



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 06:26 AM UTC

PDB ID : 2WS2 / pdb_00002ws2
Title : The 2 Angstrom structure of a Nu-class GST from Haemonchus contortus
Authors : Line, K.; Isupov, M.N.; vanRossum, A.J.; Brophy, P.M.; Littlechild, J.A.
Deposited on : 2009-09-03
Resolution : 2.01 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
Xtrriage (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

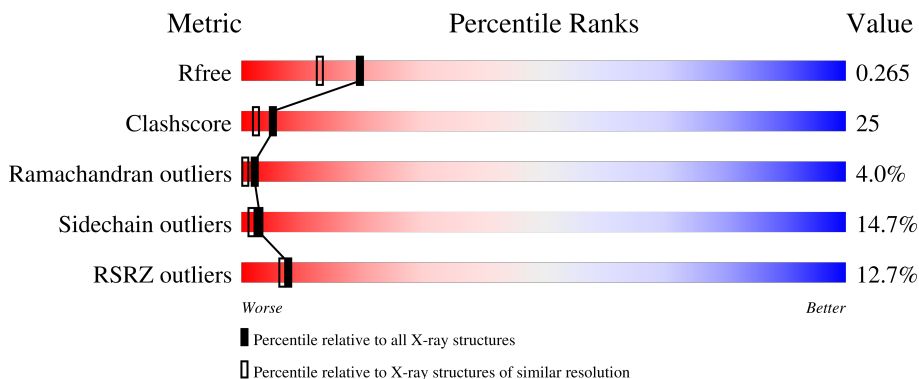
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.01 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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	204	 9% 52% 38% 8% .
1	B	204	 16% 55% 31% 11% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3520 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 GLUTATHIONE S-TRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	204	1676	1094	277	301	4	0	2	0
1	B	204	1666	1088	277	297	4	0	1	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	164	GLY	THR	SEE REMARK 999	UNP Q9NAW7
B	164	GLY	THR	SEE REMARK 999	UNP Q9NAW7

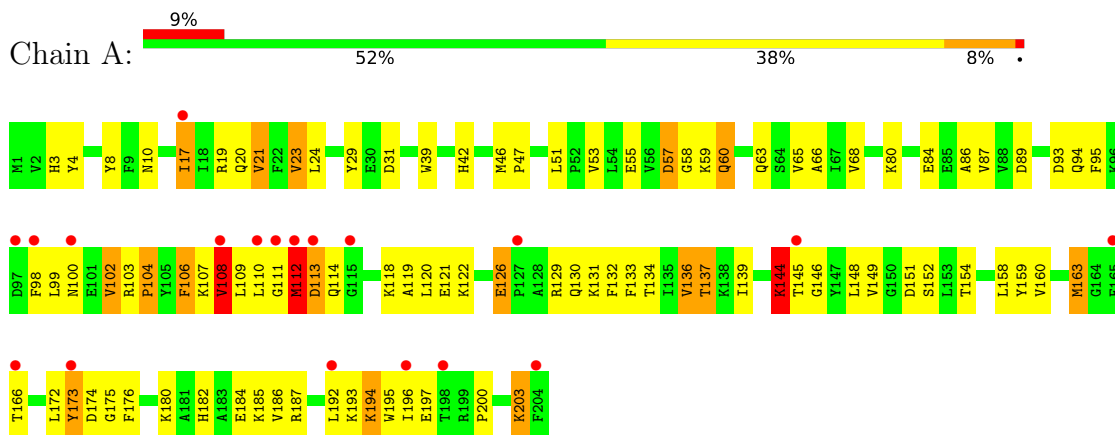
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	78	Total 78	O 78	0	0
2	B	100	Total 100	O 100	0	0

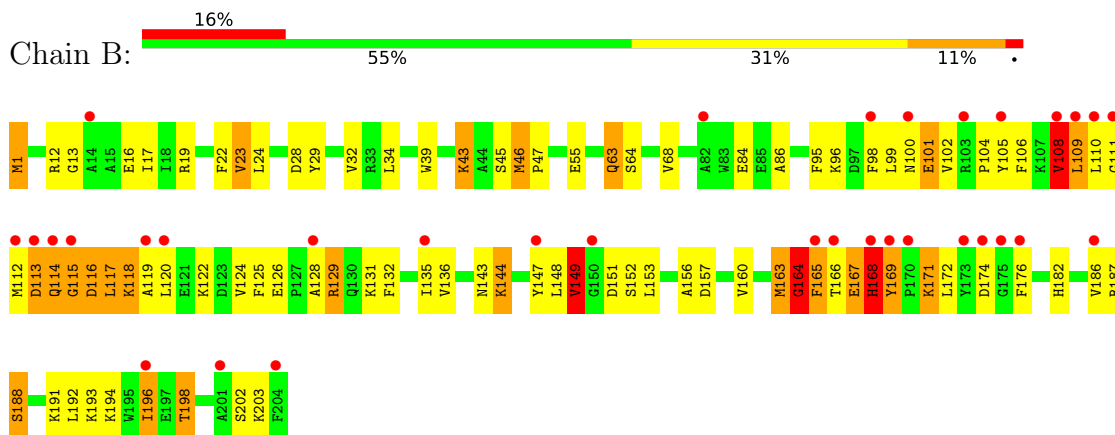
3 Residue-property plots

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: GLUTATHIONE S-TRANSFERASE



- Molecule 1: GLUTATHIONE S-TRANSFERASE



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	47.22Å 101.38Å 47.17Å 90.00° 100.46° 90.00°	Depositor
Resolution (Å)	50.71 – 2.01 50.69 – 2.01	Depositor EDS
% Data completeness (in resolution range)	96.8 (50.71-2.01) 97.3 (50.69-2.01)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.24 (at 2.01Å)	Xtriage
Refinement program	REFMAC 5.5.0088	Depositor
R, R_{free}	0.233 , 0.290 0.247 , 0.265	Depositor DCC
R_{free} test set	1433 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	26.0	Xtriage
Anisotropy	0.667	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 40.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.407 for l,-k,h	Xtriage
Reported twinning fraction	0.599 for H,K,L 0.401 for L,-K,H	Depositor
Outliers	0 of 28324 reflections	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	3520	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.22% 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 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	1.02	2/1726 (0.1%)	1.26	14/2325 (0.6%)
1	B	0.98	1/1713 (0.1%)	1.34	18/2312 (0.8%)
All	All	1.00	3/3439 (0.1%)	1.30	32/4637 (0.7%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	89	ASP	C-O	-5.76	1.17	1.24
1	B	156	ALA	CA-CB	-5.37	1.45	1.53
1	A	166	THR	CA-CB	5.36	1.60	1.53

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	168	HIS	N-CA-C	-14.39	96.31	112.57
1	B	46	MET	CA-C-N	8.90	130.97	119.84
1	B	46	MET	C-N-CA	8.90	130.97	119.84
1	A	46	MET	CA-C-N	7.87	129.68	119.84
1	A	46	MET	C-N-CA	7.87	129.68	119.84
1	B	165	PHE	N-CA-C	7.42	122.40	113.12
1	A	144	LYS	N-CA-C	7.40	121.64	112.47
1	B	188	SER	N-CA-C	-7.28	103.37	112.90
1	B	119	ALA	N-CA-C	-6.97	103.73	111.82
1	B	171	LYS	N-CA-C	6.92	119.85	111.82
1	A	113	ASP	N-CA-C	6.43	119.02	110.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	152	SER	N-CA-C	-6.30	99.75	109.14
1	A	87	VAL	CA-C-N	6.15	128.53	120.60
1	A	87	VAL	C-N-CA	6.15	128.53	120.60
1	B	144	LYS	N-CA-C	5.87	119.95	111.56
1	B	176	PHE	CA-C-N	5.73	125.26	119.19
1	B	176	PHE	C-N-CA	5.73	125.26	119.19
1	A	193	LYS	CA-C-N	5.67	128.93	120.31
1	A	193	LYS	C-N-CA	5.67	128.93	120.31
1	A	139	ILE	CB-CA-C	-5.65	104.51	112.14
1	A	21	VAL	N-CA-C	5.64	115.83	110.42
1	B	129	ARG	N-CA-C	-5.59	105.09	111.07
1	B	120	LEU	N-CA-C	5.59	117.05	111.07
1	B	86	ALA	N-CA-C	-5.56	104.86	111.69
1	B	95	PHE	N-CA-C	5.49	117.34	111.36
1	A	60	GLN	N-CA-C	5.36	118.28	109.76
1	B	115	GLY	N-CA-C	-5.33	102.13	111.46
1	B	43	LYS	N-CA-C	5.28	117.12	111.36
1	A	86	ALA	N-CA-C	-5.24	105.16	112.45
1	B	149	VAL	N-CA-C	5.18	115.36	108.11
1	B	29	TYR	N-CA-C	-5.17	100.66	108.52
1	A	136	VAL	CB-CA-C	-5.13	105.31	112.04

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	116	ASP	Peptide
1	B	164	GLY	Peptide

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	1676	0	1676	92	0
1	B	1666	0	1674	73	0
2	A	78	0	0	14	0
2	B	100	0	0	5	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	3520	0	3350	164	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 25.

All (164) 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:42:HIS:HB2	2:A:2017:HOH:O	1.21	1.30
1:B:108:VAL:HG23	1:B:109:LEU:N	1.75	1.01
1:B:101:GLU:OE1	1:B:128:ALA:HB2	1.62	0.99
1:A:133:PHE:O	1:A:137:THR:HG22	1.64	0.95
1:B:108:VAL:HG23	1:B:109:LEU:H	1.36	0.90
1:A:29:TYR:CE1	1:A:31[B]:ASP:HB3	2.05	0.90
1:B:104:PRO:O	2:B:2067:HOH:O	1.90	0.89
1:B:39:TRP:CZ2	1:B:43:LYS:HG3	2.08	0.89
1:A:145:THR:HG21	1:A:151:ASP:HB3	1.54	0.88
1:B:163:MET:O	1:B:165:PHE:N	2.07	0.87
1:A:65:VAL:HA	1:A:68:VAL:HG22	1.58	0.86
1:A:194:LYS:HE3	1:A:197:GLU:OE2	1.74	0.86
1:A:8:TYR:HB3	2:A:2009:HOH:O	1.76	0.85
1:A:19:ARG:O	1:A:23:VAL:HG23	1.77	0.85
1:A:42:HIS:NE2	2:A:2019:HOH:O	2.10	0.84
1:A:65:VAL:HA	1:A:68:VAL:CG2	2.12	0.80
1:A:42:HIS:CD2	2:A:2019:HOH:O	2.35	0.79
1:A:17:ILE:HG23	1:A:68:VAL:CG1	2.13	0.79
1:A:154:THR:HG22	2:A:2065:HOH:O	1.82	0.78
1:B:109:LEU:HD12	1:B:111:GLY:O	1.84	0.77
1:A:130:GLN:O	1:A:134:THR:HG23	1.84	0.77
1:A:42:HIS:CB	2:A:2017:HOH:O	1.96	0.77
1:A:17:ILE:HG23	1:A:68:VAL:HG11	1.65	0.76
1:A:84:GLU:HG3	1:A:149:VAL:CG1	2.15	0.76
1:A:84:GLU:HG3	1:A:149:VAL:HG12	1.68	0.75
1:A:17:ILE:CG2	1:A:68:VAL:HG11	2.17	0.74
1:B:101:GLU:OE1	1:B:128:ALA:CB	2.35	0.74
1:B:163:MET:C	1:B:165:PHE:H	1.97	0.71
1:A:119:ALA:HA	1:A:122:LYS:HG2	1.72	0.71
1:B:169:TYR:HD1	1:B:169:TYR:O	1.74	0.70
1:A:17:ILE:HG21	1:A:159:TYR:CZ	2.26	0.70
1:B:157:ASP:OD2	2:B:2086:HOH:O	2.09	0.69
1:A:173:TYR:HD1	1:A:180:LYS:N	1.92	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:194:LYS:HA	1:A:197:GLU:OE2	1.93	0.68
1:A:29:TYR:HE1	1:A:31[B]:ASP:HB3	1.53	0.67
1:B:193:LYS:O	1:B:196:ILE:HG23	1.95	0.67
1:A:59:LYS:N	1:A:59:LYS:HD3	2.07	0.67
1:A:132:PHE:O	1:A:136:VAL:HG23	1.94	0.66
1:A:187:ARG:HA	1:A:192:LEU:HD23	1.76	0.66
1:B:108:VAL:CG2	1:B:109:LEU:N	2.49	0.66
1:A:118:LYS:O	1:A:122:LYS:HE3	1.97	0.65
1:A:29:TYR:HA	2:A:2012:HOH:O	1.97	0.64
1:A:173:TYR:CD1	1:A:180:LYS:HA	2.33	0.63
1:A:100:ASN:HA	1:A:103:ARG:HD2	1.81	0.62
1:A:111:GLY:O	1:A:112:MET:HB2	1.99	0.61
1:B:117:LEU:O	1:B:118:LYS:HB2	1.99	0.61
1:A:4:TYR:HE1	2:A:2002:HOH:O	1.81	0.61
1:A:65:VAL:CA	1:A:68:VAL:HG22	2.30	0.60
1:B:174:ASP:HB3	2:B:2091:HOH:O	2.01	0.60
1:B:169:TYR:C	1:B:169:TYR:CD1	2.79	0.60
1:B:125:PHE:HD2	1:B:126:GLU:HG2	1.68	0.59
1:B:132:PHE:HE2	1:B:163:MET:HE1	1.67	0.59
1:A:173:TYR:N	1:A:173:TYR:CD2	2.69	0.59
1:A:175:GLY:O	2:A:2070:HOH:O	2.17	0.59
1:B:125:PHE:CD2	1:B:126:GLU:HG2	2.37	0.59
1:B:169:TYR:O	1:B:169:TYR:CD1	2.55	0.58
1:B:163:MET:C	1:B:165:PHE:N	2.57	0.58
1:A:4:TYR:CE1	2:A:2002:HOH:O	2.51	0.58
1:B:19:ARG:O	1:B:23:VAL:HG13	2.04	0.58
1:B:167:GLU:C	1:B:169:TYR:H	2.12	0.57
1:B:153:LEU:HD11	1:B:186:VAL:HG13	1.85	0.57
1:A:144:LYS:HB2	1:A:144:LYS:NZ	2.19	0.57
1:A:17:ILE:HD13	1:A:17:ILE:O	2.05	0.57
1:A:187:ARG:HD3	2:A:2076:HOH:O	2.05	0.56
1:B:24[B]:LEU:HD12	1:B:191:LYS:HZ2	1.70	0.56
1:A:23:VAL:HG11	1:A:195:TRP:HB2	1.87	0.56
1:A:17:ILE:HG23	1:A:68:VAL:HG12	1.87	0.55
1:B:112:MET:O	1:B:113:ASP:C	2.49	0.55
1:A:172:LEU:HD23	1:A:173:TYR:HE2	1.71	0.55
1:B:109:LEU:C	1:B:111:GLY:H	2.13	0.55
1:B:109:LEU:HD13	1:B:113:ASP:HA	1.88	0.55
1:B:98:PHE:HE2	1:B:163:MET:SD	2.30	0.55
1:A:58:GLY:C	1:A:59:LYS:HD3	2.32	0.54
1:A:17:ILE:HD13	1:A:17:ILE:C	2.33	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:100:ASN:HA	1:A:103:ARG:CD	2.38	0.54
1:A:173:TYR:CE1	1:A:180:LYS:HA	2.43	0.53
1:A:173:TYR:CD1	1:A:180:LYS:CA	2.91	0.53
1:B:109:LEU:HG	1:B:109:LEU:O	2.07	0.53
1:A:173:TYR:N	1:A:173:TYR:HD2	2.05	0.53
1:B:192:LEU:O	1:B:196:ILE:HG22	2.08	0.53
1:B:113:ASP:O	1:B:115:GLY:N	2.41	0.53
1:A:42:HIS:CG	2:A:2017:HOH:O	2.49	0.53
1:A:173:TYR:HD1	1:A:180:LYS:CA	2.21	0.53
1:A:55:GLU:HG2	1:A:60:GLN:HG3	1.92	0.52
1:A:136:VAL:HG13	1:A:148:LEU:HD21	1.91	0.52
1:B:64:SER:O	1:B:68:VAL:HG23	2.09	0.52
1:A:103:ARG:O	1:A:106:PHE:N	2.38	0.51
1:B:32:VAL:CG1	1:B:34:LEU:HD21	2.41	0.51
1:B:117:LEU:HD12	1:B:117:LEU:N	2.26	0.51
1:A:121:GLU:O	1:A:126:GLU:HG3	2.11	0.50
1:A:184:GLU:OE2	2:A:2074:HOH:O	2.20	0.50
1:A:84:GLU:CG	1:A:149:VAL:HG12	2.39	0.49
1:B:55:GLU:OE1	2:B:2042:HOH:O	2.19	0.49
1:A:112:MET:HB3	1:A:113:ASP:OD1	2.12	0.49
1:B:105:TYR:CD1	1:B:105:TYR:C	2.91	0.49
1:B:163:MET:O	1:B:164:GLY:C	2.55	0.49
1:A:94:GLN:OE1	1:B:63:GLN:NE2	2.44	0.49
1:A:129:ARG:HD2	1:A:172:LEU:O	2.14	0.48
1:A:106:PHE:C	1:A:107:LYS:HE2	2.38	0.48
1:A:134:THR:HA	1:A:137:THR:CG2	2.43	0.48
1:A:182:HIS:O	1:A:186:VAL:HG23	2.13	0.48
1:A:103:ARG:CB	1:A:104:PRO:CD	2.92	0.48
1:A:146:GLY:HA3	1:A:185:LYS:HE2	1.97	0.47
1:B:105:TYR:CD1	1:B:105:TYR:O	2.68	0.47
1:B:182:HIS:O	1:B:186:VAL:HG23	2.15	0.47
1:B:55:GLU:CD	2:B:2042:HOH:O	2.58	0.46
1:B:1:MET:SD	1:B:1:MET:N	2.83	0.46
1:B:24[A]:LEU:HD11	1:B:192:LEU:HD22	1.96	0.46
1:A:20:GLN:O	1:A:24:LEU:HD12	2.15	0.46
1:B:136:VAL:HG13	1:B:148:LEU:HD21	1.98	0.46
1:B:160:VAL:O	1:B:163:MET:HB2	2.15	0.46
1:A:20:GLN:HG2	1:A:192:LEU:HD13	1.98	0.45
1:B:194:LYS:O	1:B:198:THR:HB	2.17	0.45
1:A:114:GLN:O	1:A:114:GLN:HG2	2.16	0.45
1:B:45:SER:HG	1:B:46:MET:HE2	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:108:VAL:HG13	1:A:108:VAL:O	2.16	0.45
1:A:203:LYS:HA	1:A:203:LYS:HD2	1.61	0.45
1:B:45:SER:OG	1:B:46:MET:HE2	2.17	0.45
1:A:163:MET:HE3	1:A:163:MET:HB2	1.62	0.44
1:B:143:ASN:OD1	1:B:147:TYR:O	2.35	0.44
1:B:147:TYR:CE1	1:B:153:LEU:HD13	2.53	0.44
1:A:65:VAL:O	1:A:68:VAL:CG2	2.66	0.44
1:A:129:ARG:NH1	1:A:172:LEU:O	2.49	0.44
1:B:169:TYR:OH	1:B:171:LYS:NZ	2.48	0.44
1:A:4:TYR:HA	1:A:55:GLU:O	2.17	0.44
1:A:57:ASP:O	1:A:59:LYS:NZ	2.28	0.44
1:B:22:PHE:O	1:B:23:VAL:C	2.59	0.43
1:B:39:TRP:CH2	1:B:43:LYS:HG3	2.52	0.43
1:A:65:VAL:O	1:A:66:ALA:C	2.61	0.43
1:B:165:PHE:O	1:B:166:THR:C	2.60	0.43
1:B:186:VAL:O	1:B:192:LEU:HD23	2.18	0.43
1:A:20:GLN:HB3	1:A:158:LEU:HD13	2.00	0.43
1:A:103:ARG:CB	1:A:104:PRO:HD3	2.48	0.43
1:B:98:PHE:CE2	1:B:163:MET:SD	3.09	0.43
1:A:80:LYS:H	1:A:84:GLU:CD	2.26	0.43
1:A:111:GLY:O	1:A:112:MET:CB	2.67	0.43
1:A:20:GLN:O	1:A:24:LEU:CD1	2.66	0.43
1:A:98:PHE:O	1:A:102:VAL:HB	2.19	0.43
1:B:143:ASN:O	1:B:144:LYS:HG2	2.18	0.43
1:B:84:GLU:HG2	1:B:149:VAL:CG2	2.48	0.43
1:A:118:LYS:O	1:A:122:LYS:HG2	2.19	0.42
1:B:108:VAL:CG2	1:B:109:LEU:H	2.09	0.42
1:B:12:ARG:HB3	1:B:16:GLU:HB2	2.02	0.42
1:A:95:PHE:O	1:A:98:PHE:HB3	2.20	0.42
1:B:104:PRO:HA	1:B:110:LEU:CD1	2.50	0.42
1:A:60:GLN:HE21	1:A:60:GLN:HB2	1.60	0.42
1:A:103:ARG:HB2	1:A:104:PRO:CD	2.49	0.42
1:A:107:LYS:C	1:A:109:LEU:N	2.77	0.42
1:B:12:ARG:NH1	1:B:202:SER:OG	2.52	0.42
1:A:3:HIS:HB3	2:A:2003:HOH:O	2.20	0.41
1:B:84:GLU:HG2	1:B:149:VAL:HG23	2.02	0.41
1:A:53:VAL:CG1	1:A:60:GLN:HG2	2.51	0.41
1:A:187:ARG:HA	1:A:192:LEU:CD2	2.46	0.41
1:B:116:ASP:HA	1:B:117:LEU:HD12	2.02	0.41
1:B:117:LEU:HD12	1:B:117:LEU:H	1.84	0.41
1:B:19:ARG:HH11	1:B:19:ARG:HD2	1.73	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:135:ILE:HG22	1:B:136:VAL:N	2.36	0.41
1:B:125:PHE:CE2	1:B:129:ARG:HD3	2.56	0.40
1:B:186:VAL:C	1:B:188:SER:H	2.30	0.40
1:B:109:LEU:HD13	1:B:113:ASP:N	2.36	0.40
1:A:134:THR:HG22	1:A:176:PHE:HE1	1.86	0.40
1:A:39:TRP:CZ3	1:A:51:LEU:HG	2.57	0.40
1:B:109:LEU:HD13	1:B:113:ASP:CA	2.50	0.40
1:B:166:THR:C	1:B:168:HIS:H	2.30	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:2008:HOH:O	2:B:2072:HOH:O[1_655]	2.01	0.19

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	203/204 (100%)	179 (88%)	18 (9%)	6 (3%)	3	1
1	B	203/204 (100%)	177 (87%)	16 (8%)	10 (5%)	1	0
All	All	406/408 (100%)	356 (88%)	34 (8%)	16 (4%)	2	1

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	112	MET
1	B	106	PHE
1	B	114	GLN
1	B	118	LYS
1	B	164	GLY

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Mol	Chain	Res	Type
1	A	57	ASP
1	A	108	VAL
1	A	110	LEU
1	B	108	VAL
1	B	13	GLY
1	A	63	GLN
1	B	113	ASP
1	B	172	LEU
1	A	174	ASP
1	B	167	GLU
1	B	63	GLN

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	176/174 (101%)	152 (86%)	24 (14%)	3 2
1	B	175/174 (101%)	148 (85%)	27 (15%)	2 1
All	All	351/348 (101%)	300 (86%)	51 (14%)	3 2

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	A	17	ILE
1	A	21	VAL
1	A	23	VAL
1	A	47	PRO
1	A	93	ASP
1	A	99	LEU
1	A	102	VAL
1	A	104	PRO
1	A	106	PHE
1	A	108	VAL
1	A	112	MET

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Mol	Chain	Res	Type
1	A	120	LEU
1	A	126	GLU
1	A	131	LYS
1	A	137	THR
1	A	144	LYS
1	A	160	VAL
1	A	163	MET
1	A	173	TYR
1	A	194	LYS
1	A	196	ILE
1	A	200	PRO
1	A	203	LYS
1	B	1	MET
1	B	17	ILE
1	B	23	VAL
1	B	28	ASP
1	B	47	PRO
1	B	96	LYS
1	B	99	LEU
1	B	100	ASN
1	B	101	GLU
1	B	102	VAL
1	B	108	VAL
1	B	109	LEU
1	B	114	GLN
1	B	117	LEU
1	B	122	LYS
1	B	124	VAL
1	B	131	LYS
1	B	149	VAL
1	B	151	ASP
1	B	152	SER
1	B	163	MET
1	B	168	HIS
1	B	169	TYR
1	B	187	ARG
1	B	196	ILE
1	B	198	THR
1	B	203	LYS

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

Mol	Chain	Res	Type
1	A	60	GLN
1	A	100	ASN
1	A	189	ASN
1	B	27	GLN
1	B	114	GLN
1	B	130	GLN
1	B	143	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 oligosaccharides 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	204/204 (100%)	0.98	19 (9%) 14 13	18, 29, 41, 57	2 (0%)
1	B	204/204 (100%)	1.07	33 (16%) 4 4	16, 30, 44, 55	1 (0%)
All	All	408/408 (100%)	1.03	52 (12%) 8 7	16, 30, 43, 57	3 (0%)

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	113	ASP	4.5
1	B	165	PHE	3.8
1	A	112	MET	3.4
1	A	165	PHE	3.4
1	B	110	LEU	3.4
1	B	169	TYR	3.2
1	A	111	GLY	3.2
1	B	111	GLY	3.2
1	A	173	TYR	3.2
1	B	100	ASN	3.1
1	B	150	GLY	3.1
1	B	119	ALA	3.1
1	B	168	HIS	3.1
1	B	176	PHE	3.0
1	A	100	ASN	3.0
1	B	173	TYR	3.0
1	B	175	GLY	2.9
1	B	112	MET	2.9
1	A	110	LEU	2.8
1	B	105	TYR	2.8
1	A	108	VAL	2.8
1	A	17	ILE	2.7
1	B	115	GLY	2.7
1	A	196	ILE	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	114	GLN	2.7
1	A	204[A]	PHE	2.6
1	A	113	ASP	2.6
1	A	166	THR	2.6
1	B	120	LEU	2.6
1	A	97	ASP	2.5
1	B	170	PRO	2.5
1	B	147	TYR	2.5
1	A	198	THR	2.5
1	B	166	THR	2.5
1	B	204	PHE	2.5
1	A	115	GLY	2.5
1	B	201	ALA	2.3
1	B	82	ALA	2.3
1	A	98	PHE	2.3
1	B	14	ALA	2.3
1	B	128	ALA	2.3
1	B	98	PHE	2.2
1	B	135	ILE	2.2
1	B	196	ILE	2.2
1	B	108	VAL	2.2
1	B	109	LEU	2.2
1	B	174	ASP	2.2
1	B	103	ARG	2.1
1	A	127	PRO	2.1
1	B	186	VAL	2.1
1	A	192	LEU	2.0
1	A	145	THR	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 oligosaccharides 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.