



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 06:24 am BST

PDB ID : 4YSM
Title : Calcium-Dependent Protein Kinase from Eimeria tenella
Authors : Merritt, E.A.
Deposited on : 2015-03-17
Resolution : 3.19 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

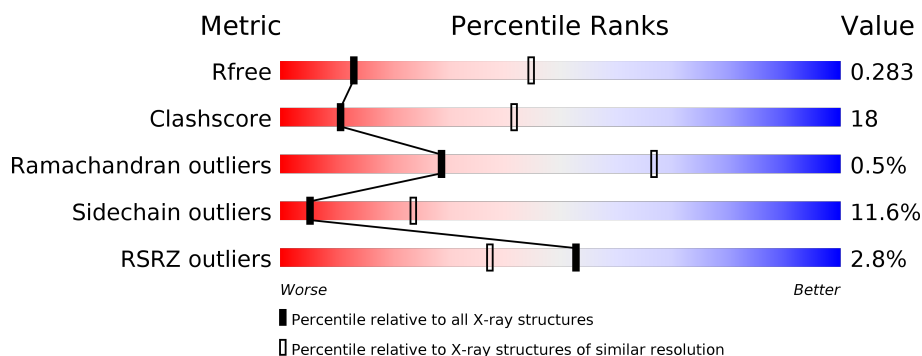
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.19 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 on 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	491	<div> <div>4%</div> <div> <div></div> <div>61%</div> <div>33%</div> <div>• •</div> </div> </div>
1	B	491	<div> <div>2%</div> <div> <div></div> <div>62%</div> <div>31%</div> <div>• •</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7528 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 Calmodulin-like domain protein kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	475	Total	C	N	O	S	0	0	0
			3765	2401	623	725	16			
1	B	475	Total	C	N	O	S	0	0	0
			3753	2393	620	724	16			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP Q3HNM4
A	-2	PRO	-	expression tag	UNP Q3HNM4
A	-1	GLY	-	expression tag	UNP Q3HNM4
A	0	SER	-	expression tag	UNP Q3HNM4
A	392	ASP	ALA	See Remark 999	UNP Q3HNM4
B	-3	GLY	-	expression tag	UNP Q3HNM4
B	-2	PRO	-	expression tag	UNP Q3HNM4
B	-1	GLY	-	expression tag	UNP Q3HNM4
B	0	SER	-	expression tag	UNP Q3HNM4
B	392	ASP	ALA	See Remark 999	UNP Q3HNM4

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	4	Total	Ca	0	0
			4	4		
2	A	4	Total	Ca	0	0
			4	4		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	O	0	0
			1	1		

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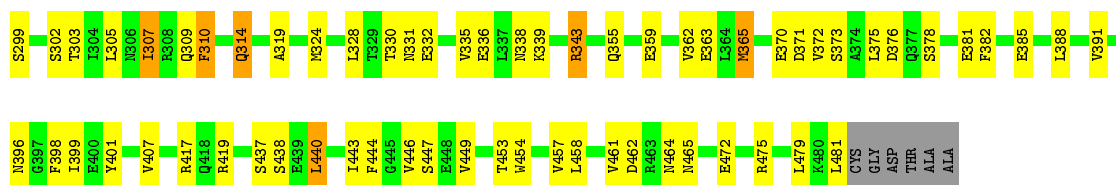
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	O	0	0
			1	1		

These plots are drawn for all protein, RNA and DNA 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 ($\text{RSRZ} > 2$). 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.

- Chain A:

Amino Acid	Count
ASP	3373
THR	A374
ALA	L375
ALA	Q376
ALA	Q377
ASP	E381
THR	F382
ALA	A291
ALA	E385
ALA	L388
THR	V391
ALA	N396
THR	G397
ALA	F398
ALA	Y401
THR	Y407
ALA	A408
THR	R417
ALA	Q418
THR	R419
ALA	D430
THR	S437
ALA	S438
THR	F439
ALA	L440
THR	I443
ALA	F444
THR	G445
ALA	V446
THR	S447
ALA	F448
ALA	Y449
THR	T453
ALA	I454
THR	R455
ALA	R456
THR	V457
ALA	L458
THR	V461
ALA	D462
THR	R463
ALA	I464
THR	L479
ALA	F480
THR	L481
ALA	CYS
THR	GLY
ALA	E180
THR	S181
ALA	L285
THR	K286
ALA	T287
THR	K183
ALA	T288
THR	D289
ALA	A290
THR	T292
ALA	D296
THR	V297
ALA	P298
THR	S299
ALA	L300
THR	E301
ALA	S302
THR	T303
ALA	I307
THR	F310
ALA	Q314
THR	A319
ALA	M324
THR	L328
ALA	T329
THR	S330
ALA	N331
THR	E332
ALA	E333
THR	T334
ALA	V335
THR	E336
ALA	L337
THR	V438
ALA	N338
THR	K339
ALA	Q342
THR	R343
ALA	D353
THR	K354
ALA	Q355
THR	E356
ALA	E363
THR	L364
ALA	M365
THR	K366
ALA	L367
THR	K368
ALA	E370
THR	S371
ALA	D372
THR	E180
THR	S181
ALA	L285
THR	K286
ALA	T287
THR	K183
ALA	T288
THR	D289
ALA	A290
THR	T292
ALA	D296
THR	V297
ALA	P298
THR	S299
ALA	L300
THR	E301
ALA	S302
THR	T303
ALA	I307
THR	F310
ALA	Q314
THR	A319
ALA	M324
THR	L328
ALA	T329
THR	S330
ALA	N331
THR	E332
ALA	E333
THR	T334
ALA	V335
THR	E336
ALA	L337
THR	V438
ALA	N338
THR	K339
ALA	Q342
THR	R343
ALA	D353
THR	K354
ALA	Q355
THR	E356
ALA	E363
THR	L364
ALA	M365
THR	K366
ALA	L367
THR	K368
ALA	E370
THR	S371
ALA	D372
THR	E180
THR	S181
ALA	L285
THR	K286
ALA	T287
THR	K183
ALA	T288
THR	D289
ALA	A290
THR	T292
ALA	D296
THR	V297
ALA	P298
THR	S299
ALA	L300
THR	E301
ALA	S302
THR	T303
ALA	I307
THR	F310
ALA	Q314
THR	A319
ALA	M324
THR	L328
ALA	T329
THR	S330
ALA	N331
THR	E332
ALA	E333
THR	T334
ALA	V335
THR	E336
ALA	L337
THR	V438
ALA	N338
THR	K339
ALA	Q342
THR	R343
ALA	D353
THR	K354
ALA	Q355
THR	E356
ALA	E363
THR	L364
ALA	M365
THR	K366
ALA	L367
THR	K368
ALA	E370
THR	S371
ALA	D372
THR	E180
THR	S181
ALA	L285
THR	K286
ALA	T287
THR	

- Chain B:
-
- | Amino Acid | Frequency (%) |
|------------|---------------|
| GLY | 2.0 |
| PRO | 1.0 |
| GLY | 1.0 |
| SER | 1.0 |
| PRO | 1.0 |
| ALA | 1.0 |
| SER | 1.0 |
| SER | 1.0 |
| LVS | 1.0 |
| SER | 1.0 |
| D7 | 1.0 |
| S20 | 1.0 |
| T21 | 1.0 |
| S25 | 1.0 |
| K36 | 1.0 |
| G37 | 1.0 |
| S38 | 1.0 |
| F39 | 1.0 |
| G40 | 1.0 |
| E41 | 1.0 |
| I42 | 1.0 |
| I43 | 1.0 |
| L44 | 1.0 |
| C45 | 1.0 |
| Q52 | 1.0 |
| V56 | 1.0 |
| S60 | 1.0 |
| K61 | 1.0 |
| R62 | 1.0 |
| Q63 | 1.0 |
| V64 | 1.0 |
| K65 | 1.0 |
| T68 | 1.0 |
| D69 | 1.0 |
| L72 | 1.0 |
| L73 | 1.0 |
| L74 | 1.0 |
| K75 | 1.0 |
| E76 | 1.0 |
| V77 | 1.0 |
| D84 | 1.0 |
| M89 | 1.0 |
| Y92 | 1.0 |
| F95 | 1.0 |
| E96 | 1.0 |
| D97 | 1.0 |
| F101 | 1.0 |
| Y102 | 1.0 |
| L103 | 1.0 |
| V104 | 1.0 |
| T105 | 1.0 |
| E106 | 1.0 |
| V107 | 1.0 |
| Y108 | 1.0 |
| L113 | 1.0 |
| F114 | 1.0 |
| D115 | 1.0 |
| E116 | 1.0 |
| I117 | 1.0 |
| I118 | 1.0 |
| K121 | 1.0 |
| R122 | 1.0 |
| F123 | 1.0 |
| A129 | 1.0 |
| R133 | 1.0 |
| Q134 | 1.0 |
| V135 | 1.0 |
| L136 | 1.0 |
| S137 | 1.0 |
| G138 | 1.0 |
| I139 | 1.0 |
| T140 | 1.0 |
| Y141 | 1.0 |
| H149 | 1.0 |
| R150 | 1.0 |
| D151 | 1.0 |
| L152 | 1.0 |
| K153 | 1.0 |
| L158 | 1.0 |
| M161 | 1.0 |
| K162 | 1.0 |
| R163 | 1.0 |
| K164 | 1.0 |
| I168 | 1.0 |
| R169 | 1.0 |
| T170 | 1.0 |
| I171 | 1.0 |
| L175 | 1.0 |
| S176 | 1.0 |
| T177 | 1.0 |
| H178 | 1.0 |
| F179 | 1.0 |
| E180 | 1.0 |
| S181 | 1.0 |
| K182 | 1.0 |
| I183 | 1.0 |
| K186 | 1.0 |
| G202 | 1.0 |
| D205 | 1.0 |
| E206 | 1.0 |
| K207 | 1.0 |
| I216 | 1.0 |
| L217 | 1.0 |
| Y218 | 1.0 |
| S222 | 1.0 |
| N228 | 1.0 |
| G229 | 1.0 |
| E232 | 1.0 |
| F233 | 1.0 |
| D234 | 1.0 |
| I235 | 1.0 |
| K237 | 1.0 |
| K238 | 1.0 |
| E239 | 1.0 |
| E240 | 1.0 |
| F246 | 1.0 |
| D247 | 1.0 |
| L248 | 1.0 |
| F249 | 1.0 |
| Q250 | 1.0 |
| W251 | 1.0 |
| V254 | 1.0 |
| S255 | 1.0 |
| E256 | 1.0 |
| P257 | 1.0 |
| K259 | 1.0 |
| D260 | 1.0 |
| L261 | 1.0 |
| T271 | 1.0 |
| L280 | 1.0 |
| E281 | 1.0 |
| H282 | 1.0 |
| E283 | 1.0 |
| W284 | 1.0 |
| K285 | 1.0 |
| K286 | 1.0 |
| T287 | 1.0 |
| T288 | 1.0 |
| A291 | 1.0 |
| T292 | 1.0 |
| D296 | 1.0 |
| V297 | 1.0 |



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	66.67Å 109.56Å 77.73Å 90.00° 92.17° 90.00°	Depositor
Resolution (Å)	38.84 – 3.19 38.84 – 3.19	Depositor EDS
% Data completeness (in resolution range)	97.7 (38.84-3.19) 97.8 (38.84-3.19)	Depositor EDS
R_{merge}	0.50	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.44 (at 3.18Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.228 , 0.280 0.230 , 0.283	Depositor DCC
R_{free} test set	910 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	74.2	Xtriage
Anisotropy	0.022	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 56.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.047 for h,-k,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	7528	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.40% 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](#)

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	0.53	0/3829	0.74	2/5156 (0.0%)
1	B	0.55	0/3817	0.75	2/5142 (0.0%)
All	All	0.54	0/7646	0.75	4/10298 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	430	ASP	CB-CG-OD1	5.60	123.34	118.30
1	A	376	ASP	CB-CG-OD2	-5.60	113.26	118.30
1	B	343	ARG	NE-CZ-NH2	5.32	122.96	120.30
1	B	310	PHE	N-CA-C	-5.15	97.10	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3765	0	3739	145	2
1	B	3753	0	3709	132	2
2	A	4	0	0	0	0
2	B	4	0	0	0	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
All	All	7528	0	7448	274	2

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 18.

All (274) 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:248:LEU:HD12	1:A:251:TRP:HE1	0.99	1.08
1:A:371:ASP:O	1:A:375:LEU:HD11	1.54	1.06
1:A:64:VAL:HG23	1:A:69:ASP:HB3	1.38	1.05
1:A:336:GLU:N	1:A:336:GLU:OE2	1.88	1.05
1:B:246:PHE:HE2	1:B:259:LYS:HB3	1.19	1.03
1:A:246:PHE:HE2	1:A:259:LYS:HB3	1.21	1.03
1:A:301:GLU:OE1	1:A:368:LYS:NZ	1.92	1.02
1:A:248:LEU:HD12	1:A:251:TRP:NE1	1.76	1.00
1:A:371:ASP:O	1:A:375:LEU:CD1	2.12	0.98
1:A:283:GLU:O	1:A:287:THR:N	1.98	0.96
1:A:284:TRP:O	1:A:288:THR:OG1	1.84	0.94
1:A:233:PHE:HA	1:A:236:LEU:HD12	1.50	0.93
1:B:64:VAL:HG13	1:B:69:ASP:HB3	1.49	0.92
1:B:283:GLU:O	1:B:287:THR:N	2.03	0.92
1:B:150:ARG:HH12	1:B:177:THR:CG2	1.82	0.92
1:B:233:PHE:HA	1:B:236:LEU:HD12	1.50	0.90
1:B:246:PHE:CE2	1:B:259:LYS:HB3	2.06	0.90
1:A:246:PHE:CE2	1:A:259:LYS:HB3	2.07	0.89
1:B:453:THR:O	1:B:457:VAL:HG23	1.73	0.89
1:B:149:HIS:CE1	1:B:151:ASP:O	2.26	0.88
1:A:453:THR:O	1:A:457:VAL:HG23	1.74	0.87
1:A:292:THR:OG1	1:A:343:ARG:NH1	2.08	0.86
1:B:150:ARG:NH1	1:B:177:THR:CG2	2.40	0.85
1:A:64:VAL:CG2	1:A:69:ASP:HB3	2.05	0.84
1:B:64:VAL:CG1	1:B:69:ASP:HB3	2.06	0.84
1:A:366:LYS:O	1:A:369:GLY:N	2.12	0.83
1:A:284:TRP:HA	1:A:287:THR:HG22	1.60	0.82
1:B:284:TRP:HA	1:B:287:THR:HG22	1.62	0.82
1:B:375:LEU:HD12	1:B:375:LEU:N	1.93	0.82
1:A:374:ALA:C	1:A:375:LEU:HD12	2.01	0.81
1:B:150:ARG:NH1	1:B:177:THR:HG22	1.96	0.81
1:B:284:TRP:O	1:B:288:THR:OG1	1.97	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:310:PHE:CD1	1:B:407:VAL:HG22	2.16	0.81
1:A:330:THR:HB	1:A:333:GLU:HG3	1.63	0.81
1:A:303:THR:HG23	1:A:408:ALA:HB1	1.63	0.80
1:B:150:ARG:HH12	1:B:177:THR:HG21	1.48	0.78
1:A:454:TRP:CE2	1:A:458:LEU:HD21	2.18	0.78
1:A:455:ARG:HA	1:A:458:LEU:HD12	1.64	0.78
1:A:66:GLN:HB3	1:A:69:ASP:HB2	1.67	0.77
1:A:296:ASP:OD1	1:A:299:SER:N	2.19	0.75
1:B:246:PHE:CE2	1:B:259:LYS:CB	2.70	0.75
1:A:375:LEU:N	1:A:375:LEU:HD12	1.99	0.75
1:B:64:VAL:HG13	1:B:69:ASP:CB	2.16	0.74
1:A:330:THR:O	1:A:333:GLU:HB2	1.88	0.74
1:A:255:SER:OG	1:A:257:PRO:HD2	1.88	0.74
1:B:257:PRO:O	1:B:260:ASP:N	2.20	0.74
1:B:122:ARG:HH12	1:B:250:GLN:HB3	1.51	0.73
1:B:255:SER:OG	1:B:257:PRO:HD2	1.88	0.73
1:A:246:PHE:CE2	1:A:259:LYS:CB	2.71	0.73
1:A:95:PHE:HB2	1:A:102:TYR:HB2	1.72	0.72
1:B:248:LEU:HB3	1:B:250:GLN:HE21	1.55	0.72
1:B:375:LEU:CD1	1:B:375:LEU:N	2.54	0.71
1:A:186:LYS:HA	1:A:202:GLY:O	1.91	0.71
1:A:36:LYS:HE3	1:A:41:GLU:OE1	1.90	0.71
1:A:343:ARG:NH2	1:A:363:GLU:OE1	2.25	0.70
1:B:36:LYS:HE3	1:B:41:GLU:OE1	1.92	0.70
1:B:296:ASP:O	1:B:299:SER:OG	2.11	0.69
1:B:95:PHE:HB2	1:B:102:TYR:HB2	1.73	0.69
1:A:391:VAL:HG13	1:A:407:VAL:HG21	1.75	0.68
1:A:335:VAL:HG13	1:A:336:GLU:N	2.07	0.68
1:B:381:GLU:O	1:B:385:GLU:CG	2.42	0.67
1:B:186:LYS:HA	1:B:202:GLY:O	1.94	0.67
1:A:248:LEU:CD1	1:A:251:TRP:HE1	1.93	0.66
1:B:464:ASN:O	1:B:465:ASN:HB2	1.94	0.66
1:A:248:LEU:HB3	1:A:250:GLN:HE21	1.61	0.66
1:B:335:VAL:HG13	1:B:336:GLU:N	2.09	0.66
1:B:391:VAL:HG13	1:B:407:VAL:HG21	1.78	0.65
1:A:296:ASP:OD1	1:A:298:PRO:N	2.29	0.65
1:B:381:GLU:O	1:B:385:GLU:HG2	1.97	0.64
1:B:382:PHE:HA	1:B:385:GLU:HG3	1.79	0.64
1:A:68:THR:HG23	1:A:69:ASP:N	2.13	0.64
1:B:68:THR:HG23	1:B:69:ASP:N	2.11	0.64
1:A:454:TRP:O	1:A:458:LEU:HG	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:149:HIS:HE1	1:B:151:ASP:O	1.80	0.63
1:B:246:PHE:CE2	1:B:259:LYS:CG	2.82	0.62
1:A:72:LEU:C	1:A:72:LEU:HD23	2.20	0.62
1:B:122:ARG:NH1	1:B:250:GLN:HB3	2.13	0.62
1:B:149:HIS:O	1:B:150:ARG:HB2	1.98	0.62
1:A:382:PHE:HA	1:A:385:GLU:HG3	1.82	0.62
1:A:246:PHE:CE2	1:A:259:LYS:CG	2.82	0.62
1:A:89:MET:SD	1:A:105:THR:HG21	2.40	0.62
1:B:151:ASP:OD2	1:B:175:LEU:HD12	2.00	0.62
1:B:375:LEU:CD1	1:B:375:LEU:H	2.13	0.61
1:B:246:PHE:CE2	1:B:259:LYS:HG2	2.35	0.61
1:B:43:ILE:HG22	1:B:45:CYS:SG	2.40	0.61
1:A:151:ASP:OD2	1:A:175:LEU:HD12	2.01	0.61
1:B:64:VAL:O	1:B:64:VAL:HG12	1.98	0.61
1:A:246:PHE:CE2	1:A:259:LYS:HG2	2.36	0.61
1:A:43:ILE:HG22	1:A:45:CYS:SG	2.41	0.61
1:B:283:GLU:HA	1:B:286:LYS:HB3	1.82	0.61
1:B:89:MET:SD	1:B:105:THR:HG21	2.42	0.59
1:A:336:GLU:CD	1:A:336:GLU:H	1.97	0.59
1:A:372:VAL:HA	1:A:375:LEU:HD13	1.84	0.58
1:A:258:ALA:HB2	1:A:284:TRP:NE1	2.18	0.58
1:A:375:LEU:N	1:A:375:LEU:CD1	2.64	0.58
1:B:462:ASP:OD1	1:B:465:ASN:HA	2.04	0.58
1:A:296:ASP:OD1	1:A:298:PRO:CD	2.51	0.58
1:A:381:GLU:OE1	1:B:271:THR:OG1	2.22	0.58
1:B:296:ASP:N	1:B:296:ASP:OD2	2.28	0.58
1:A:261:LEU:HB2	1:A:282:HIS:CD2	2.39	0.58
1:B:61:LYS:HD3	1:B:101:PHE:CZ	2.39	0.58
1:B:381:GLU:O	1:B:385:GLU:HG3	2.03	0.57
1:B:261:LEU:HB2	1:B:282:HIS:CD2	2.40	0.57
1:B:331:ASN:O	1:B:332:GLU:C	2.42	0.57
1:A:283:GLU:HA	1:A:286:LYS:HB3	1.86	0.57
1:B:61:LYS:O	1:B:65:LYS:HB2	2.04	0.57
1:A:64:VAL:HG13	1:A:64:VAL:O	2.05	0.56
1:B:258:ALA:HB2	1:B:284:TRP:NE1	2.20	0.56
1:A:353:ASP:OD1	1:A:356:GLU:HG3	2.05	0.56
1:B:61:LYS:HD2	1:B:65:LYS:HD3	1.87	0.56
1:B:454:TRP:O	1:B:458:LEU:HG	2.04	0.56
1:B:61:LYS:HD3	1:B:101:PHE:CE2	2.41	0.56
1:A:366:LYS:O	1:A:369:GLY:CA	2.54	0.55
1:A:381:GLU:O	1:A:385:GLU:CG	2.54	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:VAL:HG22	1:A:104:VAL:HG22	1.88	0.55
1:B:63:GLN:O	1:B:64:VAL:HG23	2.07	0.55
1:B:328:LEU:HB3	1:B:419:ARG:HD2	1.90	0.54
1:A:256:GLU:O	1:A:259:LYS:HB2	2.08	0.54
1:A:328:LEU:HD23	1:A:419:ARG:HG3	1.89	0.54
1:B:56:VAL:HG22	1:B:104:VAL:HG22	1.89	0.54
1:A:310:PHE:CD1	1:A:407:VAL:HG22	2.42	0.53
1:B:256:GLU:O	1:B:259:LYS:HB2	2.08	0.53
1:A:314:GLN:HB2	1:A:457:VAL:HG22	1.90	0.53
1:A:328:LEU:HB3	1:A:419:ARG:HD2	1.91	0.53
1:B:328:LEU:HD23	1:B:419:ARG:HG3	1.89	0.53
1:B:362:VAL:O	1:B:363:GLU:C	2.47	0.53
1:A:283:GLU:O	1:A:286:LYS:HB3	2.09	0.53
1:B:307:ILE:HG22	1:B:307:ILE:O	2.07	0.53
1:A:375:LEU:O	1:A:377:GLN:N	2.42	0.52
1:A:158:LEU:HD11	1:A:171:ILE:HD13	1.91	0.52
1:B:371:ASP:OD1	1:B:372:VAL:N	2.42	0.52
1:B:158:LEU:HD11	1:B:171:ILE:HD13	1.92	0.52
1:A:381:GLU:O	1:A:385:GLU:HG3	2.09	0.52
1:B:299:SER:O	1:B:303:THR:HG23	2.09	0.52
1:A:335:VAL:CG1	1:A:336:GLU:N	2.73	0.51
1:A:338:ASN:HB3	1:A:401:TYR:OH	2.10	0.51
1:B:122:ARG:HH12	1:B:250:GLN:CB	2.20	0.51
1:B:150:ARG:NH1	1:B:177:THR:HG21	2.16	0.51
1:B:324:MET:HE3	1:B:419:ARG:HB3	1.93	0.51
1:A:354:LYS:NZ	1:A:385:GLU:OE2	2.24	0.50
1:A:296:ASP:OD1	1:A:298:PRO:HD2	2.11	0.50
1:B:150:ARG:HH11	1:B:177:THR:HG22	1.73	0.50
1:A:324:MET:HE3	1:A:419:ARG:HB3	1.91	0.50
1:B:303:THR:O	1:B:307:ILE:HG13	2.11	0.50
1:B:314:GLN:HB2	1:B:457:VAL:HG22	1.93	0.50
1:B:114:PHE:O	1:B:117:ILE:HB	2.11	0.50
1:B:52:GLN:NE2	1:B:330:THR:OG1	2.45	0.50
1:A:61:LYS:HG3	1:A:99:GLY:HA2	1.94	0.50
1:B:355:GLN:O	1:B:359:GLU:HG3	2.12	0.50
1:A:114:PHE:O	1:A:117:ILE:HB	2.11	0.49
1:A:68:THR:CG2	1:A:69:ASP:N	2.75	0.49
1:B:129:ALA:O	1:B:133:ARG:HB2	2.12	0.49
1:B:284:TRP:CA	1:B:287:THR:HG22	2.39	0.49
1:B:72:LEU:C	1:B:72:LEU:HD23	2.32	0.49
1:B:68:THR:CG2	1:B:69:ASP:N	2.74	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:381:GLU:O	1:A:385:GLU:HG2	2.13	0.49
1:B:371:ASP:O	1:B:375:LEU:CD1	2.62	0.48
1:A:372:VAL:C	1:A:375:LEU:HD13	2.33	0.48
1:B:335:VAL:CG1	1:B:336:GLU:N	2.74	0.48
1:B:338:ASN:HB3	1:B:401:TYR:OH	2.13	0.48
1:A:66:GLN:O	1:A:69:ASP:N	2.46	0.48
1:A:129:ALA:O	1:A:133:ARG:HB2	2.13	0.47
1:B:251:TRP:HA	1:B:254:VAL:CG2	2.45	0.47
1:A:454:TRP:NE1	1:A:458:LEU:HD21	2.28	0.47
1:A:284:TRP:CA	1:A:287:THR:HG22	2.38	0.47
1:B:396:ASN:HD21	1:B:398:PHE:HB2	1.80	0.47
1:A:21:THR:HG23	1:A:21:THR:O	2.15	0.47
1:A:330:THR:O	1:A:333:GLU:CB	2.62	0.47
1:A:372:VAL:CA	1:A:375:LEU:HD13	2.45	0.47
1:A:65:LYS:HD2	1:A:65:LYS:HA	1.81	0.47
1:A:303:THR:O	1:A:307:ILE:HG13	2.15	0.47
1:B:161:ASN:OD1	1:B:162:LYS:N	2.48	0.47
1:B:222:SER:HB3	1:B:251:TRP:CZ2	2.50	0.47
1:A:43:ILE:CG2	1:A:45:CYS:SG	3.03	0.47
1:A:153:LYS:HA	1:A:216:ILE:HD11	1.97	0.46
1:B:153:LYS:HA	1:B:216:ILE:HD11	1.97	0.46
1:B:472:GLU:CG	1:B:475:ARG:NH2	2.79	0.46
1:A:106:GLU:CD	1:A:331:ASN:HD21	2.19	0.46
1:A:36:LYS:HG3	1:A:41:GLU:HB3	1.98	0.46
1:A:92:TYR:HE2	1:A:106:GLU:HA	1.80	0.46
1:A:366:LYS:C	1:A:369:GLY:H	2.16	0.46
1:B:454:TRP:CE2	1:B:458:LEU:HD21	2.51	0.46
1:B:65:LYS:O	1:B:65:LYS:HG3	2.15	0.46
1:B:338:ASN:OD1	1:B:339:LYS:N	2.49	0.46
1:B:43:ILE:CG2	1:B:45:CYS:SG	3.03	0.46
1:A:36:LYS:CE	1:A:41:GLU:OE1	2.63	0.46
1:A:232:GLU:HA	1:A:235:ILE:HD12	1.98	0.45
1:A:248:LEU:HB2	1:A:251:TRP:CD1	2.50	0.45
1:B:457:VAL:O	1:B:461:VAL:HG23	2.16	0.45
1:A:161:ASN:HD21	1:A:163:ARG:HD3	1.81	0.45
1:B:115:ASP:HA	1:B:118:ILE:HG12	1.98	0.45
1:B:261:LEU:HD13	1:B:282:HIS:CD2	2.51	0.45
1:B:21:THR:HG23	1:B:21:THR:O	2.16	0.45
1:B:232:GLU:HA	1:B:235:ILE:HD12	1.98	0.45
1:A:64:VAL:HG22	1:A:64:VAL:O	2.16	0.45
1:A:218:TYR:CE1	1:A:251:TRP:CZ2	3.04	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:336:GLU:O	1:A:339:LYS:HB2	2.17	0.45
1:A:457:VAL:O	1:A:461:VAL:HG23	2.17	0.45
1:A:271:THR:HG23	1:B:381:GLU:OE1	2.17	0.45
1:A:108:TYR:CE1	1:A:169:ARG:HG3	2.52	0.45
1:A:161:ASN:OD1	1:A:162:LYS:N	2.50	0.45
1:A:366:LYS:O	1:A:369:GLY:HA2	2.17	0.45
1:B:108:TYR:CE1	1:B:169:ARG:HG3	2.52	0.45
1:B:123:PHE:N	1:B:123:PHE:CD2	2.85	0.45
1:A:335:VAL:CG1	1:A:336:GLU:OE2	2.65	0.45
1:A:66:GLN:CB	1:A:69:ASP:HB2	2.44	0.45
1:A:222:SER:HB3	1:A:251:TRP:CZ2	2.52	0.44
1:A:396:ASN:HD21	1:A:398:PHE:HB2	1.82	0.44
1:A:335:VAL:HG13	1:A:336:GLU:H	1.81	0.44
1:A:372:VAL:HA	1:A:375:LEU:CD1	2.46	0.44
1:B:138:GLY:O	1:B:141:TYR:HB3	2.18	0.44
1:A:372:VAL:HG12	1:A:372:VAL:O	2.18	0.44
1:A:123:PHE:N	1:A:123:PHE:CD2	2.86	0.44
1:A:261:LEU:HD13	1:A:282:HIS:HD2	1.83	0.44
1:A:330:THR:CB	1:A:333:GLU:HG3	2.41	0.43
1:B:261:LEU:HD13	1:B:282:HIS:HD2	1.82	0.43
1:A:138:GLY:O	1:A:141:TYR:HB3	2.18	0.43
1:B:36:LYS:HG3	1:B:41:GLU:HB3	2.01	0.43
1:A:133:ARG:HB3	1:A:133:ARG:CZ	2.48	0.43
1:A:150:ARG:NH2	1:A:175:LEU:O	2.49	0.43
1:A:261:LEU:HD13	1:A:282:HIS:CD2	2.53	0.43
1:B:92:TYR:HE2	1:B:106:GLU:HA	1.84	0.43
1:A:367:LEU:C	1:A:369:GLY:H	2.22	0.43
1:B:248:LEU:HB2	1:B:251:TRP:CD1	2.53	0.43
1:A:115:ASP:HA	1:A:118:ILE:HG12	2.01	0.43
1:B:362:VAL:O	1:B:365:MET:N	2.51	0.43
1:B:205:ASP:OD1	1:B:207:LYS:HB2	2.19	0.42
1:A:205:ASP:OD1	1:A:207:LYS:HB2	2.19	0.42
1:A:440:LEU:O	1:A:443:ILE:HG22	2.20	0.42
1:A:66:GLN:OE1	1:A:68:THR:HG21	2.19	0.42
1:B:297:VAL:N	1:B:298:PRO:CD	2.83	0.42
1:B:106:GLU:CD	1:B:331:ASN:HD21	2.22	0.42
1:B:149:HIS:O	1:B:150:ARG:CB	2.63	0.42
1:A:149:HIS:O	1:A:150:ARG:HB2	2.18	0.42
1:B:149:HIS:ND1	1:B:151:ASP:O	2.51	0.42
1:B:305:LEU:O	1:B:309:GLN:HG3	2.20	0.42
1:B:319:ALA:HB2	1:B:444:PHE:CE1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:LEU:HA	1:A:139:ILE:HG12	2.02	0.42
1:A:258:ALA:HB2	1:A:284:TRP:CE2	2.55	0.42
1:A:74:LEU:O	1:A:77:VAL:HB	2.20	0.42
1:B:310:PHE:O	1:B:310:PHE:CD2	2.73	0.42
1:B:133:ARG:CZ	1:B:133:ARG:HB3	2.50	0.41
1:B:218:TYR:CE1	1:B:251:TRP:CZ2	3.08	0.41
1:B:440:LEU:O	1:B:443:ILE:HG22	2.20	0.41
1:A:455:ARG:CA	1:A:458:LEU:HD12	2.43	0.41
1:B:251:TRP:O	1:B:254:VAL:HG23	2.20	0.41
1:A:134:GLN:OE1	1:A:168:ILE:HB	2.21	0.41
1:B:134:GLN:OE1	1:B:168:ILE:HB	2.20	0.41
1:A:454:TRP:CD2	1:A:458:LEU:HD21	2.56	0.41
1:A:106:GLU:OE2	1:A:331:ASN:OD1	2.38	0.41
1:A:218:TYR:CZ	1:A:251:TRP:HZ2	2.38	0.41
1:A:319:ALA:HB2	1:A:444:PHE:CE1	2.55	0.41
1:A:257:PRO:O	1:A:260:ASP:HB3	2.20	0.41
1:A:39:PHE:CD2	1:A:40:GLY:N	2.89	0.41
1:A:60:SER:OG	1:A:63:GLN:CB	2.69	0.41
1:B:257:PRO:O	1:B:260:ASP:HB3	2.21	0.41
1:B:39:PHE:CD2	1:B:40:GLY:N	2.89	0.41
1:A:455:ARG:HA	1:A:458:LEU:CD1	2.43	0.41
1:A:39:PHE:CE1	1:A:57:LYS:HE2	2.55	0.41
1:B:136:LEU:HA	1:B:139:ILE:HG12	2.02	0.41
1:B:37:GLY:N	1:B:39:PHE:HE2	2.18	0.41
1:B:74:LEU:O	1:B:77:VAL:HB	2.20	0.41
1:B:153:LYS:CA	1:B:216:ILE:HD11	2.51	0.41
1:B:291:ALA:O	1:B:292:THR:C	2.60	0.41
1:A:269:VAL:HG12	1:B:381:GLU:OE2	2.21	0.40
1:B:106:GLU:OE2	1:B:331:ASN:OD1	2.38	0.40
1:A:120:ARG:C	1:A:121:LYS:HG2	2.41	0.40
1:A:133:ARG:NH1	1:A:342:GLN:CD	2.74	0.40
1:A:335:VAL:HG12	1:A:336:GLU:OE2	2.21	0.40
1:A:261:LEU:CB	1:A:282:HIS:CD2	3.05	0.40
1:A:391:VAL:HG13	1:A:407:VAL:CG2	2.49	0.40
1:B:310:PHE:CD2	1:B:310:PHE:C	2.94	0.40
1:B:257:PRO:O	1:B:258:ALA:C	2.59	0.40
1:B:399:ILE:O	1:B:399:ILE:HG22	2.22	0.40

All (2) 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)
1:A:376:ASP:OD2	1:B:25:SER:OG[2_355]	1.95	0.25
1:A:25:SER:OG	1:B:376:ASP:OD2[2_454]	1.99	0.21

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	473/491 (96%)	443 (94%)	28 (6%)	2 (0%)	34	69
1	B	473/491 (96%)	443 (94%)	27 (6%)	3 (1%)	25	64
All	All	946/982 (96%)	886 (94%)	55 (6%)	5 (0%)	29	67

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	250	GLN
1	A	376	ASP
1	B	64	VAL
1	B	121	LYS
1	B	250	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	406/426 (95%)	360 (89%)	46 (11%)	6	25
1	B	402/426 (94%)	354 (88%)	48 (12%)	5	22

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	808/852 (95%)	714 (88%)	94 (12%)	5 24

All (94) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	LYS
1	A	20	SER
1	A	34	LEU
1	A	39	PHE
1	A	52	GLN
1	A	75	LYS
1	A	84	ASP
1	A	97	ASP
1	A	103	LEU
1	A	105	THR
1	A	113	LEU
1	A	122	ARG
1	A	164	LYS
1	A	168	ILE
1	A	178	HIS
1	A	179	PHE
1	A	180	GLU
1	A	228	ASN
1	A	231	ASN
1	A	232	GLU
1	A	238	LYS
1	A	240	GLU
1	A	250	GLN
1	A	280	LEU
1	A	288	THR
1	A	302	SER
1	A	307	ILE
1	A	314	GLN
1	A	336	GLU
1	A	343	ARG
1	A	363	GLU
1	A	365	MET
1	A	370	GLU
1	A	373	SER
1	A	388	LEU
1	A	417	ARG
1	A	437	SER

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Mol	Chain	Res	Type
1	A	438	SER
1	A	440	LEU
1	A	446	VAL
1	A	447	SER
1	A	458	LEU
1	A	463	ARG
1	A	464	ASN
1	A	479	LEU
1	A	481	LEU
1	B	20	SER
1	B	39	PHE
1	B	60	SER
1	B	61	LYS
1	B	69	ASP
1	B	75	LYS
1	B	84	ASP
1	B	97	ASP
1	B	103	LEU
1	B	105	THR
1	B	113	LEU
1	B	122	ARG
1	B	163	ARG
1	B	164	LYS
1	B	168	ILE
1	B	178	HIS
1	B	179	PHE
1	B	180	GLU
1	B	186	LYS
1	B	228	ASN
1	B	232	GLU
1	B	237	LYS
1	B	238	LYS
1	B	240	GLU
1	B	250	GLN
1	B	254	VAL
1	B	271	THR
1	B	280	LEU
1	B	288	THR
1	B	296	ASP
1	B	302	SER
1	B	307	ILE
1	B	314	GLN

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Mol	Chain	Res	Type
1	B	343	ARG
1	B	365	MET
1	B	370	GLU
1	B	373	SER
1	B	378	SER
1	B	388	LEU
1	B	417	ARG
1	B	437	SER
1	B	438	SER
1	B	440	LEU
1	B	446	VAL
1	B	447	SER
1	B	449	VAL
1	B	479	LEU
1	B	481	LEU

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

Mol	Chain	Res	Type
1	A	19	HIS
1	A	250	GLN
1	A	306	ASN
1	A	331	ASN
1	B	19	HIS
1	B	52	GLN
1	B	250	GLN
1	B	331	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry

Of 8 ligands modelled in this entry, 8 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

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	475/491 (96%)	-0.03	18 (3%) 40 26	43, 72, 119, 139	0
1	B	475/491 (96%)	-0.16	9 (1%) 66 53	40, 68, 113, 149	0
All	All	950/982 (96%)	-0.10	27 (2%) 53 37	40, 70, 116, 149	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	7	ASP	7.1
1	A	288	THR	5.3
1	A	287	THR	4.5
1	A	181	SER	4.3
1	A	7	ASP	4.3
1	B	288	THR	4.1
1	B	182	THR	3.8
1	B	180	GLU	3.7
1	A	228	ASN	3.5
1	B	287	THR	3.5
1	A	38	SER	3.4
1	A	182	THR	3.4
1	A	230	ALA	3.2
1	B	181	SER	3.1
1	A	183	LYS	3.0
1	B	68	THR	2.8
1	A	178	HIS	2.7
1	A	186	LYS	2.6
1	B	183	LYS	2.5
1	A	188	LYS	2.4
1	A	180	GLU	2.4
1	A	290	ALA	2.4
1	A	292	THR	2.2
1	B	229	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	185	MET	2.1
1	A	449	VAL	2.1
1	A	189	ILE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no carbohydrates 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	CA	B	503	1/1	0.84	0.11	91,91,91,91	0
2	CA	A	503	1/1	0.87	0.09	83,83,83,83	0
2	CA	B	504	1/1	0.89	0.10	84,84,84,84	0
2	CA	A	504	1/1	0.91	0.16	104,104,104,104	0
2	CA	B	502	1/1	0.95	0.11	58,58,58,58	0
2	CA	A	502	1/1	0.96	0.11	58,58,58,58	0
2	CA	A	501	1/1	0.97	0.10	56,56,56,56	0
2	CA	B	501	1/1	0.99	0.08	53,53,53,53	0

6.5 Other polymers [i](#)

There are no such residues in this entry.