



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:43 AM UTC

PDB ID : 8FJD / pdb_00008fjd
Title : Structure of chlorophyllase from *Triticum aestivum*
Authors : Boggs, D.; Jo, M.; Bridwell-Rabb, J.
Deposited on : 2022-12-19
Resolution : 4.46 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

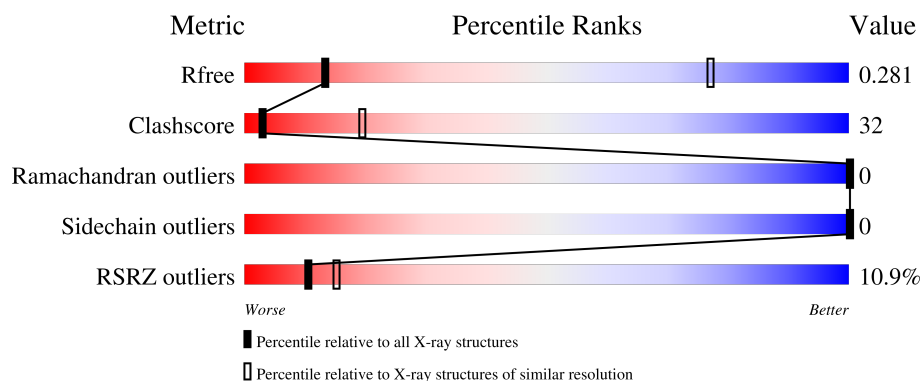
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.46 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	1119 (5.02-3.90)
Clashscore	190562	1024 (5.00-3.92)
Ramachandran outliers	187476	1055 (5.02-3.90)
Sidechain outliers	187428	1038 (5.02-3.90)
RSRZ outliers	180081	1114 (5.02-3.90)

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	325	9% 42% 48% 8%
1	B	325	11% 45% 46% 9%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4497 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 Chlorophyllase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	298	Total	C	N	O	S	0	0	0
			2245	1446	376	410	13			
1	B	297	Total	C	N	O	S	0	0	0
			2236	1441	375	407	13			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	320	GLU	-	expression tag	UNP W6EIP8
A	321	ASN	-	expression tag	UNP W6EIP8
A	322	LEU	-	expression tag	UNP W6EIP8
A	323	TYR	-	expression tag	UNP W6EIP8
A	324	PHE	-	expression tag	UNP W6EIP8
A	325	GLN	-	expression tag	UNP W6EIP8
B	320	GLU	-	expression tag	UNP W6EIP8
B	321	ASN	-	expression tag	UNP W6EIP8
B	322	LEU	-	expression tag	UNP W6EIP8
B	323	TYR	-	expression tag	UNP W6EIP8
B	324	PHE	-	expression tag	UNP W6EIP8
B	325	GLN	-	expression tag	UNP W6EIP8

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	9	Total	O	0	0
			9	9		

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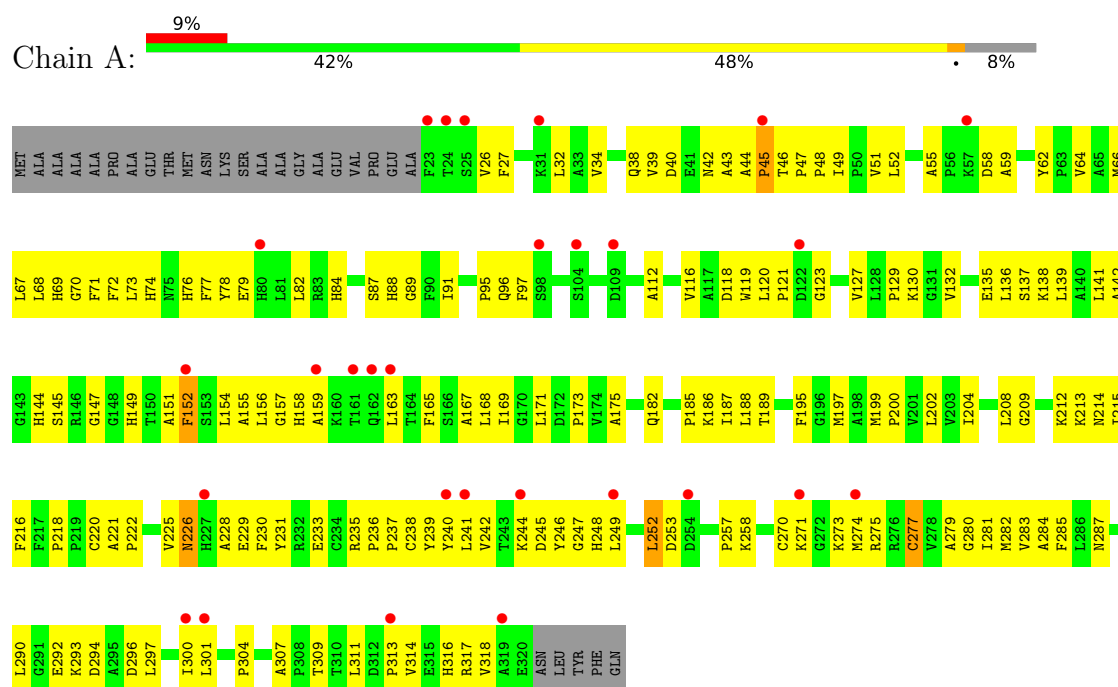
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	6	Total	O	0	0
			6	6		

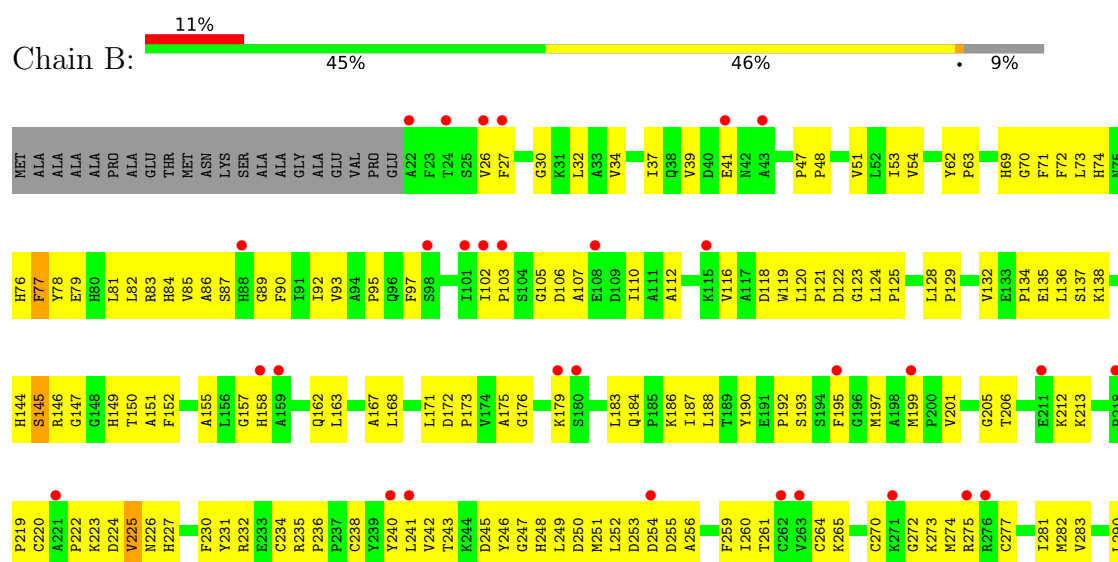
3 Residue-property plots [i](#)

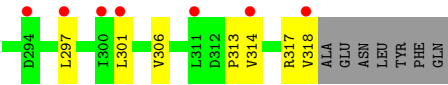
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Chlorophyllase



• Molecule 1: Chlorophyllase





4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	197.52Å 197.52Å 96.83Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.13 – 4.46 49.13 – 4.46	Depositor EDS
% Data completeness (in resolution range)	95.1 (49.13-4.46) 95.3 (49.13-4.46)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.34 (at 4.45Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.266 , 0.278 0.267 , 0.281	Depositor DCC
R_{free} test set	344 reflections (3.37%)	wwPDB-VP
Wilson B-factor (Å ²)	118.9	Xtriage
Anisotropy	0.689	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 134.3	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	0.83	EDS
Total number of atoms	4497	wwPDB-VP
Average B, all atoms (Å ²)	129.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.65% 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: CA

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	0.93	1/2306 (0.0%)	1.22	7/3142 (0.2%)
1	B	0.96	0/2297	1.20	3/3130 (0.1%)
All	All	0.94	1/4603 (0.0%)	1.21	10/6272 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	244	LYS	CA-C	5.09	1.59	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	226	ASN	CB-CA-C	-7.54	101.24	113.37
1	A	245	ASP	N-CA-C	6.92	121.39	113.15
1	A	252	LEU	N-CA-C	-6.64	101.73	110.43
1	A	226	ASN	N-CA-C	6.60	121.02	109.80
1	A	45	PRO	N-CD-CG	-5.86	96.77	103.80
1	B	77	PHE	N-CA-C	-5.81	106.04	113.01
1	B	145	SER	CB-CA-C	-5.67	110.02	116.54
1	A	277	CYS	N-CA-C	-5.54	105.14	111.07
1	B	225	VAL	N-CA-C	-5.33	106.67	112.80
1	A	152	PHE	N-CA-C	-5.02	105.81	111.28

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	2245	0	2243	145	0
1	B	2236	0	2237	150	0
2	A	1	0	0	0	0
3	A	9	0	0	2	0
3	B	6	0	0	3	0
All	All	4497	0	4480	286	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 32.

All (286) 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:240:TYR:HE2	1:A:313:PRO:HG2	1.25	0.99
1:B:82:LEU:HG	1:B:92:ILE:HD13	1.57	0.87
1:A:195:PHE:HB3	1:A:197:MET:HE3	1.60	0.84
1:A:96:GLN:HG3	3:A:509:HOH:O	1.77	0.83
1:B:168:LEU:HB3	1:B:201:VAL:HG22	1.58	0.83
1:A:45:PRO:CG	1:A:123:GLY:HA2	2.09	0.82
1:A:212:LYS:HE3	1:A:215:ILE:HA	1.61	0.80
1:B:41:GLU:HA	1:B:47:PRO:HD2	1.63	0.80
1:A:238:CYS:SG	1:A:317:ARG:HB2	2.20	0.80
1:A:240:TYR:CE2	1:A:313:PRO:HG2	2.14	0.80
1:B:227:HIS:HA	1:B:230:PHE:HD2	1.48	0.78
1:A:27:PHE:CE2	1:A:307:ALA:HA	2.19	0.77
1:A:246:TYR:HB3	1:A:274:MET:SD	2.26	0.75
1:B:79:GLU:CD	3:B:402:HOH:O	2.31	0.73
1:A:270:CYS:HB3	1:A:273:LYS:HG3	1.70	0.73
1:B:168:LEU:HB2	1:B:199:MET:SD	2.29	0.73
1:A:292:GLU:O	1:A:292:GLU:HG3	1.88	0.73
1:A:138:LYS:HB3	1:A:290:LEU:HD23	1.72	0.72
1:A:246:TYR:CB	1:A:274:MET:SD	2.77	0.72
1:A:257:PRO:HA	1:B:83:ARG:HE	1.55	0.70
1:B:270:CYS:HB3	1:B:273:LYS:HG3	1.74	0.69
1:B:186:LYS:O	1:B:186:LYS:HG3	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:LEU:HD13	1:A:163:LEU:HD11	1.75	0.68
1:A:68:LEU:HD12	1:A:151:ALA:HB2	1.75	0.68
1:B:76:HIS:CE1	3:B:402:HOH:O	2.46	0.67
1:A:182:GLN:HB2	1:A:186:LYS:HG2	1.76	0.67
1:A:145:SER:HB2	1:A:248:HIS:CE1	2.30	0.66
1:A:241:LEU:HD23	1:A:311:LEU:HD13	1.76	0.65
1:A:45:PRO:HG3	1:A:123:GLY:HA2	1.79	0.65
1:B:175:ALA:HB3	1:B:225:VAL:HB	1.78	0.64
1:A:45:PRO:HG2	1:A:123:GLY:HA2	1.79	0.63
1:A:69:HIS:NE2	1:A:97:PHE:N	2.46	0.63
1:A:118:ASP:O	1:A:121:PRO:HD2	1.98	0.63
1:B:223:LYS:HG3	1:B:226:ASN:ND2	2.13	0.63
1:A:200:PRO:HA	1:A:237:PRO:HG2	1.80	0.62
1:B:51:VAL:HG12	1:B:95:PRO:CB	2.29	0.62
1:A:88:HIS:HD2	1:A:283:VAL:HG21	1.63	0.62
1:B:158:HIS:HE1	1:B:187:ILE:HG22	1.65	0.62
1:B:231:TYR:CD1	1:B:240:TYR:HB2	2.35	0.62
1:B:222:PRO:HB2	1:B:225:VAL:HG22	1.81	0.62
1:A:44:ALA:HA	1:A:45:PRO:C	2.24	0.62
1:A:121:PRO:HA	1:A:136:LEU:HD11	1.81	0.61
1:B:205:GLY:O	1:B:243:THR:N	2.33	0.61
1:B:188:LEU:HD21	1:B:230:PHE:CD1	2.35	0.61
1:B:188:LEU:HD21	1:B:230:PHE:CE1	2.35	0.61
1:B:241:LEU:HG	1:B:314:VAL:HG13	1.82	0.61
1:B:254:ASP:CG	1:B:275:ARG:HH22	2.08	0.61
1:A:212:LYS:HG3	1:A:218:PRO:HA	1.81	0.61
1:A:71:PHE:O	1:A:73:LEU:HG	2.01	0.60
1:A:182:GLN:OE1	1:A:188:LEU:HB2	2.01	0.60
1:B:51:VAL:HG12	1:B:95:PRO:HB3	1.83	0.60
1:A:154:LEU:HD12	1:A:159:ALA:HB3	1.83	0.60
1:A:271:LYS:HB3	1:A:275:ARG:HH12	1.67	0.60
1:B:34:VAL:HG21	1:B:83:ARG:HG2	1.82	0.60
1:A:67:LEU:HD23	1:A:82:LEU:HD21	1.84	0.59
1:B:213:LYS:HB2	1:B:265:LYS:HD3	1.83	0.59
1:B:238:CYS:SG	1:B:317:ARG:HB2	2.42	0.59
1:B:240:TYR:HE2	1:B:313:PRO:HG2	1.68	0.59
1:A:74:HIS:HA	3:A:509:HOH:O	2.03	0.59
1:B:47:PRO:HA	1:B:119:TRP:CD1	2.39	0.58
1:B:26:VAL:HB	1:B:283:VAL:CG2	2.34	0.58
1:B:171:LEU:O	1:B:172:ASP:C	2.47	0.58
1:B:51:VAL:HG12	1:B:95:PRO:CA	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:CYS:SG	1:A:317:ARG:NE	2.77	0.58
1:B:51:VAL:HG12	1:B:95:PRO:HA	1.85	0.58
1:B:124:LEU:HD23	1:B:136:LEU:HD21	1.86	0.58
1:A:112:ALA:O	1:A:116:VAL:HG23	2.04	0.57
1:B:176:GLY:O	1:B:225:VAL:HG21	2.04	0.57
1:B:97:PHE:CE1	1:B:112:ALA:HB3	2.39	0.57
1:A:67:LEU:O	1:A:95:PRO:HD2	2.05	0.56
1:A:188:LEU:HA	1:A:233:GLU:OE1	2.06	0.56
1:B:145:SER:HB2	1:B:248:HIS:NE2	2.20	0.56
1:B:241:LEU:HA	1:B:314:VAL:HG22	1.88	0.56
1:B:39:VAL:HG23	1:B:47:PRO:HG3	1.88	0.56
1:B:51:VAL:HA	1:B:95:PRO:HA	1.87	0.56
1:A:195:PHE:HB3	1:A:197:MET:CE	2.35	0.56
1:B:32:LEU:HD12	1:B:89:GLY:HA2	1.87	0.56
1:A:241:LEU:HG	1:A:314:VAL:HG13	1.88	0.55
1:B:213:LYS:HB2	1:B:265:LYS:CD	2.35	0.55
1:A:145:SER:HB2	1:A:248:HIS:HE1	1.71	0.55
1:A:238:CYS:HG	1:A:317:ARG:HB2	1.71	0.55
1:B:272:GLY:HA2	1:B:275:ARG:HE	1.70	0.55
1:B:248:HIS:O	1:B:251:MET:HE3	2.07	0.55
1:A:235:ARG:HG3	1:A:236:PRO:HD2	1.88	0.54
1:B:72:PHE:CE2	1:B:260:ILE:HG23	2.42	0.54
1:B:69:HIS:CD2	1:B:97:PHE:H	2.26	0.54
1:A:175:ALA:HB3	1:A:225:VAL:HB	1.89	0.54
1:B:122:ASP:OD1	1:B:122:ASP:O	2.25	0.54
1:A:280:GLY:O	1:A:281:ILE:C	2.51	0.53
1:A:43:ALA:O	1:A:46:THR:HA	2.09	0.53
1:B:30:GLY:HA3	1:B:87:SER:C	2.33	0.53
1:A:58:ASP:O	1:A:62:TYR:HE2	1.91	0.53
1:A:136:LEU:O	1:A:137:SER:C	2.51	0.53
1:B:97:PHE:HE1	1:B:112:ALA:HB3	1.71	0.53
1:B:246:TYR:CD2	1:B:274:MET:HB2	2.44	0.53
1:B:250:ASP:HB2	1:B:274:MET:HE1	1.90	0.53
1:B:81:LEU:HD11	1:B:282:MET:SD	2.49	0.53
1:A:68:LEU:HD22	1:A:97:PHE:CZ	2.44	0.53
1:A:214:ASN:O	1:A:216:PHE:N	2.39	0.53
1:A:120:LEU:HB2	1:A:121:PRO:HD3	1.91	0.53
1:B:102:ILE:HB	1:B:103:PRO:HD3	1.90	0.53
1:B:231:TYR:CE1	1:B:240:TYR:HB2	2.44	0.52
1:B:70:GLY:O	1:B:73:LEU:HB2	2.10	0.52
1:A:76:HIS:NE2	1:B:76:HIS:HE1	2.06	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:78:TYR:O	1:A:82:LEU:HG	2.09	0.52
1:A:246:TYR:CD2	1:A:274:MET:HB2	2.44	0.52
1:A:27:PHE:CD2	1:A:307:ALA:HA	2.44	0.52
1:B:193:SER:HA	1:B:234:CYS:O	2.09	0.52
1:B:249:LEU:HG	1:B:264:CYS:SG	2.50	0.52
1:B:26:VAL:HB	1:B:283:VAL:HG23	1.91	0.52
1:B:297:LEU:O	1:B:301:LEU:HG	2.09	0.52
1:B:213:LYS:HD2	1:B:265:LYS:HD2	1.92	0.51
1:A:271:LYS:HB3	1:A:275:ARG:NH1	2.25	0.51
1:B:144:HIS:HA	1:B:171:LEU:HB2	1.92	0.51
1:B:195:PHE:HB3	1:B:197:MET:HE2	1.91	0.51
1:A:34:VAL:O	1:B:259:PHE:CE2	2.63	0.51
1:B:120:LEU:HB2	1:B:121:PRO:HD3	1.93	0.51
1:B:79:GLU:CG	3:B:402:HOH:O	2.57	0.51
1:B:231:TYR:HA	1:B:234:CYS:SG	2.50	0.51
1:B:79:GLU:HB2	1:B:253:ASP:OD2	2.11	0.51
1:B:192:PRO:HD3	1:B:232:ARG:HH21	1.76	0.51
1:B:179:LYS:HG3	1:B:190:TYR:CE2	2.45	0.51
1:B:134:PRO:HB2	1:B:136:LEU:CD2	2.41	0.50
1:A:171:LEU:HD21	1:A:282:MET:SD	2.51	0.50
1:B:71:PHE:HB2	1:B:146:ARG:HD3	1.93	0.50
1:A:88:HIS:CD2	1:A:283:VAL:HG21	2.44	0.50
1:B:27:PHE:HE2	1:B:306:VAL:HG23	1.76	0.50
1:A:155:ALA:C	1:A:157:GLY:N	2.66	0.50
1:A:240:TYR:OH	1:A:242:VAL:HG21	2.11	0.50
1:A:39:VAL:HG21	1:A:127:VAL:HG21	1.92	0.49
1:A:141:LEU:HB2	1:A:165:PHE:CD2	2.46	0.49
1:A:270:CYS:HB3	1:A:273:LYS:CG	2.41	0.49
1:B:223:LYS:O	1:B:224:ASP:HB2	2.12	0.49
1:A:26:VAL:HG11	1:A:296:ASP:CG	2.37	0.49
1:A:284:ALA:O	1:A:285:PHE:C	2.56	0.49
1:B:240:TYR:CZ	1:B:242:VAL:CG2	2.95	0.49
1:A:212:LYS:HG2	1:A:213:LYS:H	1.77	0.48
1:A:240:TYR:HE2	1:A:313:PRO:CG	2.12	0.48
1:B:173:PRO:HG2	1:B:230:PHE:CD2	2.48	0.48
1:A:32:LEU:HD22	1:A:89:GLY:HA2	1.94	0.48
1:A:136:LEU:HD13	1:A:163:LEU:CD1	2.42	0.48
1:B:124:LEU:O	1:B:128:LEU:HG	2.12	0.48
1:B:247:GLY:H	1:B:250:ASP:CG	2.20	0.48
1:B:149:HIS:HE1	1:B:184:GLN:O	1.97	0.48
1:B:84:HIS:O	1:B:85:VAL:C	2.55	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:49:ILE:O	1:A:51:VAL:HG13	2.13	0.48
1:B:270:CYS:HB3	1:B:273:LYS:CG	2.42	0.48
1:A:154:LEU:CD1	1:A:159:ALA:HB3	2.44	0.48
1:A:149:HIS:CE1	1:A:185:PRO:O	2.67	0.47
1:B:53:ILE:HG12	1:B:93:VAL:HG22	1.96	0.47
1:A:64:VAL:O	1:A:139:LEU:HA	2.15	0.47
1:A:304:PRO:HB3	1:A:311:LEU:HB2	1.96	0.47
1:B:47:PRO:HA	1:B:119:TRP:NE1	2.29	0.47
1:A:195:PHE:CZ	1:A:233:GLU:HB2	2.49	0.47
1:A:240:TYR:CZ	1:A:242:VAL:CG2	2.97	0.47
1:B:212:LYS:HD3	1:B:219:PRO:HD3	1.96	0.47
1:B:277:CYS:O	1:B:281:ILE:HG13	2.15	0.47
1:A:59:ALA:HA	1:A:132:VAL:HG22	1.96	0.47
1:B:39:VAL:CG2	1:B:47:PRO:HG3	2.44	0.47
1:B:124:LEU:HB3	1:B:125:PRO:HD3	1.97	0.47
1:A:249:LEU:HD22	1:A:252:LEU:HD11	1.96	0.47
1:A:258:LYS:HZ3	1:B:83:ARG:HB3	1.80	0.47
1:B:86:ALA:O	1:B:89:GLY:N	2.33	0.47
1:A:34:VAL:O	1:B:259:PHE:HE2	1.98	0.46
1:A:246:TYR:HE2	1:A:309:THR:CG2	2.29	0.46
1:A:26:VAL:HG11	1:A:296:ASP:CB	2.44	0.46
1:A:229:GLU:O	1:A:230:PHE:C	2.59	0.46
1:B:74:HIS:HB2	1:B:77:PHE:CE1	2.51	0.46
1:B:158:HIS:CE1	1:B:187:ILE:HG22	2.46	0.46
1:A:49:ILE:HD13	1:A:112:ALA:HB1	1.97	0.46
1:A:76:HIS:NE2	1:B:76:HIS:CE1	2.83	0.46
1:A:258:LYS:NZ	1:B:83:ARG:HB3	2.31	0.46
1:A:292:GLU:O	1:A:292:GLU:CG	2.60	0.46
1:A:296:ASP:O	1:A:300:ILE:HG13	2.15	0.46
1:A:240:TYR:C	1:A:241:LEU:HD12	2.41	0.46
1:A:282:MET:O	1:A:283:VAL:C	2.59	0.46
1:B:54:VAL:HB	1:B:92:ILE:CG2	2.46	0.46
1:B:255:ASP:O	1:B:256:ALA:C	2.60	0.45
1:A:202:LEU:HD21	1:A:204:ILE:HD11	1.98	0.45
1:B:121:PRO:HG3	1:B:163:LEU:HD21	1.99	0.45
1:A:74:HIS:HB2	1:A:77:PHE:CE1	2.51	0.45
1:A:209:GLY:C	1:A:221:ALA:HB3	2.41	0.45
1:A:231:TYR:CG	1:A:240:TYR:HB2	2.51	0.45
1:A:246:TYR:HB2	1:A:274:MET:SD	2.57	0.45
1:B:128:LEU:HD12	1:B:134:PRO:HD3	1.98	0.45
1:A:297:LEU:O	1:A:301:LEU:HG	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:256:ALA:HB1	1:B:261:THR:HG21	1.98	0.45
1:A:293:LYS:O	1:A:294:ASP:C	2.59	0.45
1:B:106:ASP:O	1:B:110:ILE:HG13	2.17	0.45
1:A:231:TYR:CD2	1:A:240:TYR:HB2	2.52	0.45
1:A:27:PHE:CE2	1:A:307:ALA:CA	2.94	0.44
1:A:257:PRO:HA	1:B:83:ARG:NE	2.28	0.44
1:A:277:CYS:SG	1:A:311:LEU:HD21	2.57	0.44
1:B:63:PRO:HG2	1:B:90:PHE:CD1	2.52	0.44
1:B:105:GLY:HA3	1:B:184:GLN:HB2	1.99	0.44
1:B:138:LYS:HB3	1:B:290:LEU:HD22	1.98	0.44
1:B:37:ILE:HD11	1:B:129:PRO:HG3	1.98	0.44
1:B:78:TYR:O	1:B:82:LEU:HD13	2.17	0.44
1:B:121:PRO:HA	1:B:136:LEU:HD12	2.00	0.44
1:A:208:LEU:HB2	1:A:247:GLY:HA2	2.00	0.44
1:A:257:PRO:HA	1:B:83:ARG:HH21	1.82	0.44
1:B:149:HIS:O	1:B:150:THR:C	2.59	0.44
1:B:220:CYS:O	1:B:222:PRO:HD3	2.18	0.44
1:A:144:HIS:O	1:A:147:GLY:N	2.50	0.43
1:B:48:PRO:HG2	1:B:116:VAL:HG22	2.00	0.43
1:B:106:ASP:O	1:B:107:ALA:C	2.61	0.43
1:A:55:ALA:HB2	1:A:91:ILE:HG23	1.99	0.43
1:A:138:LYS:HB3	1:A:290:LEU:CD2	2.45	0.43
1:B:231:TYR:OH	1:B:317:ARG:HG3	2.19	0.43
1:A:27:PHE:CD1	1:A:280:GLY:HA3	2.53	0.43
1:B:236:PRO:HG3	1:B:317:ARG:HB3	2.00	0.43
1:B:26:VAL:HG23	1:B:27:PHE:N	2.32	0.43
1:B:62:TYR:HD2	1:B:132:VAL:HG13	1.83	0.43
1:B:246:TYR:CB	1:B:274:MET:SD	3.06	0.43
1:B:89:GLY:O	1:B:90:PHE:CG	2.71	0.43
1:B:167:ALA:N	1:B:199:MET:HB2	2.34	0.43
1:B:27:PHE:O	1:B:84:HIS:HE1	2.02	0.43
1:B:136:LEU:O	1:B:137:SER:C	2.62	0.43
1:A:27:PHE:HD1	1:A:280:GLY:HA3	1.83	0.43
1:A:284:ALA:O	1:A:287:ASN:N	2.52	0.43
1:A:173:PRO:HB2	1:A:230:PHE:CE2	2.54	0.42
1:B:118:ASP:CG	1:B:162:GLN:H	2.26	0.42
1:B:135:GLU:HG2	1:B:137:SER:HG	1.84	0.42
1:B:252:LEU:HD23	1:B:252:LEU:HA	1.89	0.42
1:A:155:ALA:O	1:A:157:GLY:N	2.52	0.42
1:A:220:CYS:C	1:A:222:PRO:HD3	2.43	0.42
1:B:231:TYR:O	1:B:317:ARG:NH2	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:32:LEU:HD22	1:A:89:GLY:CA	2.49	0.42
1:B:27:PHE:O	1:B:84:HIS:CE1	2.72	0.42
1:B:124:LEU:N	1:B:125:PRO:CD	2.82	0.42
1:B:155:ALA:C	1:B:157:GLY:H	2.26	0.42
1:B:245:ASP:O	1:B:246:TYR:CG	2.72	0.42
1:B:128:LEU:HD23	1:B:128:LEU:HA	1.85	0.42
1:B:152:PHE:CG	1:B:168:LEU:HD21	2.54	0.42
1:B:206:THR:HG21	1:B:248:HIS:HA	2.01	0.42
1:A:45:PRO:CG	1:A:123:GLY:CA	2.91	0.42
1:A:135:GLU:O	1:A:136:LEU:C	2.62	0.42
1:A:189:THR:H	1:A:233:GLU:CD	2.28	0.42
1:A:77:PHE:N	1:A:77:PHE:CD1	2.84	0.42
1:B:234:CYS:HB2	1:B:317:ARG:HH21	1.83	0.42
1:B:235:ARG:O	1:B:236:PRO:C	2.63	0.42
1:B:236:PRO:HB3	1:B:318:VAL:CA	2.49	0.42
1:A:38:GLN:HG2	1:A:52:LEU:HD13	2.00	0.42
1:B:145:SER:OG	1:B:146:ARG:N	2.53	0.42
1:B:146:ARG:O	1:B:147:GLY:C	2.63	0.42
1:B:240:TYR:OH	1:B:242:VAL:HG21	2.19	0.42
1:B:246:TYR:HB3	1:B:274:MET:SD	2.59	0.42
1:A:45:PRO:HG3	1:A:123:GLY:CA	2.49	0.42
1:B:119:TRP:CZ2	1:B:123:GLY:HA3	2.55	0.42
1:B:145:SER:HB2	1:B:248:HIS:CE1	2.55	0.42
1:B:175:ALA:O	1:B:183:LEU:HG	2.20	0.42
1:A:152:PHE:CG	1:A:168:LEU:HD21	2.55	0.41
1:A:84:HIS:O	1:A:87:SER:OG	2.33	0.41
1:A:239:TYR:HD1	1:A:316:HIS:HB2	1.85	0.41
1:B:69:HIS:NE2	1:B:97:PHE:N	2.68	0.41
1:A:66:MET:O	1:A:142:ALA:N	2.44	0.41
1:A:40:ASP:C	1:A:42:ASN:N	2.78	0.41
1:A:149:HIS:CE1	1:A:187:ILE:HG12	2.55	0.41
1:A:156:LEU:HD23	1:A:158:HIS:HE1	1.84	0.41
1:A:220:CYS:O	1:A:222:PRO:HD3	2.20	0.41
1:A:226:ASN:OD1	1:A:228:ALA:HB3	2.20	0.41
1:B:186:LYS:O	1:B:186:LYS:CG	2.63	0.41
1:A:62:TYR:HD2	1:A:132:VAL:HG13	1.85	0.41
1:A:79:GLU:HB3	1:A:253:ASP:OD2	2.20	0.41
1:B:121:PRO:HA	1:B:136:LEU:CD1	2.50	0.41
1:A:156:LEU:HD23	1:A:158:HIS:CE1	2.55	0.41
1:A:279:ALA:O	1:A:283:VAL:HG23	2.20	0.41
1:A:39:VAL:HG12	1:A:47:PRO:HG3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:69:HIS:HD2	1:A:95:PRO:O	2.03	0.41
1:A:167:ALA:N	1:A:199:MET:SD	2.93	0.41
1:A:48:PRO:HD3	1:A:119:TRP:CG	2.56	0.41
1:A:169:ILE:HG21	1:A:282:MET:HG2	2.02	0.41
1:B:119:TRP:HE3	1:B:120:LEU:HD23	1.85	0.41
1:B:151:ALA:O	1:B:152:PHE:C	2.64	0.41
1:A:70:GLY:HA3	1:A:73:LEU:HD12	2.03	0.41
1:B:168:LEU:O	1:B:201:VAL:HA	2.20	0.41
1:B:254:ASP:OD1	1:B:275:ARG:NH2	2.45	0.41
1:A:119:TRP:CE2	1:A:123:GLY:HA3	2.55	0.40
1:B:222:PRO:HB2	1:B:225:VAL:CG2	2.49	0.40
1:A:239:TYR:HE1	1:A:318:VAL:CG1	2.35	0.40
1:B:220:CYS:C	1:B:222:PRO:HD3	2.46	0.40
1:B:282:MET:O	1:B:283:VAL:C	2.63	0.40
1:A:129:PRO:O	1:A:130:LYS:C	2.64	0.40
1:A:155:ALA:O	1:A:156:LEU:C	2.62	0.40
1:A:213:LYS:HG2	1:A:214:ASN:ND2	2.36	0.40
1:A:71:PHE:CD2	1:A:72:PHE:HB2	2.57	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	296/325 (91%)	266 (90%)	30 (10%)	0	100	100
1	B	295/325 (91%)	268 (91%)	27 (9%)	0	100	100
All	All	591/650 (91%)	534 (90%)	57 (10%)	0	100	100

There are no Ramachandran outliers to report.

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	239/256 (93%)	239 (100%)	0	100	100
1	B	238/256 (93%)	238 (100%)	0	100	100
All	All	477/512 (93%)	477 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	80	HIS
1	A	158	HIS
1	A	184	GLN
1	A	214	ASN
1	A	248	HIS
1	B	76	HIS
1	B	158	HIS
1	B	184	GLN

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

Of 1 ligands modelled in this entry, 1 is 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

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	298/325 (91%)	0.87	28 (9%)	14 18	88, 119, 147, 178	0
1	B	297/325 (91%)	0.90	37 (12%)	8 13	101, 137, 176, 208	0
All	All	595/650 (91%)	0.88	65 (10%)	10 15	88, 126, 163, 208	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	240	TYR	6.7
1	B	271	LYS	4.8
1	B	102	ILE	4.3
1	B	254	ASP	3.8
1	B	179	LYS	3.6
1	B	195	PHE	3.4
1	B	180	SER	3.4
1	A	24	THR	3.4
1	B	159	ALA	3.3
1	B	241	LEU	3.3
1	A	301	LEU	3.3
1	B	158	HIS	3.2
1	B	24	THR	3.1
1	A	254	ASP	3.1
1	B	98	SER	3.0
1	A	319	ALA	3.0
1	A	57	LYS	3.0
1	A	300	ILE	2.9
1	A	249	LEU	2.9
1	B	276	ARG	2.9
1	A	109	ASP	2.9
1	B	262	CYS	2.9
1	A	240	TYR	2.7
1	B	300	ILE	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	227	HIS	2.7
1	A	31	LYS	2.7
1	B	294	ASP	2.7
1	B	275	ARG	2.7
1	A	161	THR	2.6
1	A	159	ALA	2.6
1	B	301	LEU	2.6
1	A	98	SER	2.5
1	A	45	PRO	2.5
1	B	43	ALA	2.5
1	A	244	LYS	2.4
1	A	313	PRO	2.4
1	A	241	LEU	2.4
1	B	108	GLU	2.4
1	B	318	VAL	2.4
1	B	199	MET	2.4
1	B	27	PHE	2.3
1	B	88	HIS	2.3
1	A	122	ASP	2.3
1	B	314	VAL	2.3
1	B	311	LEU	2.2
1	A	104	SER	2.2
1	A	23	PHE	2.2
1	B	41	GLU	2.2
1	B	211	GLU	2.2
1	B	218	PRO	2.2
1	B	103	PRO	2.1
1	A	152	PHE	2.1
1	B	297	LEU	2.1
1	B	26	VAL	2.1
1	A	274	MET	2.1
1	A	271	LYS	2.1
1	A	80	HIS	2.1
1	A	162	GLN	2.1
1	B	101	ILE	2.1
1	A	163	LEU	2.1
1	B	22	ALA	2.0
1	B	263	VAL	2.0
1	A	25	SER	2.0
1	B	221	ALA	2.0
1	B	115	LYS	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](#)

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($\text{\AA}^2$)	Q<0.9
2	CA	A	401	1/1	1.00	0.07	73,73,73,73	0

6.5 Other polymers [i](#)

There are no such residues in this entry.