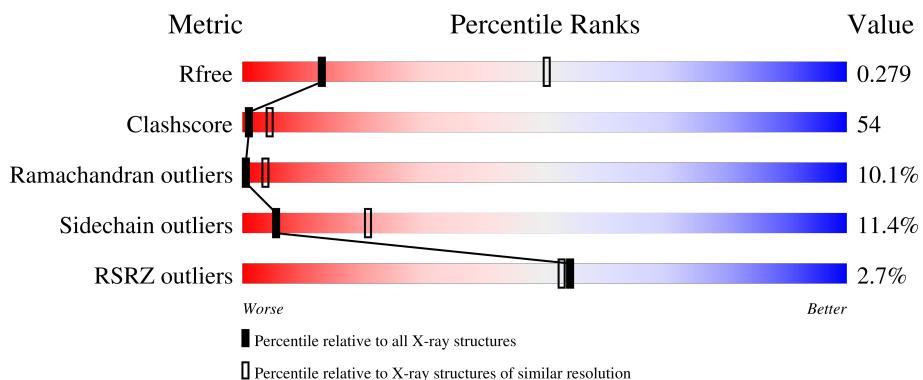
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	130704	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	255	.% 27% 40% 10% · 21%
1	B	255	3% 26% 42% 10% · 21%
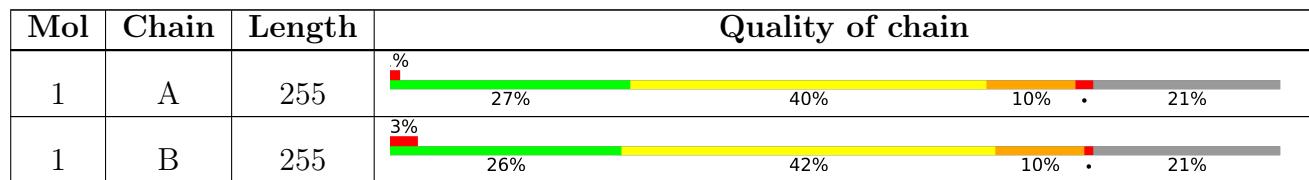
2 Entry composition ⓘ

There is only 1 type of molecule in this entry. The entry contains 3282 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 CELL DIVISION PROTEIN FTSQ.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	202	Total	C	N	O	S	0	0	1
			1639	1042	294	297	6			
1	B	202	Total	C	N	O	S	0	0	1
			1643	1045	297	295	6			

3 Residue-property plots ⓘ

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: CELL DIVISION PROTEIN FTSQ
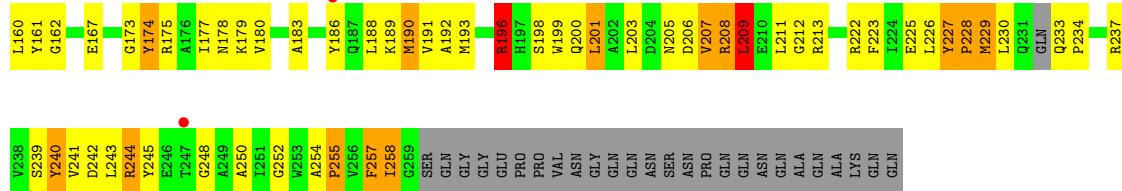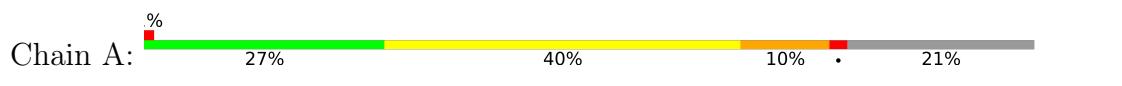
• Molecule 1: CELL DIVISION PROTEIN FTSQ

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 62	Depositor
Cell constants a, b, c, α, β, γ	160.76Å 160.76Å 54.58Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	35.00 – 3.40 35.35 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.4 (35.00-3.40) 99.1 (35.35-3.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.52 (at 3.18Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.277 , 0.323 0.281 , 0.279	Depositor DCC
R_{free} test set	659 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å^2)	135.4	Xtriage
Anisotropy	0.420	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 91.3	EDS
L-test for twinning[2]	$< |L| > = 0.47, < L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.054 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	3282	wwPDB-VP
Average B, all atoms (Å^2)	151.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.73% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	A	0.50	0/1675	0.72	0/2268
1	B	0.47	0/1678	0.68	2/2271 (0.1%)
All	All	0.48	0/3353	0.70	2/4539 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	205	ASN	N-CA-C	-5.76	95.45	111.00
1	B	115	TRP	N-CA-C	5.02	124.56	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1639	0	1638	180	0
1	B	1643	0	1650	183	0
All	All	3282	0	3288	354	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 54.

All (354) 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:245:TYR:HE2	1:A:250:ALA:HB2	1.19	1.04
1:B:104:PRO:HG2	1:B:106:ILE:HD13	1.38	1.03
1:B:71:THR:HB	1:B:74:ASP:OD1	1.59	1.03
1:B:177:ILE:HD11	1:B:216:ARG:NH1	1.71	1.03
1:B:177:ILE:HD11	1:B:216:ARG:HH12	1.17	1.03
1:A:102:ARG:C	1:A:104:PRO:HA	1.80	1.02
1:A:61:LEU:HD11	1:A:76:ARG:HH11	1.29	0.97
1:B:198:SER:HA	1:B:212:GLY:O	1.64	0.96
1:B:88:PHE:CD2	1:B:88:PHE:O	2.18	0.96
1:B:97:GLN:O	1:B:100:ILE:HG22	1.68	0.93
1:B:157:LEU:HD22	1:B:158:PRO:HD2	1.51	0.93
1:A:201:LEU:HD21	1:A:211:LEU:HD23	1.50	0.91
1:A:196:ARG:HB2	1:B:68:HIS:NE2	1.88	0.88
1:A:196:ARG:HB2	1:B:68:HIS:CE1	2.08	0.87
1:B:238:VAL:HG12	1:B:239:SER:H	1.38	0.86
1:B:114:GLN:HB2	1:B:118:GLU:HG3	1.56	0.85
1:A:245:TYR:CE2	1:A:250:ALA:HB2	2.12	0.82
1:B:203:LEU:HB2	1:B:207:VAL:HG12	1.61	0.82
1:B:200:GLN:NE2	1:B:208:ARG:HD2	1.94	0.82
1:B:88:PHE:O	1:B:88:PHE:HD2	1.59	0.81
1:A:61:LEU:CD1	1:A:76:ARG:HH11	1.92	0.81
1:B:61:LEU:HD11	1:B:76:ARG:HH11	1.44	0.80
1:B:101:GLU:O	1:B:103:LEU:N	2.14	0.80
1:B:245:TYR:HE2	1:B:250:ALA:HB2	1.47	0.80
1:A:103:LEU:N	1:A:104:PRO:HA	1.98	0.79
1:A:157:LEU:HD22	1:A:158:PRO:HD2	1.64	0.79
1:B:101:GLU:HG3	1:B:102:ARG:H	1.47	0.79
1:B:71:THR:HG22	1:B:73:ASP:H	1.48	0.78
1:B:104:PRO:HB2	1:B:105:TRP:CE3	2.19	0.78
1:B:114:GLN:HB2	1:B:118:GLU:CG	2.14	0.77
1:B:79:ILE:CD1	1:B:96:ILE:HG23	2.14	0.76
1:B:227:TYR:O	1:B:230:LEU:HG	1.86	0.76
1:B:207:VAL:HG22	1:B:208:ARG:H	1.50	0.76
1:A:198:SER:HA	1:A:212:GLY:O	1.86	0.75
1:B:108:GLN:O	1:B:124:VAL:HG22	1.85	0.75
1:A:245:TYR:HD1	1:B:72:ASN:ND2	1.84	0.75
1:B:130:ALA:HB1	1:B:160:LEU:HD13	1.69	0.74
1:B:88:PHE:O	1:B:89:MET:O	2.07	0.73
1:A:245:TYR:CD1	1:B:72:ASN:ND2	2.57	0.72
1:B:101:GLU:C	1:B:103:LEU:H	1.91	0.72
1:A:79:ILE:HD11	1:A:95:ILE:HD12	1.71	0.72
1:A:104:PRO:HG2	1:A:146:SER:H	1.55	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:71:THR:HB	1:A:74:ASP:OD1	1.90	0.71
1:A:213:ARG:HH12	1:B:152:VAL:HG12	1.54	0.71
1:A:188:LEU:HD21	1:A:190:MET:O	1.90	0.71
1:A:64:THR:CG2	1:A:120:LYS:HE3	2.20	0.71
1:A:89:MET:HG3	1:A:90:THR:N	2.04	0.71
1:A:188:LEU:HD23	1:A:189:LYS:N	2.05	0.70
1:B:79:ILE:HD13	1:B:96:ILE:HG23	1.74	0.70
1:A:239:SER:O	1:A:240:TYR:HB3	1.92	0.69
1:A:208:ARG:HG2	1:A:209:LEU:H	1.56	0.69
1:A:115:TRP:O	1:A:116:PRO:C	2.31	0.69
1:A:188:LEU:HD23	1:A:190:MET:N	2.07	0.69
1:B:100:ILE:HD13	1:B:100:ILE:O	1.93	0.69
1:A:101:GLU:O	1:A:102:ARG:C	2.31	0.68
1:A:186:TYR:HB3	1:A:203:LEU:HD12	1.75	0.68
1:B:97:GLN:HE21	1:B:110:SER:HA	1.58	0.66
1:A:208:ARG:CG	1:A:209:LEU:H	2.07	0.66
1:B:130:ALA:HA	1:B:157:LEU:HD11	1.77	0.66
1:A:132:TRP:CH2	1:A:167:GLU:HA	2.29	0.66
1:B:101:GLU:O	1:B:104:PRO:HD2	1.95	0.66
1:B:104:PRO:CG	1:B:106:ILE:HD13	2.20	0.66
1:B:130:ALA:O	1:B:138:VAL:HG12	1.96	0.66
1:B:188:LEU:HD23	1:B:188:LEU:C	2.16	0.66
1:A:103:LEU:N	1:A:104:PRO:CA	2.59	0.66
1:B:241:VAL:HG12	1:B:243:LEU:CD1	2.25	0.65
1:A:79:ILE:CD1	1:A:95:ILE:HG23	2.25	0.65
1:A:213:ARG:NH1	1:B:152:VAL:HA	2.12	0.65
1:A:257:PHE:HD1	1:A:258:ILE:N	1.94	0.65
1:A:233:GLN:CD	1:A:234:PRO:HD2	2.16	0.65
1:A:188:LEU:HD23	1:A:188:LEU:C	2.17	0.65
1:B:114:GLN:CB	1:B:118:GLU:HG3	2.27	0.65
1:B:61:LEU:CD1	1:B:76:ARG:HH11	2.10	0.65
1:A:61:LEU:N	1:A:61:LEU:HD12	2.12	0.64
1:B:132:TRP:CH2	1:B:167:GLU:HA	2.32	0.64
1:B:101:GLU:HG3	1:B:102:ARG:N	2.13	0.64
1:B:202:ALA:O	1:B:203:LEU:HD12	1.98	0.64
1:B:177:ILE:CD1	1:B:216:ARG:HH12	2.02	0.64
1:B:181:LEU:CD1	1:B:188:LEU:HD12	2.28	0.64
1:B:93:VAL:HG23	1:B:94:ASN:H	1.62	0.63
1:A:61:LEU:CD1	1:A:76:ARG:NH1	2.59	0.63
1:B:180:VAL:O	1:B:183:ALA:HB3	1.99	0.63
1:A:79:ILE:HG23	1:A:80:LEU:N	2.14	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:201:LEU:CD2	1:A:211:LEU:HD23	2.26	0.63
1:A:257:PHE:CD1	1:A:258:ILE:N	2.67	0.63
1:A:233:GLN:OE1	1:A:234:PRO:HD2	1.97	0.63
1:B:138:VAL:HG22	1:B:139:ASP:N	2.14	0.63
1:A:79:ILE:CG2	1:A:80:LEU:N	2.61	0.62
1:B:203:LEU:HD22	1:B:207:VAL:HG11	1.81	0.62
1:B:196:ARG:O	1:B:198:SER:N	2.32	0.61
1:A:205:ASN:HB3	1:A:207:VAL:HG12	1.83	0.61
1:A:62:VAL:O	1:A:120:LYS:HD2	2.01	0.61
1:B:226:LEU:N	1:B:226:LEU:HD12	2.15	0.61
1:B:237:ARG:HG2	1:B:237:ARG:HH21	1.65	0.61
1:A:222:ARG:NH1	1:A:248:GLY:C	2.54	0.61
1:B:241:VAL:HG12	1:B:243:LEU:HD11	1.82	0.61
1:B:79:ILE:HG23	1:B:80:LEU:N	2.16	0.61
1:B:127:VAL:O	1:B:139:ASP:HB3	2.01	0.61
1:A:188:LEU:HD23	1:A:190:MET:H	1.65	0.60
1:B:242:ASP:OD1	1:B:244:ARG:HD2	2.00	0.60
1:A:188:LEU:HD11	1:A:191:VAL:CG2	2.31	0.60
1:B:101:GLU:HG3	1:B:102:ARG:HG3	1.83	0.60
1:A:64:THR:HG21	1:A:120:LYS:HE3	1.84	0.59
1:A:148:PRO:C	1:A:150:GLU:H	2.06	0.59
1:A:188:LEU:CD2	1:A:190:MET:N	2.65	0.59
1:A:203:LEU:HB2	1:A:207:VAL:HG13	1.84	0.59
1:B:82:LEU:N	1:B:82:LEU:HD22	2.17	0.59
1:A:130:ALA:HB1	1:A:160:LEU:HD13	1.85	0.59
1:A:159:LEU:C	1:A:160:LEU:HD12	2.23	0.59
1:A:130:ALA:CA	1:A:157:LEU:HD11	2.33	0.59
1:B:130:ALA:CA	1:B:157:LEU:HD11	2.33	0.59
1:B:200:GLN:HE21	1:B:208:ARG:HD2	1.68	0.59
1:A:100:ILE:HG13	1:A:109:ALA:H	1.69	0.58
1:B:129:PHE:C	1:B:157:LEU:HD21	2.24	0.58
1:B:93:VAL:HG23	1:B:94:ASN:N	2.19	0.58
1:A:64:THR:HG23	1:A:120:LYS:HE3	1.86	0.58
1:A:227:TYR:O	1:A:229:MET:N	2.37	0.58
1:A:102:ARG:HB3	1:A:104:PRO:HA	1.86	0.57
1:B:138:VAL:HG23	1:B:143:ARG:O	2.04	0.57
1:B:190:MET:SD	1:B:191:VAL:N	2.77	0.57
1:B:152:VAL:HG23	1:B:153:GLY:H	1.68	0.57
1:A:227:TYR:C	1:A:229:MET:H	2.08	0.57
1:A:245:TYR:HE2	1:A:250:ALA:CB	2.07	0.57
1:A:245:TYR:HD1	1:B:72:ASN:HD21	1.53	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:94:ASN:O	1:B:98:GLN:HB2	2.04	0.57
1:A:152:VAL:HG23	1:A:153:GLY:H	1.69	0.57
1:B:205:ASN:O	1:B:207:VAL:N	2.38	0.57
1:A:203:LEU:N	1:A:203:LEU:HD22	2.20	0.57
1:B:223:PHE:CE1	1:B:227:TYR:HB2	2.40	0.57
1:A:98:GLN:O	1:A:101:GLU:HB3	2.05	0.56
1:A:71:THR:HG22	1:A:73:ASP:H	1.70	0.56
1:A:86:GLY:O	1:A:88:PHE:N	2.39	0.56
1:B:103:LEU:HB2	1:B:104:PRO:CD	2.34	0.56
1:A:96:ILE:O	1:A:98:GLN:N	2.39	0.56
1:B:205:ASN:O	1:B:205:ASN:OD1	2.23	0.56
1:A:156:LYS:HE2	1:A:156:LYS:HA	1.85	0.56
1:B:148:PRO:C	1:B:150:GLU:H	2.09	0.56
1:A:127:VAL:O	1:A:139:ASP:HB3	2.06	0.56
1:A:201:LEU:HD23	1:A:201:LEU:N	2.21	0.56
1:A:223:PHE:HE1	1:A:241:VAL:HG21	1.70	0.56
1:B:138:VAL:HG22	1:B:139:ASP:H	1.71	0.56
1:B:200:GLN:HE21	1:B:208:ARG:CG	2.19	0.56
1:A:102:ARG:H	1:A:102:ARG:HD3	1.71	0.55
1:B:123:LEU:HD12	1:B:123:LEU:O	2.07	0.55
1:B:130:ALA:HA	1:B:157:LEU:CD1	2.36	0.55
1:A:180:VAL:O	1:A:183:ALA:HB3	2.07	0.55
1:A:226:LEU:HD12	1:A:226:LEU:H	1.71	0.55
1:B:106:ILE:N	1:B:106:ILE:HD12	2.21	0.55
1:B:199:TRP:NE1	1:B:216:ARG:HD3	2.21	0.55
1:B:215:ASP:OD2	1:B:218:GLY:HA3	2.05	0.55
1:B:97:GLN:NE2	1:B:110:SER:HA	2.21	0.55
1:A:95:ILE:O	1:A:96:ILE:O	2.25	0.55
1:A:130:ALA:HA	1:A:157:LEU:CD1	2.36	0.55
1:B:157:LEU:HD22	1:B:158:PRO:CD	2.33	0.55
1:A:100:ILE:HD11	1:A:108:GLN:HA	1.89	0.55
1:A:213:ARG:NH1	1:B:152:VAL:HG12	2.22	0.55
1:A:130:ALA:HA	1:A:157:LEU:HD11	1.89	0.54
1:A:63:VAL:HA	1:A:121:ILE:O	2.08	0.54
1:B:217:MET:O	1:B:220:LEU:HB3	2.07	0.54
1:B:79:ILE:CG2	1:B:80:LEU:N	2.70	0.54
1:A:100:ILE:O	1:A:102:ARG:N	2.40	0.54
1:A:92:ASP:C	1:A:94:ASN:N	2.60	0.54
1:A:82:LEU:N	1:A:82:LEU:HD22	2.23	0.54
1:A:98:GLN:O	1:A:101:GLU:N	2.38	0.54
1:B:61:LEU:HD12	1:B:61:LEU:N	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:98:GLN:O	1:A:101:GLU:CB	2.55	0.54
1:A:111:VAL:HG13	1:A:121:ILE:HG13	1.90	0.54
1:A:84:ALA:HB1	1:A:89:MET:SD	2.48	0.54
1:A:124:VAL:O	1:A:124:VAL:HG23	2.07	0.53
1:A:188:LEU:HD11	1:A:191:VAL:HG22	1.90	0.53
1:A:173:GLY:C	1:A:177:ILE:HD12	2.28	0.53
1:B:71:THR:HG22	1:B:73:ASP:N	2.22	0.53
1:A:75:ILE:HG12	1:A:99:GLN:OE1	2.08	0.53
1:B:188:LEU:HD23	1:B:190:MET:N	2.23	0.53
1:A:76:ARG:O	1:A:79:ILE:HG22	2.08	0.53
1:B:199:TRP:CD1	1:B:216:ARG:HD3	2.43	0.53
1:B:185:LYS:O	1:B:185:LYS:HG2	2.09	0.53
1:B:139:ASP:O	1:B:142:GLY:N	2.41	0.53
1:B:61:LEU:CD1	1:B:76:ARG:NH1	2.71	0.52
1:B:112:ARG:HG2	1:B:120:LYS:HB3	1.91	0.52
1:A:208:ARG:HG2	1:A:209:LEU:N	2.25	0.52
1:B:156:LYS:HE2	1:B:156:LYS:HA	1.91	0.52
1:A:208:ARG:CG	1:A:209:LEU:N	2.72	0.52
1:B:238:VAL:HG12	1:B:239:SER:N	2.15	0.52
1:B:245:TYR:HB2	1:B:248:GLY:O	2.10	0.52
1:B:79:ILE:HD13	1:B:96:ILE:CG2	2.39	0.52
1:B:225:GLU:O	1:B:228:PRO:HD2	2.10	0.52
1:A:173:GLY:O	1:A:177:ILE:HD12	2.10	0.51
1:A:175:ARG:HG3	1:A:175:ARG:HH21	1.76	0.51
1:A:174:TYR:CE2	1:A:178:ASN:HB2	2.45	0.51
1:B:173:GLY:O	1:B:174:TYR:C	2.48	0.51
1:B:200:GLN:HE22	1:B:208:ARG:HD2	1.70	0.51
1:B:71:THR:O	1:B:74:ASP:N	2.43	0.51
1:B:188:LEU:HD21	1:B:190:MET:O	2.11	0.51
1:A:188:LEU:HD21	1:A:190:MET:C	2.30	0.51
1:A:188:LEU:CD2	1:A:190:MET:H	2.23	0.51
1:B:111:VAL:HG13	1:B:121:ILE:CD1	2.41	0.51
1:A:160:LEU:HD21	1:A:174:TYR:HD1	1.75	0.50
1:B:127:VAL:O	1:B:139:ASP:CB	2.58	0.50
1:A:100:ILE:CG1	1:A:108:GLN:HA	2.41	0.50
1:A:102:ARG:HB3	1:A:104:PRO:CA	2.41	0.50
1:A:119:LEU:O	1:A:121:ILE:HD12	2.11	0.50
1:B:160:LEU:HD11	1:B:174:TYR:CD1	2.47	0.50
1:B:209:LEU:N	1:B:209:LEU:CD1	2.74	0.50
1:A:101:GLU:O	1:A:102:ARG:O	2.29	0.50
1:A:92:ASP:C	1:A:94:ASN:H	2.14	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:ILE:CG2	1:A:80:LEU:H	2.24	0.49
1:B:114:GLN:HG3	1:B:118:GLU:HG3	1.94	0.49
1:A:227:TYR:CE1	1:A:230:LEU:HD11	2.47	0.49
1:A:81:SER:HB2	1:A:98:GLN:NE2	2.28	0.49
1:A:94:ASN:O	1:A:97:GLN:HB3	2.13	0.49
1:B:174:TYR:C	1:B:174:TYR:CD2	2.86	0.49
1:B:200:GLN:HE21	1:B:208:ARG:CD	2.26	0.49
1:A:203:LEU:N	1:A:203:LEU:CD2	2.76	0.49
1:B:76:ARG:O	1:B:79:ILE:HG22	2.13	0.48
1:A:127:VAL:O	1:A:127:VAL:HG13	2.12	0.48
1:B:207:VAL:HG22	1:B:208:ARG:N	2.22	0.48
1:A:79:ILE:HD13	1:A:95:ILE:HG23	1.96	0.48
1:B:243:LEU:N	1:B:243:LEU:HD12	2.28	0.48
1:A:174:TYR:CD2	1:A:178:ASN:HB2	2.49	0.48
1:B:196:ARG:HB3	1:B:213:ARG:NH1	2.29	0.48
1:A:174:TYR:CD2	1:A:174:TYR:C	2.88	0.48
1:B:221:GLN:O	1:B:224:ILE:CG1	2.62	0.48
1:B:241:VAL:HG12	1:B:243:LEU:HD12	1.95	0.48
1:B:237:ARG:HG2	1:B:237:ARG:NH2	2.28	0.47
1:B:104:PRO:HB2	1:B:105:TRP:CZ3	2.49	0.47
1:B:114:GLN:HB2	1:B:118:GLU:HG2	1.94	0.47
1:B:251:ILE:HG22	1:B:252:GLY:N	2.29	0.47
1:A:79:ILE:HD11	1:A:95:ILE:CD1	2.43	0.47
1:B:174:TYR:CE2	1:B:178:ASN:HB2	2.50	0.47
1:A:72:ASN:O	1:A:75:ILE:HB	2.15	0.47
1:A:127:VAL:O	1:A:139:ASP:CB	2.62	0.47
1:A:75:ILE:O	1:A:78:ALA:N	2.33	0.47
1:A:95:ILE:O	1:A:96:ILE:C	2.52	0.47
1:B:101:GLU:CG	1:B:102:ARG:H	2.12	0.47
1:B:254:ALA:HA	1:B:255:PRO:HD3	1.58	0.47
1:B:103:LEU:HB2	1:B:104:PRO:HD3	1.96	0.47
1:A:92:ASP:HB2	1:A:111:VAL:HB	1.97	0.46
1:A:148:PRO:O	1:A:150:GLU:N	2.42	0.46
1:B:245:TYR:HE2	1:B:250:ALA:CB	2.22	0.46
1:B:257:PHE:H	1:B:257:PHE:HD2	1.62	0.46
1:B:241:VAL:O	1:B:243:LEU:CD1	2.63	0.46
1:A:160:LEU:HA	1:A:191:VAL:O	2.14	0.46
1:A:96:ILE:O	1:A:97:GLN:C	2.53	0.46
1:A:174:TYR:HE2	1:A:178:ASN:CG	2.19	0.46
1:B:181:LEU:HD12	1:B:188:LEU:HD12	1.98	0.46
1:B:227:TYR:HB3	1:B:228:PRO:HD3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:60:LYS:C	1:B:61:LEU:HD12	2.36	0.46
1:B:132:TRP:O	1:B:160:LEU:O	2.34	0.46
1:B:242:ASP:C	1:B:243:LEU:HD12	2.36	0.46
1:A:160:LEU:HD11	1:A:174:TYR:CD1	2.51	0.46
1:A:227:TYR:C	1:A:229:MET:N	2.69	0.46
1:A:226:LEU:HD12	1:A:226:LEU:N	2.30	0.46
1:A:254:ALA:HA	1:A:255:PRO:HD3	1.66	0.46
1:B:226:LEU:N	1:B:226:LEU:CD1	2.78	0.46
1:A:91:GLN:HE21	1:A:91:GLN:HB2	1.56	0.45
1:B:152:VAL:HG23	1:B:153:GLY:N	2.30	0.45
1:A:188:LEU:C	1:A:188:LEU:CD2	2.85	0.45
1:A:201:LEU:HD21	1:A:211:LEU:CD2	2.34	0.45
1:B:174:TYR:CD2	1:B:178:ASN:HB2	2.52	0.45
1:A:60:LYS:C	1:A:61:LEU:HD12	2.37	0.45
1:A:121:ILE:HD12	1:A:121:ILE:N	2.32	0.45
1:B:220:LEU:O	1:B:221:GLN:C	2.55	0.45
1:A:92:ASP:HA	1:A:95:ILE:HG12	1.99	0.44
1:A:103:LEU:HD12	1:A:106:ILE:HD13	1.99	0.44
1:B:63:VAL:HG13	1:B:121:ILE:HG22	1.98	0.44
1:A:227:TYR:H	1:A:228:PRO:CD	2.29	0.44
1:A:152:VAL:HG23	1:A:153:GLY:N	2.33	0.44
1:B:101:GLU:CD	1:B:108:GLN:HA	2.38	0.44
1:B:129:PHE:O	1:B:157:LEU:HD21	2.17	0.44
1:B:209:LEU:HD21	1:B:223:PHE:CE2	2.53	0.44
1:A:207:VAL:O	1:A:207:VAL:HG22	2.17	0.44
1:A:114:GLN:HB3	1:A:116:PRO:HD2	1.99	0.44
1:A:148:PRO:C	1:A:150:GLU:N	2.69	0.44
1:A:92:ASP:HA	1:A:95:ILE:CG1	2.48	0.43
1:A:102:ARG:CA	1:A:104:PRO:HA	2.45	0.43
1:B:175:ARG:HH21	1:B:175:ARG:HG3	1.83	0.43
1:A:243:LEU:C	1:A:245:TYR:H	2.21	0.43
1:B:59:SER:HB3	1:B:117:ASP:O	2.18	0.43
1:A:139:ASP:O	1:A:142:GLY:N	2.50	0.43
1:A:173:GLY:O	1:A:174:TYR:C	2.57	0.43
1:A:257:PHE:CD1	1:A:257:PHE:C	2.92	0.43
1:B:115:TRP:O	1:B:116:PRO:C	2.54	0.43
1:B:221:GLN:O	1:B:224:ILE:HG12	2.19	0.43
1:B:226:LEU:CD1	1:B:226:LEU:H	2.32	0.43
1:A:82:LEU:HD21	1:A:98:GLN:NE2	2.33	0.43
1:A:162:GLY:HA2	1:A:193:MET:O	2.18	0.43
1:B:121:ILE:HG22	1:B:121:ILE:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:73:ASP:C	1:A:75:ILE:N	2.70	0.43
1:A:223:PHE:CE1	1:A:241:VAL:HG21	2.52	0.43
1:B:114:GLN:CG	1:B:118:GLU:HG3	2.49	0.43
1:B:171:LEU:O	1:B:172:GLU:C	2.57	0.43
1:B:174:TYR:HD2	1:B:174:TYR:O	2.01	0.43
1:B:188:LEU:HD21	1:B:191:VAL:HG23	2.01	0.43
1:A:91:GLN:CG	1:A:93:VAL:HG23	2.49	0.42
1:B:71:THR:O	1:B:74:ASP:HB2	2.18	0.42
1:B:106:ILE:N	1:B:106:ILE:CD1	2.82	0.42
1:A:196:ARG:NE	1:B:68:HIS:CE1	2.87	0.42
1:A:201:LEU:HD23	1:A:209:LEU:O	2.19	0.42
1:B:111:VAL:HG13	1:B:121:ILE:HD11	2.00	0.42
1:B:159:LEU:C	1:B:160:LEU:HD12	2.39	0.42
1:A:132:TRP:HB3	1:A:136:HIS:HB3	2.01	0.42
1:A:156:LYS:HE2	1:A:156:LYS:CA	2.50	0.42
1:B:132:TRP:HB3	1:B:136:HIS:HB3	2.00	0.42
1:A:222:ARG:O	1:A:223:PHE:C	2.57	0.42
1:B:207:VAL:HG13	1:B:208:ARG:N	2.34	0.42
1:B:103:LEU:CB	1:B:104:PRO:CD	2.98	0.42
1:A:200:GLN:C	1:A:201:LEU:HD23	2.40	0.42
1:B:105:TRP:O	1:B:126:TYR:HD1	2.02	0.42
1:B:245:TYR:CE2	1:B:250:ALA:HB2	2.39	0.42
1:B:101:GLU:C	1:B:103:LEU:N	2.62	0.42
1:A:95:ILE:HG12	1:A:95:ILE:H	1.66	0.42
1:B:199:TRP:CE2	1:B:216:ARG:HD3	2.55	0.42
1:A:97:GLN:CA	1:A:100:ILE:HG22	2.50	0.41
1:A:102:ARG:CB	1:A:104:PRO:HA	2.50	0.41
1:A:161:TYR:HB2	1:A:192:ALA:CB	2.50	0.41
1:B:93:VAL:O	1:B:95:ILE:N	2.53	0.41
1:B:188:LEU:C	1:B:188:LEU:CD2	2.87	0.41
1:B:238:VAL:HG13	1:B:251:ILE:HG23	2.03	0.41
1:B:177:ILE:O	1:B:178:ASN:C	2.56	0.41
1:A:114:GLN:C	1:A:116:PRO:HD2	2.40	0.41
1:A:129:PHE:HB3	1:A:139:ASP:HA	2.02	0.41
1:A:199:TRP:CD1	1:A:199:TRP:N	2.89	0.41
1:B:101:GLU:CD	1:B:109:ALA:H	2.23	0.41
1:A:59:SER:HB3	1:A:88:PHE:CE1	2.56	0.41
1:A:75:ILE:O	1:A:76:ARG:C	2.59	0.41
1:A:239:SER:O	1:A:240:TYR:CB	2.65	0.41
1:B:203:LEU:HD22	1:B:207:VAL:CG1	2.50	0.41
1:B:138:VAL:CG2	1:B:139:ASP:N	2.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:220:LEU:O	1:B:222:ARG:N	2.54	0.41
1:A:69:TYR:HD2	1:A:125:GLU:OE2	2.04	0.41
1:A:91:GLN:O	1:A:94:ASN:HB3	2.21	0.41
1:A:138:VAL:HG22	1:A:139:ASP:N	2.35	0.41
1:A:205:ASN:C	1:A:207:VAL:H	2.24	0.41
1:B:173:GLY:O	1:B:176:ALA:N	2.54	0.41
1:B:194:SER:O	1:B:195:ALA:C	2.59	0.41
1:B:240:TYR:CD1	1:B:240:TYR:C	2.95	0.41
1:A:111:VAL:CG1	1:A:119:LEU:HD22	2.51	0.41
1:A:64:THR:OG1	1:A:122:HIS:CD2	2.74	0.40
1:A:240:TYR:CZ	1:A:252:GLY:HA3	2.56	0.40
1:B:226:LEU:HD12	1:B:226:LEU:H	1.83	0.40
1:A:79:ILE:HG22	1:A:80:LEU:H	1.87	0.40
1:B:111:VAL:HG13	1:B:121:ILE:HD12	2.03	0.40
1:B:240:TYR:CE2	1:B:252:GLY:HA3	2.57	0.40
1:A:242:ASP:OD1	1:A:244:ARG:HD2	2.22	0.40
1:A:132:TRP:O	1:A:160:LEU:O	2.39	0.40
1:A:139:ASP:O	1:A:140:GLU:C	2.59	0.40
1:B:147:VAL:HA	1:B:148:PRO:HD3	1.96	0.40
1:B:196:ARG:HD3	1:B:213:ARG:HH12	1.87	0.40
1:A:81:SER:HB2	1:A:98:GLN:HE21	1.85	0.40
1:A:178:ASN:O	1:A:179:LYS:C	2.60	0.40
1:B:69:TYR:HB2	1:B:105:TRP:NE1	2.37	0.40
1:B:150:GLU:HB3	1:B:151:ARG:H	1.62	0.40
1:B:160:LEU:HD12	1:B:160:LEU:N	2.37	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	198/255 (78%)	129 (65%)	50 (25%)	19 (10%)	0	4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	198/255 (78%)	134 (68%)	43 (22%)	21 (11%)	0	3
All	All	396/510 (78%)	263 (66%)	93 (24%)	40 (10%)	0	4

All (40) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	87	THR
1	A	96	ILE
1	A	97	GLN
1	A	117	ASP
1	A	227	TYR
1	B	88	PHE
1	B	89	MET
1	B	100	ILE
1	B	102	ARG
1	B	104	PRO
1	B	197	HIS
1	B	206	ASP
1	A	102	ARG
1	A	208	ARG
1	B	67	ARG
1	B	101	GLU
1	B	216	ARG
1	A	98	GLN
1	A	101	GLU
1	A	149	SER
1	A	209	LEU
1	A	225	GLU
1	A	228	PRO
1	A	240	TYR
1	A	244	ARG
1	B	94	ASN
1	B	117	ASP
1	B	185	LYS
1	B	149	SER
1	B	150	GLU
1	A	103	LEU
1	B	214	ASP
1	A	147	VAL
1	A	196	ARG
1	B	83	GLY
1	B	239	SER

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Mol	Chain	Res	Type
1	A	255	PRO
1	B	116	PRO
1	B	147	VAL
1	B	238	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	176/220 (80%)	153 (87%)	23 (13%)	4	15
1	B	176/220 (80%)	159 (90%)	17 (10%)	8	28
All	All	352/440 (80%)	312 (89%)	40 (11%)	5	21

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	90	THR
1	A	91	GLN
1	A	93	VAL
1	A	97	GLN
1	A	100	ILE
1	A	102	ARG
1	A	107	GLN
1	A	119	LEU
1	A	123	LEU
1	A	136	HIS
1	A	149	SER
1	A	156	LYS
1	A	174	TYR
1	A	190	MET
1	A	196	ARG
1	A	201	LEU
1	A	206	ASP
1	A	207	VAL
1	A	209	LEU

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Mol	Chain	Res	Type
1	A	229	MET
1	A	237	ARG
1	A	257	PHE
1	A	258	ILE
1	B	74	ASP
1	B	88	PHE
1	B	98	GLN
1	B	100	ILE
1	B	107	GLN
1	B	136	HIS
1	B	137	MET
1	B	149	SER
1	B	156	LYS
1	B	174	TYR
1	B	190	MET
1	B	201	LEU
1	B	204	ASP
1	B	236	LYS
1	B	240	TYR
1	B	251	ILE
1	B	257	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	68	HIS
1	A	98	GLN
1	A	114	GLN
1	A	122	HIS
1	A	221	GLN
1	B	72	ASN
1	B	97	GLN
1	B	114	GLN
1	B	200	GLN
1	B	221	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 monosaccharides 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, 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	202/255 (79%)	0.15	3 (1%)	73	72	91, 149, 192, 199	0
1	B	202/255 (79%)	0.12	8 (3%)	38	37	98, 154, 192, 199	0
All	All	404/510 (79%)	0.14	11 (2%)	54	53	91, 152, 192, 199	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	232	GLN	4.8
1	B	231	GLN	4.1
1	B	56	LEU	3.1
1	B	87	THR	2.5
1	A	186	TYR	2.4
1	A	247	THR	2.4
1	A	104	PRO	2.4
1	B	102	ARG	2.3
1	B	55	ARG	2.1
1	B	195	ALA	2.0
1	B	65	GLY	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.