



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:56 AM UTC

PDB ID : 1XGM / pdb_00001xgm
Title : METHIONINE AMINOPEPTIDASE FROM HYPERTHERMOPHILE PY-
ROCOCCUS FURIOSUS
Authors : Tahirov, T.H.; Tsukihara, T.
Deposited on : 1997-11-17
Resolution : 2.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

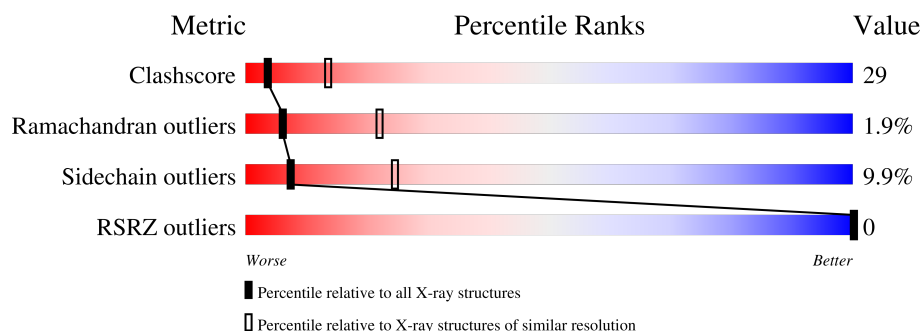
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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))
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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 $\leq 5\%$. 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	295	44% 44% 10% .
1	B	295	46% 43% 9% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4638 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 METHIONINE AMINOPEPTIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	295	Total	C	N	O	S	0	0	0
			2312	1490	390	423	9			
1	B	295	Total	C	N	O	S	0	0	0
			2312	1490	390	423	9			

- Molecule 2 is COBALT (II) ION (CCD ID: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Co	0	0
			2	2		
2	B	2	Total	Co	0	0
			2	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	5	Total	O	0	0
			5	5		
3	B	5	Total	O	0	0
			5	5		

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	53.38Å 85.06Å 72.70Å 90.00° 107.71° 90.00°	Depositor
Resolution (Å)	15.00 – 2.80 15.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	76.0 (15.00-2.80) 79.4 (15.00-2.80)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.35 (at 2.81Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.181 , 0.263 0.183 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	59.9	Xtriage
Anisotropy	0.426	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.16 , 56.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4638	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.70% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

5.1 Standard geometry

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

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	0.88	2/2353 (0.1%)	1.25	26/3176 (0.8%)
1	B	0.87	2/2353 (0.1%)	1.22	20/3176 (0.6%)
All	All	0.87	4/4706 (0.1%)	1.23	46/6352 (0.7%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	12	ILE	CA-CB	-6.07	1.47	1.54
1	B	96	VAL	CA-CB	-5.50	1.47	1.55
1	A	16	VAL	CA-CB	-5.30	1.48	1.54
1	B	134	ALA	CA-CB	-5.04	1.45	1.53

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	217	ALA	N-CA-C	10.36	122.26	110.97
1	B	162	ALA	N-CA-C	7.91	122.56	113.15
1	B	271	ILE	N-CA-C	7.57	117.69	110.42
1	B	237	TYR	N-CA-C	-7.25	103.38	111.28
1	A	228	ARG	N-CA-C	7.24	119.25	111.36
1	A	166	ILE	CA-C-N	7.08	128.69	119.84
1	A	166	ILE	C-N-CA	7.08	128.69	119.84
1	A	32	GLU	N-CA-C	-6.57	104.04	111.07
1	A	162	ALA	N-CA-C	6.26	120.60	113.15
1	A	271	ILE	N-CA-C	6.22	116.70	110.23
1	B	91	ILE	N-CA-C	6.21	116.82	110.05
1	B	56	ILE	N-CA-C	6.20	116.85	108.17
1	B	168	ASN	N-CA-C	-6.19	105.67	112.72
1	B	57	ASN	CB-CA-C	-6.13	109.50	116.54
1	A	91	ILE	N-CA-C	6.05	116.65	110.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	294	THR	N-CA-C	5.97	119.32	112.57
1	B	37	ILE	CB-CA-C	-5.96	104.25	111.88
1	B	265	TYR	CA-C-N	5.93	127.25	119.84
1	B	265	TYR	C-N-CA	5.93	127.25	119.84
1	B	228	ARG	N-CA-C	5.89	118.66	111.82
1	A	9	ALA	N-CA-C	-5.88	104.78	111.07
1	A	92	ALA	N-CA-C	-5.83	97.46	107.61
1	A	99	ARG	N-CA-C	-5.76	99.74	108.67
1	B	40	MET	N-CA-C	-5.75	104.70	110.97
1	A	177	VAL	N-CA-C	5.74	116.11	107.80
1	A	56	ILE	N-CA-C	5.72	116.34	107.99
1	A	168	ASN	N-CA-C	-5.71	106.20	112.72
1	B	176	TYR	N-CA-C	-5.63	102.56	110.50
1	B	131	LEU	N-CA-C	-5.61	105.07	111.07
1	B	209	VAL	N-CA-C	5.43	120.64	109.34
1	A	140	ARG	N-CA-C	5.43	117.28	111.36
1	A	233	LEU	CA-C-N	5.35	125.25	119.85
1	A	233	LEU	C-N-CA	5.35	125.25	119.85
1	A	57	ASN	CB-CA-C	-5.30	110.44	116.54
1	A	37	ILE	CB-CA-C	-5.25	105.16	111.88
1	A	40	MET	N-CA-C	-5.18	105.33	110.97
1	B	150	LEU	N-CA-C	-5.18	100.96	109.40
1	A	66	TYR	N-CA-C	-5.15	101.25	109.23
1	A	265	TYR	CA-C-N	5.14	126.27	119.84
1	A	265	TYR	C-N-CA	5.14	126.27	119.84
1	A	225	LYS	N-CA-C	-5.14	104.61	111.24
1	B	9	ALA	N-CA-C	-5.08	105.64	111.07
1	B	171	ARG	CA-C-N	5.07	126.18	119.84
1	B	171	ARG	C-N-CA	5.07	126.18	119.84
1	A	288	ASP	N-CA-C	5.07	119.56	113.17
1	A	241	GLN	N-CA-C	5.06	118.94	112.87

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	2312	0	2407	135	0
1	B	2312	0	2407	144	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
All	All	4638	0	4814	276	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 29.

All (276) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:207:MET:HB2	1:B:265:TYR:HE2	1.27	0.99
1:A:133:LYS:HG2	1:A:137:ASN:HD21	1.36	0.91
1:A:86:HIS:HD2	1:A:89:GLY:H	1.19	0.91
1:A:208:TYR:HA	1:A:262:ILE:HG22	1.57	0.87
1:B:86:HIS:HD2	1:B:89:GLY:H	1.18	0.87
1:B:223:LEU:HB2	1:B:256:LEU:HD21	1.56	0.86
1:B:224:ALA:HA	1:B:227:LYS:HD3	1.60	0.83
1:A:66:TYR:HA	1:A:238:ARG:HB2	1.62	0.81
1:B:208:TYR:HA	1:B:262:ILE:HG22	1.64	0.80
1:B:133:LYS:HG2	1:B:137:ASN:HD21	1.47	0.79
1:A:242:ASN:H	1:A:242:ASN:HD22	1.30	0.78
1:B:209:VAL:HG13	1:B:262:ILE:HA	1.67	0.77
1:A:238:ARG:HH11	1:A:238:ARG:HG2	1.48	0.77
1:A:86:HIS:HD2	1:A:89:GLY:N	1.83	0.76
1:A:149:ASN:HB2	1:B:171:ARG:HA	1.69	0.75
1:B:25:ARG:O	1:B:28:MET:HB2	1.88	0.74
1:B:86:HIS:HD2	1:B:89:GLY:N	1.84	0.73
1:B:99:ARG:HG3	1:B:99:ARG:HH11	1.53	0.73
1:B:207:MET:HB2	1:B:265:TYR:CE2	2.18	0.72
1:A:242:ASN:H	1:A:242:ASN:ND2	1.84	0.72
1:B:230:TYR:HE2	1:B:240:LEU:HD21	1.54	0.71
1:B:178:LEU:HB3	1:B:285:VAL:HG11	1.71	0.70
1:A:99:ARG:HH11	1:A:99:ARG:HG3	1.56	0.70
1:B:150:LEU:HD13	1:B:189:PHE:CZ	2.26	0.70
1:B:256:LEU:HB3	1:B:262:ILE:HG12	1.74	0.69
1:A:150:LEU:HD13	1:A:189:PHE:CZ	2.26	0.69
1:B:37:ILE:HG21	1:B:52:VAL:HG21	1.74	0.69
1:A:212:VAL:CG1	1:A:261:ALA:HB2	2.23	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:ASP:HB3	1:A:4:GLU:HG2	1.74	0.68
1:B:2:ASP:HB3	1:B:4:GLU:HG2	1.76	0.68
1:A:17:ARG:O	1:A:21:ILE:HD12	1.94	0.68
1:B:244:MET:HB2	1:B:245:PRO:HD2	1.76	0.67
1:A:186:ILE:HD11	1:A:283:ILE:HD13	1.75	0.67
1:A:25:ARG:O	1:A:28:MET:HB2	1.96	0.66
1:A:84:GLY:HA2	1:A:92:ALA:O	1.97	0.65
1:A:145:LYS:HE3	1:A:145:LYS:N	2.11	0.65
1:B:223:LEU:HA	1:B:226:ILE:HD12	1.79	0.65
1:A:242:ASN:HD22	1:A:242:ASN:N	1.92	0.65
1:B:33:LEU:O	1:B:37:ILE:HG12	1.97	0.64
1:B:29:LEU:HD22	1:B:31:LEU:H	1.62	0.64
1:A:86:HIS:CD2	1:A:89:GLY:H	2.10	0.63
1:A:222:LEU:HD21	1:A:253:LEU:HD23	1.79	0.63
1:A:155:ILE:HB	1:A:183:VAL:CG1	2.28	0.63
1:A:20:ALA:HB2	1:A:37:ILE:HD12	1.80	0.62
1:B:222:LEU:HD23	1:B:256:LEU:HD12	1.81	0.62
1:B:222:LEU:HD23	1:B:256:LEU:CD1	2.29	0.62
1:A:94:THR:HB	1:A:294:THR:HG21	1.81	0.62
1:A:269:LYS:HE3	1:A:273:ASN:OD1	2.00	0.61
1:A:50:PHE:CE1	1:A:84:GLY:HA3	2.36	0.61
1:A:212:VAL:O	1:A:214:VAL:HG23	2.01	0.61
1:B:50:PHE:CE1	1:B:84:GLY:HA3	2.36	0.61
1:B:94:THR:HB	1:B:294:THR:HG21	1.82	0.61
1:A:244:MET:HG3	1:A:249:LEU:HB2	1.82	0.61
1:A:37:ILE:HG21	1:A:52:VAL:HG21	1.83	0.61
1:B:20:ALA:HB2	1:B:37:ILE:HD12	1.83	0.61
1:B:91:ILE:HG22	1:B:92:ALA:N	2.15	0.61
1:B:207:MET:CB	1:B:265:TYR:HE2	2.08	0.61
1:B:29:LEU:HD23	1:B:71:THR:O	2.00	0.60
1:B:269:LYS:HE3	1:B:273:ASN:OD1	2.01	0.60
1:A:285:VAL:HA	1:A:290:VAL:HG12	1.83	0.60
1:B:155:ILE:HB	1:B:183:VAL:CG1	2.32	0.60
1:A:128:ILE:HD12	1:A:166:ILE:HG12	1.83	0.60
1:B:115:LEU:O	1:B:119:ILE:HD12	2.02	0.59
1:A:187:GLU:HB2	1:A:280:GLU:HB2	1.84	0.59
1:B:84:GLY:HA2	1:B:92:ALA:O	2.02	0.59
1:B:66:TYR:HA	1:B:238:ARG:HB2	1.83	0.59
1:B:209:VAL:HG22	1:B:261:ALA:O	2.02	0.59
1:A:171:ARG:HA	1:B:149:ASN:HB2	1.85	0.59
1:A:178:LEU:HB3	1:A:285:VAL:HG11	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:225:LYS:O	1:B:228:ARG:HG3	2.02	0.59
1:B:224:ALA:HA	1:B:227:LYS:CD	2.30	0.59
1:A:3:THR:O	1:A:7:MET:HG2	2.02	0.59
1:B:223:LEU:HB2	1:B:256:LEU:CD2	2.28	0.59
1:B:285:VAL:HA	1:B:290:VAL:HG12	1.85	0.58
1:B:91:ILE:N	1:B:91:ILE:HD12	2.18	0.58
1:B:29:LEU:HA	1:B:72:VAL:HG12	1.84	0.58
1:B:31:LEU:HD12	1:B:31:LEU:O	2.04	0.58
1:B:212:VAL:CG1	1:B:261:ALA:HB2	2.34	0.58
1:A:219:ALA:O	1:A:222:LEU:HB3	2.04	0.57
1:B:154:LYS:HB2	1:B:184:PHE:CE1	2.40	0.57
1:B:223:LEU:O	1:B:226:ILE:HB	2.04	0.57
1:A:150:LEU:HD13	1:A:189:PHE:CE1	2.39	0.57
1:A:16:VAL:CG1	1:A:37:ILE:HG23	2.35	0.57
1:A:244:MET:HB2	1:A:245:PRO:HD2	1.87	0.57
1:A:33:LEU:O	1:A:37:ILE:HG12	2.05	0.57
1:B:187:GLU:HB2	1:B:280:GLU:HB2	1.87	0.56
1:A:191:THR:HG21	1:A:195:GLY:HA2	1.88	0.56
1:B:254:LYS:O	1:B:257:GLU:N	2.38	0.56
1:A:91:ILE:HG22	1:A:92:ALA:N	2.18	0.56
1:B:16:VAL:CG1	1:B:37:ILE:HG23	2.36	0.56
1:A:166:ILE:HD11	1:A:184:PHE:CD1	2.41	0.56
1:A:66:TYR:CD2	1:A:66:TYR:N	2.74	0.56
1:A:115:LEU:O	1:A:119:ILE:HD12	2.06	0.56
1:B:91:ILE:CG2	1:B:92:ALA:N	2.68	0.56
1:A:91:ILE:CG2	1:A:92:ALA:N	2.69	0.55
1:B:166:ILE:HD11	1:B:184:PHE:CD1	2.42	0.55
1:B:39:LYS:O	1:B:42:MET:HB2	2.07	0.54
1:B:202:PRO:HG2	1:B:204:LEU:HD21	1.89	0.54
1:B:66:TYR:N	1:B:66:TYR:CD2	2.75	0.54
1:A:37:ILE:O	1:A:41:ILE:HG13	2.08	0.54
1:A:219:ALA:HA	1:A:252:ALA:HB1	1.89	0.54
1:B:17:ARG:O	1:B:21:ILE:HD12	2.07	0.54
1:B:86:HIS:CD2	1:B:89:GLY:H	2.10	0.54
1:A:187:GLU:CB	1:A:280:GLU:HB2	2.38	0.53
1:A:74:LYS:HE3	1:A:77:ASP:OD1	2.08	0.53
1:A:91:ILE:HD12	1:A:91:ILE:N	2.23	0.53
1:B:16:VAL:HG21	1:B:41:ILE:HG12	1.89	0.53
1:A:124:ALA:HA	1:A:178:LEU:O	2.09	0.53
1:B:230:TYR:CE2	1:B:240:LEU:HD21	2.42	0.53
1:B:64:THR:O	1:B:204:LEU:HD13	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:212:VAL:HG12	1:A:261:ALA:HB2	1.89	0.53
1:B:209:VAL:HG22	1:B:261:ALA:C	2.33	0.53
1:A:66:TYR:HA	1:A:238:ARG:CB	2.36	0.53
1:B:3:THR:O	1:B:7:MET:HG2	2.09	0.53
1:B:86:HIS:CD2	1:B:89:GLY:N	2.73	0.52
1:A:64:THR:O	1:A:204:LEU:HD13	2.10	0.52
1:B:63:TYR:CE2	1:B:204:LEU:HD11	2.45	0.52
1:A:121:VAL:CG2	1:A:131:LEU:HD23	2.39	0.52
1:B:74:LYS:HE3	1:B:77:ASP:OD1	2.10	0.52
1:B:182:ASP:HB2	1:B:285:VAL:HB	1.91	0.52
1:B:220:ARG:O	1:B:223:LEU:HB3	2.09	0.52
1:A:123:ARG:O	1:A:124:ALA:C	2.53	0.52
1:A:147:ILE:HA	1:A:195:GLY:O	2.09	0.52
1:A:86:HIS:HA	1:A:90:PHE:O	2.09	0.52
1:A:99:ARG:HD3	1:A:103:GLU:O	2.11	0.51
1:A:99:ARG:HH11	1:A:99:ARG:CG	2.24	0.51
1:A:38:GLU:OE2	1:A:51:PRO:HA	2.10	0.51
1:A:242:ASN:HD22	1:A:243:ASP:H	1.58	0.51
1:B:155:ILE:O	1:B:183:VAL:HG12	2.10	0.51
1:A:238:ARG:HG2	1:A:238:ARG:NH1	2.23	0.51
1:B:133:LYS:O	1:B:134:ALA:C	2.53	0.51
1:A:133:LYS:O	1:A:134:ALA:C	2.54	0.50
1:B:245:PRO:HG2	1:B:248:GLN:HB3	1.93	0.50
1:B:86:HIS:HA	1:B:90:PHE:O	2.12	0.50
1:A:61:ALA:O	1:A:62:HIS:HB2	2.10	0.50
1:A:133:LYS:O	1:A:137:ASN:ND2	2.45	0.50
1:A:171:ARG:HG2	1:B:149:ASN:HA	1.94	0.50
1:A:20:ALA:HB2	1:A:37:ILE:CD1	2.41	0.49
1:B:16:VAL:HG12	1:B:37:ILE:HG23	1.94	0.49
1:B:147:ILE:HA	1:B:195:GLY:O	2.12	0.49
1:A:121:VAL:HG23	1:A:131:LEU:HD23	1.94	0.49
1:B:63:TYR:HE2	1:B:204:LEU:HD11	1.78	0.49
1:B:37:ILE:CG2	1:B:52:VAL:HG21	2.40	0.49
1:B:128:ILE:HD12	1:B:166:ILE:HG12	1.93	0.49
1:B:61:ALA:O	1:B:62:HIS:HB2	2.12	0.49
1:B:39:LYS:N	1:B:39:LYS:HD2	2.27	0.49
1:B:66:TYR:CE2	1:B:69:ASP:HB2	2.48	0.48
1:A:191:THR:HA	1:A:275:ILE:O	2.14	0.48
1:A:242:ASN:ND2	1:A:243:ASP:H	2.12	0.48
1:B:186:ILE:HD11	1:B:283:ILE:HD13	1.95	0.48
1:B:257:GLU:C	1:B:259:ALA:H	2.21	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:6:LEU:HD23	1:B:90:PHE:HB3	1.93	0.48
1:B:31:LEU:HD22	1:B:66:TYR:O	2.13	0.48
1:B:270:GLU:OE1	1:B:272:ARG:N	2.46	0.48
1:A:207:MET:SD	1:A:232:THR:O	2.71	0.48
1:B:13:ALA:HB2	1:B:85:VAL:HG23	1.95	0.48
1:A:203:THR:HG23	1:A:266:PRO:HD3	1.95	0.48
1:A:82:ASP:HA	1:A:95:ALA:HB2	1.96	0.48
1:A:209:VAL:HG13	1:A:261:ALA:O	2.14	0.47
1:A:80:LYS:HD3	1:A:276:VAL:O	2.14	0.47
1:B:37:ILE:O	1:B:41:ILE:HG13	2.15	0.47
1:B:40:MET:O	1:B:41:ILE:C	2.57	0.47
1:A:81:ILE:O	1:A:95:ALA:HA	2.15	0.47
1:B:145:LYS:HE3	1:B:145:LYS:N	2.30	0.47
1:B:202:PRO:CG	1:B:204:LEU:HD21	2.45	0.47
1:B:10:GLY:HA3	1:B:293:THR:HB	1.96	0.47
1:B:206:TYR:CD1	1:B:262:ILE:HD12	2.50	0.47
1:A:29:LEU:HD22	1:A:31:LEU:H	1.80	0.47
1:A:31:LEU:HD22	1:A:66:TYR:O	2.15	0.47
1:A:66:TYR:CE2	1:A:69:ASP:HB2	2.50	0.47
1:B:63:TYR:CE2	1:B:204:LEU:CD1	2.99	0.46
1:B:228:ARG:HD2	1:B:229:GLU:HG3	1.97	0.46
1:B:96:VAL:HG22	1:B:97:THR:N	2.29	0.46
1:B:223:LEU:O	1:B:227:LYS:HG3	2.15	0.46
1:A:100:VAL:O	1:A:102:MET:HG3	2.14	0.46
1:B:225:LYS:HA	1:B:228:ARG:CZ	2.46	0.46
1:B:253:LEU:HD23	1:B:253:LEU:HA	1.65	0.46
1:B:155:ILE:HB	1:B:183:VAL:HG13	1.97	0.46
1:A:8:LYS:O	1:A:12:ILE:HG13	2.15	0.45
1:A:16:VAL:HG12	1:A:37:ILE:HG23	1.98	0.45
1:B:80:LYS:HD3	1:B:276:VAL:O	2.15	0.45
1:B:82:ASP:HA	1:B:95:ALA:HB2	1.98	0.45
1:B:29:LEU:HD21	1:B:69:ASP:O	2.15	0.45
1:B:271:ILE:CG2	1:B:272:ARG:N	2.79	0.45
1:A:30:LEU:HD23	1:A:30:LEU:HA	1.81	0.45
1:A:37:ILE:CG2	1:A:52:VAL:HG21	2.46	0.45
1:B:88:ASP:O	1:B:158:TYR:CE2	2.70	0.45
1:A:96:VAL:HG22	1:A:97:THR:N	2.31	0.45
1:B:245:PRO:O	1:B:246:GLU:C	2.60	0.45
1:A:182:ASP:HB2	1:A:285:VAL:HB	1.99	0.45
1:A:218:GLN:NE2	1:A:244:MET:HE1	2.32	0.45
1:A:29:LEU:HA	1:A:72:VAL:HG12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:20:ALA:HB2	1:B:37:ILE:CD1	2.46	0.44
1:B:222:LEU:HD21	1:B:253:LEU:HD21	1.99	0.44
1:B:225:LYS:HG3	1:B:228:ARG:HH21	1.81	0.44
1:A:31:LEU:HD12	1:A:31:LEU:O	2.16	0.44
1:A:166:ILE:CD1	1:A:184:PHE:CD1	3.00	0.44
1:A:29:LEU:HD23	1:A:71:THR:O	2.18	0.44
1:A:113:GLU:HG3	1:A:142:ARG:NH2	2.32	0.44
1:A:56:ILE:HD13	1:A:79:LEU:HA	1.99	0.44
1:A:224:ALA:O	1:A:228:ARG:HG2	2.17	0.44
1:A:245:PRO:O	1:A:246:GLU:C	2.60	0.44
1:B:225:LYS:HA	1:B:228:ARG:NE	2.33	0.44
1:A:67:LYS:N	1:A:241:GLN:OE1	2.49	0.44
1:B:203:THR:HG23	1:B:266:PRO:HD3	2.00	0.44
1:B:251:LEU:O	1:B:252:ALA:C	2.60	0.44
1:A:155:ILE:HB	1:A:183:VAL:HG12	1.99	0.43
1:A:242:ASN:O	1:A:244:MET:N	2.51	0.43
1:A:265:TYR:HA	1:A:266:PRO:HD2	1.83	0.43
1:A:39:LYS:O	1:A:42:MET:HB2	2.18	0.43
1:A:208:TYR:CG	1:A:209:VAL:N	2.86	0.43
1:B:99:ARG:HH11	1:B:99:ARG:CG	2.23	0.43
1:A:85:VAL:O	1:A:91:ILE:HA	2.18	0.43
1:A:238:ARG:HH11	1:A:238:ARG:CG	2.21	0.43
1:A:222:LEU:HG	1:A:226:ILE:HD12	1.99	0.43
1:B:222:LEU:HD21	1:B:253:LEU:CD2	2.48	0.43
1:B:153:HIS:CG	1:B:161:HIS:CD2	3.07	0.43
1:A:114:ALA:O	1:A:115:LEU:C	2.62	0.43
1:A:224:ALA:HA	1:A:227:LYS:HD3	2.00	0.43
1:A:76:GLY:HA2	1:A:102:MET:SD	2.59	0.42
1:B:182:ASP:O	1:B:284:ILE:HA	2.18	0.42
1:A:218:GLN:NE2	1:A:218:GLN:O	2.53	0.42
1:B:257:GLU:C	1:B:259:ALA:N	2.76	0.42
1:A:150:LEU:HA	1:A:150:LEU:HD23	1.60	0.42
1:B:30:LEU:HA	1:B:30:LEU:HD23	1.74	0.42
1:B:38:GLU:OE2	1:B:51:PRO:HA	2.19	0.42
1:A:270:GLU:OE1	1:A:272:ARG:N	2.52	0.42
1:B:121:VAL:CG2	1:B:131:LEU:HD23	2.49	0.42
1:B:242:ASN:C	1:B:242:ASN:HD22	2.26	0.42
1:A:209:VAL:HG13	1:A:262:ILE:HA	2.01	0.42
1:B:88:ASP:O	1:B:158:TYR:CZ	2.73	0.42
1:B:187:GLU:CB	1:B:280:GLU:HB2	2.49	0.42
1:A:57:ASN:O	1:A:59:ILE:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:ALA:HB3	1:A:280:GLU:HB3	2.02	0.42
1:B:226:ILE:O	1:B:227:LYS:C	2.61	0.42
1:B:245:PRO:HG2	1:B:248:GLN:CB	2.50	0.42
1:B:256:LEU:HB3	1:B:262:ILE:CG1	2.47	0.42
1:A:237:TYR:CE1	1:A:249:LEU:HD23	2.55	0.41
1:B:29:LEU:CD2	1:B:31:LEU:H	2.32	0.41
1:B:40:MET:HE3	1:B:40:MET:HB2	1.89	0.41
1:A:271:ILE:CG2	1:A:272:ARG:N	2.82	0.41
1:B:250:LYS:O	1:B:251:LEU:C	2.63	0.41
1:A:40:MET:O	1:A:41:ILE:C	2.62	0.41
1:B:10:GLY:HA2	1:B:92:ALA:HB1	2.01	0.41
1:B:254:LYS:O	1:B:255:THR:C	2.64	0.41
1:A:209:VAL:CG2	1:A:210:ARG:N	2.84	0.41
1:A:129:LYS:HB3	1:A:174:ASP:HB2	2.02	0.41
1:B:38:GLU:OE2	1:B:239:TRP:HZ2	2.03	0.41
1:B:86:HIS:O	1:B:86:HIS:CG	2.73	0.41
1:B:113:GLU:O	1:B:114:ALA:C	2.63	0.41
1:B:17:ARG:O	1:B:18:GLU:C	2.63	0.41
1:A:4:GLU:O	1:A:8:LYS:HD3	2.21	0.41
1:A:51:PRO:O	1:A:52:VAL:C	2.63	0.41
1:A:131:LEU:O	1:A:132:GLY:C	2.64	0.41
1:A:186:ILE:CD1	1:A:283:ILE:HD13	2.46	0.41
1:A:189:PHE:CZ	1:A:278:GLN:OE1	2.74	0.41
1:B:113:GLU:HG3	1:B:142:ARG:NH2	2.36	0.41
1:B:254:LYS:O	1:B:258:LYS:N	2.47	0.41
1:A:59:ILE:HD12	1:A:267:VAL:HG11	2.02	0.41
1:A:238:ARG:NH1	1:A:238:ARG:CG	2.80	0.41
1:A:249:LEU:O	1:A:250:LYS:C	2.63	0.41
1:B:91:ILE:CG2	1:B:92:ALA:H	2.33	0.41
1:B:253:LEU:O	1:B:256:LEU:HB2	2.21	0.41
1:A:4:GLU:O	1:A:7:MET:HB2	2.21	0.41
1:B:275:ILE:HG22	1:B:276:VAL:N	2.35	0.41
1:A:23:LEU:O	1:A:28:MET:HG3	2.21	0.40
1:A:160:LEU:HD23	1:A:161:HIS:CE1	2.56	0.40
1:A:29:LEU:HD22	1:A:31:LEU:HB3	2.03	0.40
1:A:264:GLY:O	1:A:266:PRO:HD2	2.21	0.40
1:B:59:ILE:HD12	1:B:267:VAL:HG11	2.04	0.40
1:B:114:ALA:O	1:B:115:LEU:C	2.64	0.40
1:B:136:GLU:HB2	1:B:169:ILE:HA	2.02	0.40
1:B:233:LEU:HA	1:B:233:LEU:HD23	1.67	0.40
1:A:14:LYS:HD2	1:A:295:GLU:O	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:127:GLU:OE1	1:A:175:ASN:HB2	2.21	0.40
1:B:212:VAL:O	1:B:214:VAL:HG23	2.22	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	293/295 (99%)	257 (88%)	29 (10%)	7 (2%)	4	17
1	B	293/295 (99%)	251 (86%)	38 (13%)	4 (1%)	9	30
All	All	586/590 (99%)	508 (87%)	67 (11%)	11 (2%)	6	22

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	243	ASP
1	B	266	PRO
1	A	246	GLU
1	A	266	PRO
1	A	287	LYS
1	B	287	LYS
1	B	58	GLU
1	A	58	GLU
1	A	178	LEU
1	A	193	GLY
1	B	172	PRO

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	243/243 (100%)	219 (90%)	24 (10%)	7	24
1	B	243/243 (100%)	219 (90%)	24 (10%)	7	24
All	All	486/486 (100%)	438 (90%)	48 (10%)	7	24

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	GLU
1	A	28	MET
1	A	31	LEU
1	A	36	SER
1	A	42	MET
1	A	64	THR
1	A	66	TYR
1	A	83	VAL
1	A	99	ARG
1	A	145	LYS
1	A	183	VAL
1	A	202	PRO
1	A	207	MET
1	A	209	VAL
1	A	211	ASP
1	A	212	VAL
1	A	226	ILE
1	A	242	ASN
1	A	255	THR
1	A	262	ILE
1	A	271	ILE
1	A	278	GLN
1	A	281	HIS
1	A	284	ILE
1	B	4	GLU
1	B	28	MET
1	B	29	LEU

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Mol	Chain	Res	Type
1	B	31	LEU
1	B	36	SER
1	B	42	MET
1	B	64	THR
1	B	66	TYR
1	B	83	VAL
1	B	145	LYS
1	B	183	VAL
1	B	202	PRO
1	B	209	VAL
1	B	212	VAL
1	B	232	THR
1	B	242	ASN
1	B	243	ASP
1	B	246	GLU
1	B	255	THR
1	B	262	ILE
1	B	271	ILE
1	B	278	GLN
1	B	281	HIS
1	B	284	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	86	HIS
1	A	137	ASN
1	A	161	HIS
1	A	168	ASN
1	A	196	GLN
1	A	242	ASN
1	B	86	HIS
1	B	137	ASN
1	B	161	HIS
1	B	196	GLN
1	B	242	ASN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 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	A	295/295 (100%)	-0.90	0 100 100	5, 32, 72, 113	0
1	B	295/295 (100%)	-0.91	0 100 100	6, 32, 72, 106	0
All	All	590/590 (100%)	-0.90	0 100 100	5, 32, 72, 113	0

There are no RSRZ outliers to report.

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 oligosaccharides 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
2	CO	B	296	1/1	0.99	0.01	14,14,14,14	0
2	CO	B	297	1/1	0.99	0.03	20,20,20,20	0
2	CO	A	296	1/1	1.00	0.01	14,14,14,14	0
2	CO	A	297	1/1	1.00	0.01	13,13,13,13	0

6.5 Other polymers [i](#)

There are no such residues in this entry.