



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 09:00 PM EDT

PDB ID : 5U7Q / pdb_00005u7q
Title : Identification of A New Class of Potent Cdc7 Inhibitors Designed by Putative Pharmacophore Model: Synthesis and Biological Evaluation of 2,3-Dihydrothieno[3,2-d]pyrimidin-4(1H)-ones
Authors : Hoffman, I.D.
Deposited on : 2016-12-12
Resolution : 3.15 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

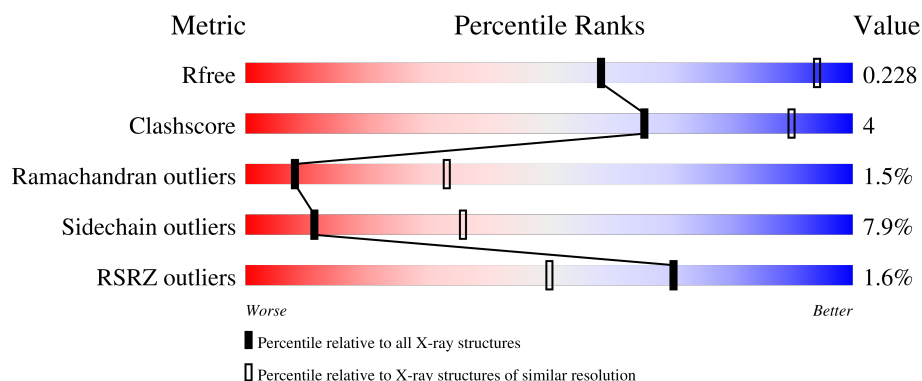
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.15 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	2361 (3.20-3.12)
Clashscore	190562	2486 (3.20-3.12)
Ramachandran outliers	187476	2405 (3.20-3.12)
Sidechain outliers	187428	2404 (3.20-3.12)
RSRZ outliers	180081	2361 (3.20-3.12)

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	395	% 84% 13% ..
1	B	395	2% 81% 13% ..
1	C	395	% 85% 12% ..
1	D	395	3% 80% 12% ...

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12540 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 Rho-associated protein kinase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	388	Total	C	N	O	S	0	0	0
			3147	2018	528	581	20			
1	B	385	Total	C	N	O	S	0	0	0
			3121	2004	521	576	20			
1	C	390	Total	C	N	O	S	0	0	0
			3156	2023	530	583	20			
1	D	383	Total	C	N	O	S	0	0	0
			3106	1996	518	573	19			

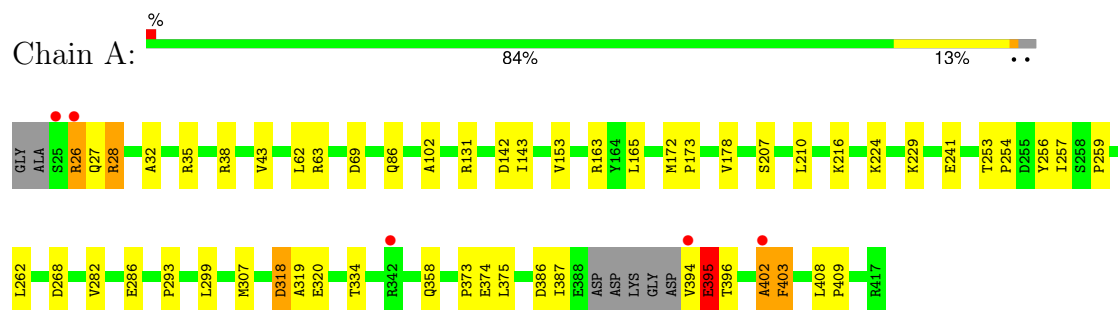
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	O	0	0
			2	2		
2	B	3	Total	O	0	0
			3	3		
2	C	2	Total	O	0	0
			2	2		
2	D	3	Total	O	0	0
			3	3		

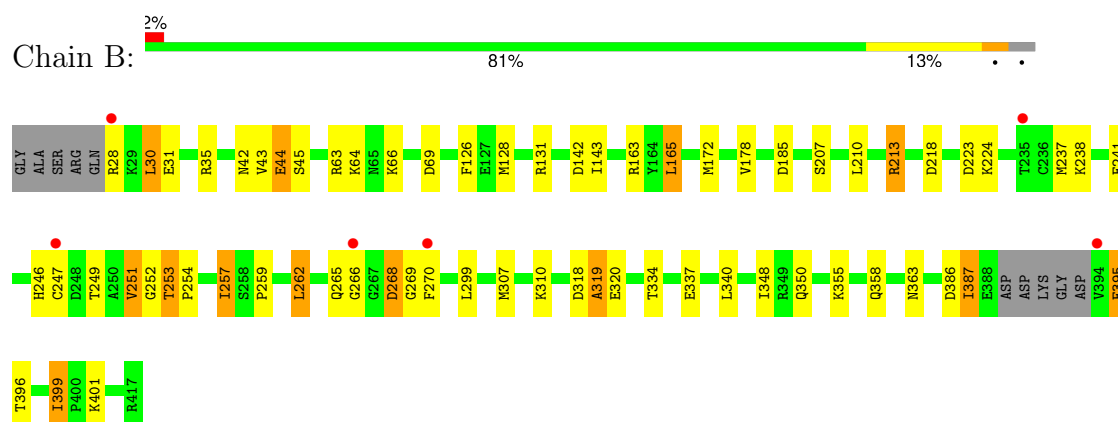
3 Residue-property plots [i](#)

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.

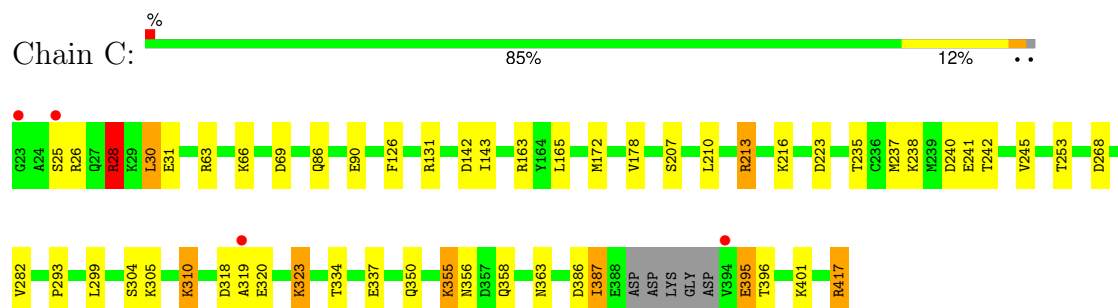
- Molecule 1: Rho-associated protein kinase 2



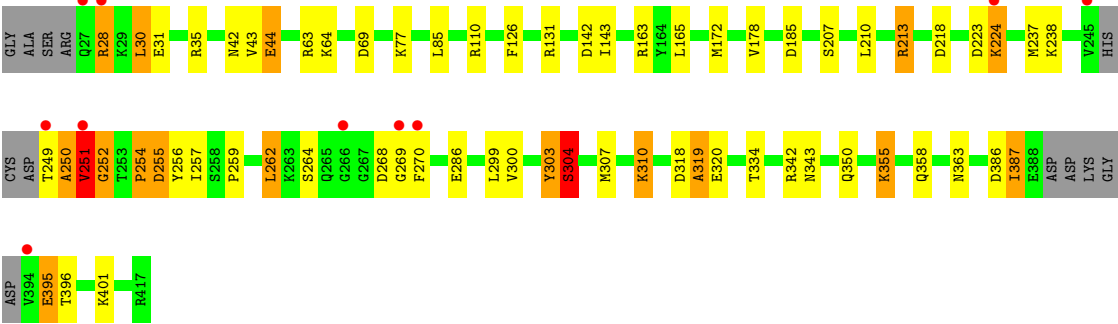
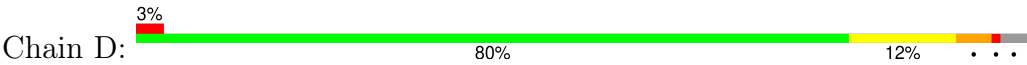
- Molecule 1: Rho-associated protein kinase 2



- Molecule 1: Rho-associated protein kinase 2



- Molecule 1: Rho-associated protein kinase 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	91.19Å 146.46Å 112.42Å 90.00° 96.34° 90.00°	Depositor
Resolution (Å)	30.00 – 3.15 30.00 – 3.15	Depositor EDS
% Data completeness (in resolution range)	97.9 (30.00-3.15) 99.7 (30.00-3.15)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 3.11Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.205 , 0.235 0.203 , 0.228	Depositor DCC
R_{free} test set	2611 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	67.7	Xtriage
Anisotropy	0.082	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 35.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	12540	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.57% 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

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	0.80	0/3225	1.04	9/4357 (0.2%)
1	B	0.76	2/3199 (0.1%)	1.02	7/4323 (0.2%)
1	C	0.75	0/3234	0.99	1/4369 (0.0%)
1	D	0.79	4/3182 (0.1%)	1.05	10/4298 (0.2%)
All	All	0.78	6/12840 (0.0%)	1.02	27/17347 (0.2%)

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
1	D	0	2
All	All	0	4

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	254	PRO	C-O	-6.68	1.15	1.24
1	D	251	VAL	N-CA	6.50	1.54	1.46
1	D	251	VAL	CA-C	6.49	1.60	1.52
1	B	399	ILE	CA-CB	5.21	1.60	1.54
1	D	251	VAL	CA-CB	5.17	1.61	1.54
1	D	304	SER	CA-C	-5.09	1.46	1.52

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	303	TYR	N-CA-C	-12.36	91.99	110.28
1	A	26	ARG	N-CA-C	9.30	124.65	108.75
1	D	304	SER	N-CA-CB	7.74	123.57	110.49
1	D	355	LYS	CA-CB-CG	7.62	129.35	114.10

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	252	GLY	N-CA-C	7.59	121.16	111.37
1	A	403	PHE	N-CA-C	-7.39	95.06	110.80
1	B	252	GLY	N-CA-C	-6.78	103.29	112.57
1	A	403	PHE	N-CA-CB	6.74	121.89	110.49
1	A	402	ALA	N-CA-C	6.55	121.39	112.68
1	D	251	VAL	N-CA-C	6.09	122.01	109.34
1	A	28	ARG	N-CA-C	-5.99	104.68	112.23
1	B	247	CYS	N-CA-C	5.99	119.08	109.02
1	B	253	THR	CA-C-N	5.96	126.48	120.04
1	B	253	THR	C-N-CA	5.96	126.48	120.04
1	A	224	LYS	N-CA-C	5.82	118.37	111.33
1	C	86	GLN	N-CA-C	5.80	118.42	110.24
1	D	85	LEU	CA-C-N	5.79	129.33	120.82
1	D	85	LEU	C-N-CA	5.79	129.33	120.82
1	D	224	LYS	CB-CG-CD	5.43	123.80	111.30
1	D	110	ARG	CG-CD-NE	5.43	123.95	112.00
1	A	163	ARG	N-CA-C	5.36	120.09	113.50
1	B	254	PRO	CB-CA-C	-5.29	103.06	111.04
1	A	318	ASP	N-CA-C	5.27	116.83	111.14
1	B	254	PRO	N-CA-C	5.24	121.34	114.27
1	D	255	ASP	N-CA-CB	5.22	119.31	110.49
1	B	224	LYS	N-CA-C	5.04	117.43	111.33
1	A	86	GLN	N-CA-C	5.04	117.41	110.35

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	246	HIS	Peptide
1	B	269	GLY	Peptide
1	D	251	VAL	Peptide
1	D	252	GLY	Peptide

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	3147	0	3074	31	0
1	B	3121	0	3048	20	0
1	C	3156	0	3082	21	0
1	D	3106	0	3039	27	0
2	A	2	0	0	0	0
2	B	3	0	0	0	0
2	C	2	0	0	0	0
2	D	3	0	0	1	0
All	All	12540	0	12243	95	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 4.

All (95) 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:172:MET:CE	1:A:229:LYS:HD2	1.72	1.19
1:A:172:MET:HE1	1:A:229:LYS:CD	1.74	1.16
1:A:153:VAL:HG22	1:A:172:MET:HE2	1.45	0.98
1:A:153:VAL:HG22	1:A:172:MET:CE	2.09	0.83
1:A:172:MET:HE1	1:A:229:LYS:HD2	0.83	0.77
1:D:28:ARG:HD2	1:D:28:ARG:H	1.55	0.71
1:D:257:ILE:HG21	1:D:262:LEU:HD13	1.72	0.70
1:A:62:LEU:HD21	1:A:402:ALA:O	1.94	0.68
1:B:257:ILE:HG21	1:B:262:LEU:HD13	1.76	0.67
1:D:264:SER:HB2	1:D:269:GLY:HA3	1.78	0.66
1:D:213:ARG:HH11	1:D:213:ARG:HG2	1.60	0.65
1:A:394:VAL:O	1:A:395:GLU:OE1	2.15	0.65
1:D:300:VAL:O	1:D:303:TYR:O	2.14	0.64
1:C:323:LYS:HG3	1:D:343:ASN:HD21	1.62	0.64
1:A:216:LYS:NZ	1:A:253:THR:HG21	2.12	0.64
1:C:216:LYS:NZ	1:C:253:THR:HG21	2.12	0.63
1:D:254:PRO:O	1:D:256:TYR:N	2.32	0.62
1:C:355:LYS:HE3	1:C:356:ASN:H	1.66	0.61
1:C:240:ASP:OD1	1:C:242:THR:OG1	2.18	0.60
1:B:386:ASP:C	1:B:387:ILE:HG12	2.27	0.60
1:A:102:ALA:HB1	1:A:131:ARG:HH12	1.67	0.59
1:C:386:ASP:C	1:C:387:ILE:HG12	2.27	0.59
1:A:173:PRO:HB2	1:A:375:LEU:HD21	1.82	0.59
1:C:213:ARG:NH1	1:C:235:THR:O	2.35	0.59
1:B:268:ASP:N	1:B:268:ASP:OD1	2.37	0.58
1:D:386:ASP:C	1:D:387:ILE:HG12	2.27	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:262:LEU:HD23	1:A:307:MET:HE3	1.85	0.57
1:A:254:PRO:O	1:A:257:ILE:HG22	2.06	0.56
1:A:62:LEU:CD2	1:A:402:ALA:O	2.54	0.56
1:A:256:TYR:OH	1:A:286:GLU:OE1	2.18	0.56
1:A:26:ARG:C	1:A:28:ARG:H	2.15	0.55
1:A:62:LEU:HD21	1:A:402:ALA:C	2.32	0.54
1:A:216:LYS:HZ2	1:A:253:THR:HG21	1.73	0.53
1:C:323:LYS:H	1:C:323:LYS:HE2	1.72	0.53
1:A:172:MET:HE3	1:A:229:LYS:HB2	1.91	0.53
1:B:143:ILE:HD11	1:B:210:LEU:HD13	1.90	0.52
1:A:143:ILE:HD11	1:A:210:LEU:HD13	1.92	0.52
1:D:143:ILE:HD11	1:D:210:LEU:HD13	1.92	0.51
1:B:257:ILE:CG2	1:B:262:LEU:HD13	2.40	0.51
1:C:143:ILE:HD11	1:C:210:LEU:HD13	1.92	0.51
1:B:249:THR:O	1:B:265:GLN:NE2	2.44	0.50
1:C:355:LYS:HE3	1:C:356:ASN:N	2.26	0.50
1:C:25:SER:OG	1:C:28:ARG:HD3	2.11	0.50
1:A:102:ALA:HB1	1:A:131:ARG:NH1	2.27	0.49
1:D:257:ILE:CG2	1:D:262:LEU:HD13	2.40	0.49
1:D:318:ASP:O	1:D:319:ALA:C	2.55	0.49
1:A:374:GLU:C	1:A:375:LEU:HD12	2.39	0.48
1:B:318:ASP:O	1:B:319:ALA:C	2.55	0.48
1:D:42:ASN:OD1	1:D:44:GLU:HG2	2.14	0.47
1:A:38:ARG:NH1	1:A:142:ASP:OD1	2.42	0.47
1:A:63:ARG:NH1	1:A:69:ASP:OD1	2.47	0.46
1:D:63:ARG:NH1	1:D:69:ASP:OD1	2.47	0.46
1:D:28:ARG:HD2	1:D:28:ARG:N	2.27	0.46
1:C:63:ARG:NH1	1:C:69:ASP:OD1	2.48	0.46
1:A:386:ASP:C	1:A:387:ILE:HG13	2.42	0.45
1:C:417:ARG:HH11	1:C:417:ARG:HG3	1.81	0.45
1:A:26:ARG:HG3	1:A:28:ARG:NH1	2.31	0.45
1:B:42:ASN:OD1	1:B:44:GLU:HG2	2.16	0.45
1:B:266:GLY:O	1:C:305:LYS:HE2	2.17	0.45
1:C:323:LYS:HG3	1:D:343:ASN:ND2	2.29	0.45
1:D:303:TYR:O	1:D:304:SER:CB	2.65	0.45
1:D:256:TYR:OH	1:D:286:GLU:OE1	2.22	0.44
1:D:264:SER:CB	1:D:269:GLY:HA3	2.46	0.44
1:C:310:LYS:HB3	1:D:310:LYS:HD3	1.98	0.43
1:B:63:ARG:NH1	1:B:69:ASP:OD1	2.47	0.43
1:D:251:VAL:HG12	2:D:503:HOH:O	2.18	0.43
1:D:172:MET:HE1	1:D:223:ASP:HB3	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:259:PRO:HA	1:B:307:MET:HE1	2.00	0.43
1:C:216:LYS:HZ3	1:C:253:THR:HG21	1.83	0.43
1:B:318:ASP:O	1:B:320:GLU:HG3	2.19	0.43
1:C:126:PHE:CD1	1:C:395:GLU:HG2	2.54	0.43
1:D:250:ALA:O	1:D:251:VAL:HB	2.19	0.43
1:A:373:PRO:HB2	1:A:375:LEU:CD1	2.49	0.42
1:B:172:MET:HE1	1:B:223:ASP:HB3	2.01	0.42
1:D:318:ASP:O	1:D:320:GLU:HG3	2.19	0.42
1:B:251:VAL:HG13	1:B:265:GLN:OE1	2.19	0.42
1:A:32:ALA:O	1:A:35:ARG:HG2	2.20	0.42
1:A:259:PRO:HA	1:A:307:MET:HE1	2.00	0.42
1:B:355:LYS:HE3	1:B:355:LYS:HA	2.02	0.42
1:D:259:PRO:HA	1:D:307:MET:HE1	2.02	0.42
1:D:126:PHE:CD1	1:D:395:GLU:HG2	2.55	0.42
1:B:340:LEU:HG	1:B:348:ILE:HG12	2.02	0.42
1:D:264:SER:HB2	1:D:269:GLY:CA	2.48	0.41
1:B:218:ASP:OD1	1:B:218:ASP:N	2.52	0.41
1:A:282:VAL:HG13	1:A:293:PRO:HD2	2.03	0.41
1:A:318:ASP:O	1:A:320:GLU:HG3	2.21	0.41
1:B:126:PHE:CD1	1:B:395:GLU:HG2	2.56	0.41
1:B:213:ARG:O	1:B:213:ARG:HD2	2.21	0.41
1:C:237:MET:HE2	1:C:245:VAL:HB	2.03	0.41
1:A:408:LEU:N	1:A:409:PRO:CD	2.84	0.41
1:C:172:MET:HE1	1:C:223:ASP:HB3	2.02	0.41
1:C:318:ASP:O	1:C:320:GLU:HG3	2.21	0.41
1:C:282:VAL:HG13	1:C:293:PRO:HD2	2.03	0.40
1:B:128:MET:HE1	1:B:165:LEU:HD22	2.03	0.40
1:D:218:ASP:OD1	1:D:218:ASP:N	2.55	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	384/395 (97%)	368 (96%)	11 (3%)	5 (1%)	9	36
1	B	381/395 (96%)	364 (96%)	13 (3%)	4 (1%)	12	41
1	C	386/395 (98%)	371 (96%)	10 (3%)	5 (1%)	9	36
1	D	377/395 (95%)	359 (95%)	9 (2%)	9 (2%)	4	23
All	All	1528/1580 (97%)	1462 (96%)	43 (3%)	23 (2%)	8	33

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	268	ASP
1	B	395	GLU
1	C	268	ASP
1	C	395	GLU
1	D	250	ALA
1	D	251	VAL
1	D	255	ASP
1	D	304	SER
1	D	395	GLU
1	A	395	GLU
1	A	403	PHE
1	B	253	THR
1	C	28	ARG
1	D	254	PRO
1	D	268	ASP
1	B	319	ALA
1	D	319	ALA
1	A	319	ALA
1	B	30	LEU
1	C	319	ALA
1	D	30	LEU
1	A	27	GLN
1	C	30	LEU

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	342/346 (99%)	332 (97%)	10 (3%)	37	63
1	B	339/346 (98%)	303 (89%)	36 (11%)	6	24
1	C	342/346 (99%)	313 (92%)	29 (8%)	10	33
1	D	337/346 (97%)	304 (90%)	33 (10%)	7	28
All	All	1360/1384 (98%)	1252 (92%)	108 (8%)	11	36

All (108) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	43	VAL
1	A	165	LEU
1	A	178	VAL
1	A	207	SER
1	A	241	GLU
1	A	299	LEU
1	A	334	THR
1	A	358	GLN
1	A	395	GLU
1	A	396	THR
1	B	28	ARG
1	B	30	LEU
1	B	31	GLU
1	B	35	ARG
1	B	43	VAL
1	B	44	GLU
1	B	45	SER
1	B	64	LYS
1	B	66	LYS
1	B	131	ARG
1	B	142	ASP
1	B	163	ARG
1	B	165	LEU
1	B	178	VAL
1	B	185	ASP
1	B	207	SER
1	B	213	ARG
1	B	237	MET
1	B	238	LYS
1	B	241	GLU
1	B	251	VAL
1	B	257	ILE
1	B	262	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	268	ASP
1	B	270	PHE
1	B	299	LEU
1	B	310	LYS
1	B	334	THR
1	B	337	GLU
1	B	350	GLN
1	B	358	GLN
1	B	363	ASN
1	B	387	ILE
1	B	396	THR
1	B	399	ILE
1	B	401	LYS
1	C	26	ARG
1	C	28	ARG
1	C	30	LEU
1	C	31	GLU
1	C	66	LYS
1	C	90	GLU
1	C	131	ARG
1	C	142	ASP
1	C	163	ARG
1	C	165	LEU
1	C	178	VAL
1	C	207	SER
1	C	213	ARG
1	C	238	LYS
1	C	241	GLU
1	C	299	LEU
1	C	304	SER
1	C	310	LYS
1	C	323	LYS
1	C	334	THR
1	C	337	GLU
1	C	350	GLN
1	C	355	LYS
1	C	358	GLN
1	C	363	ASN
1	C	387	ILE
1	C	396	THR
1	C	401	LYS
1	C	417	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	28	ARG
1	D	30	LEU
1	D	31	GLU
1	D	35	ARG
1	D	43	VAL
1	D	44	GLU
1	D	64	LYS
1	D	77	LYS
1	D	131	ARG
1	D	142	ASP
1	D	163	ARG
1	D	165	LEU
1	D	178	VAL
1	D	185	ASP
1	D	207	SER
1	D	213	ARG
1	D	224	LYS
1	D	237	MET
1	D	238	LYS
1	D	249	THR
1	D	262	LEU
1	D	270	PHE
1	D	299	LEU
1	D	310	LYS
1	D	334	THR
1	D	342	ARG
1	D	350	GLN
1	D	355	LYS
1	D	358	GLN
1	D	363	ASN
1	D	387	ILE
1	D	396	THR
1	D	401	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	107	GLN
1	A	115	GLN
1	A	148	ASN
1	A	183	ASN
1	A	246	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	363	ASN
1	B	86	GLN
1	B	107	GLN
1	B	115	GLN
1	B	183	ASN
1	C	107	GLN
1	C	115	GLN
1	C	148	ASN
1	C	183	ASN
1	C	246	HIS
1	C	351	HIS
1	C	358	GLN
1	D	107	GLN
1	D	115	GLN
1	D	183	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [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	388/395 (98%)	-0.25	5 (1%) 75 55	38, 66, 100, 141	0
1	B	385/395 (97%)	-0.16	6 (1%) 70 50	41, 69, 108, 141	0
1	C	390/395 (98%)	-0.17	4 (1%) 79 62	42, 71, 107, 136	0
1	D	383/395 (96%)	-0.09	10 (2%) 57 36	46, 72, 110, 138	0
All	All	1546/1580 (97%)	-0.17	25 (1%) 70 50	38, 70, 108, 141	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	249	THR	4.5
1	B	28	ARG	3.9
1	D	394	VAL	3.8
1	A	394	VAL	3.6
1	D	270	PHE	3.4
1	C	394	VAL	3.3
1	C	25	SER	3.3
1	B	394	VAL	3.2
1	B	270	PHE	3.1
1	C	319	ALA	2.8
1	D	245	VAL	2.6
1	D	251	VAL	2.5
1	B	247	CYS	2.4
1	C	23	GLY	2.4
1	A	342	ARG	2.4
1	A	25	SER	2.2
1	B	235	THR	2.2
1	D	28	ARG	2.2
1	D	27	GLN	2.2
1	D	266	GLY	2.2
1	D	224	LYS	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	26	ARG	2.2
1	A	402	ALA	2.1
1	D	269	GLY	2.1
1	B	266	GLY	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.