



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:58 AM UTC

PDB ID : 3U51 / pdb_00003u51
Title : Src in complex with DNA-templated macrocyclic inhibitor MC1
Authors : Seeliger, M.A.; Liu, D.R.; Georghiou, G.; Kleiner, R.E.; Pulkoski-Gross, M.
Deposited on : 2011-10-10
Resolution : 2.24 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

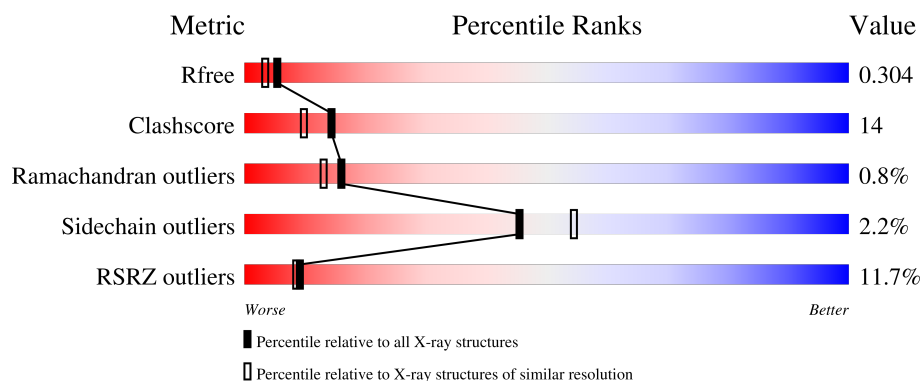
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.24 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	3416 (2.26-2.22)
Clashscore	190562	3556 (2.26-2.22)
Ramachandran outliers	187476	3500 (2.26-2.22)
Sidechain outliers	187428	3501 (2.26-2.22)
RSRZ outliers	180081	3415 (2.26-2.22)

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	275	9% 64% 29% 7%
1	B	275	13% 65% 26% 7%
2	C	6	17% 33% 50%
2	D	6	50% 50%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4337 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 Proto-oncogene tyrosine-protein kinase Src.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	256	Total	C	N	O	S	0	0	0
			2059	1321	343	378	17			
1	B	255	Total	C	N	O	S	0	0	0
			2048	1312	342	377	17			

- Molecule 2 is a protein called macrocyclic inhibitor MC1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	6	Total	C	N	O	0	0	1
			54	38	9	7			
2	D	6	Total	C	N	O	0	0	1
			54	38	9	7			

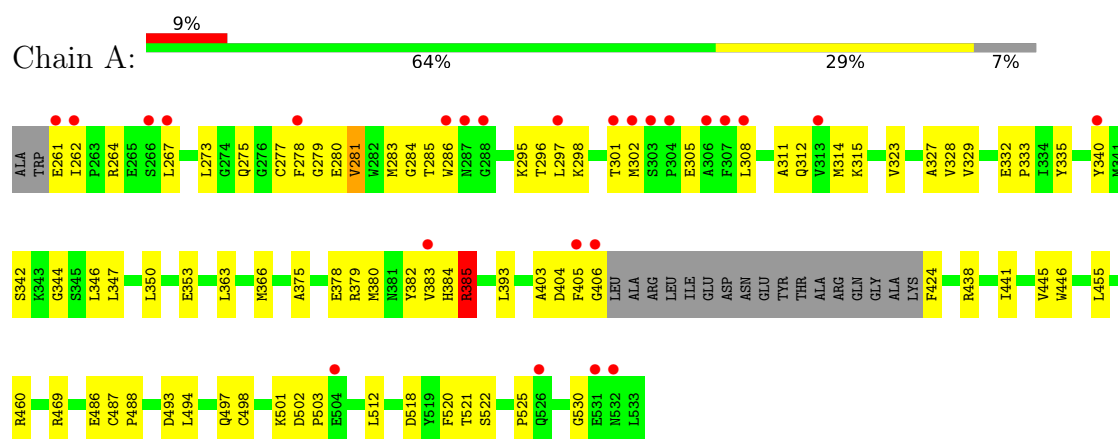
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	59	Total	O	0	0
			59	59		
3	B	61	Total	O	0	0
			61	61		
3	C	2	Total	O	0	0
			2	2		

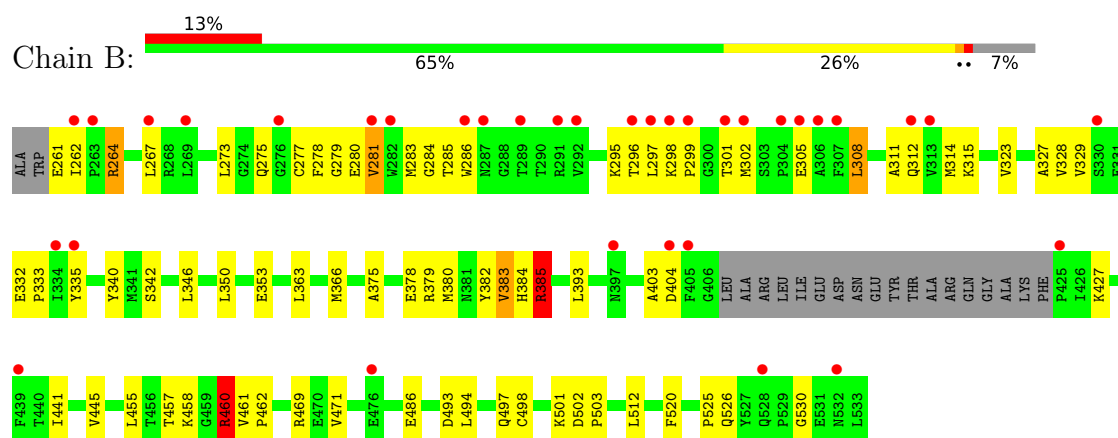
3 Residue-property plots

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.

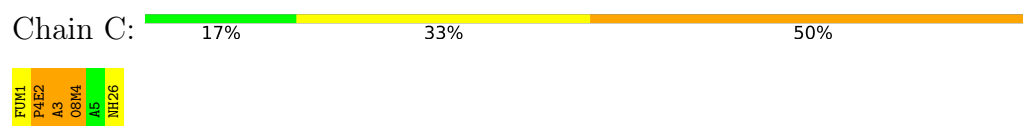
- Molecule 1: Proto-oncogene tyrosine-protein kinase Src



- Molecule 1: Proto-oncogene tyrosine-protein kinase Src



- Molecule 2: macrocyclic inhibitor MC1



- Molecule 2: macrocyclic inhibitor MC1



F0M1
P4E2
A3
O8M4
A5
NH26

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	42.17Å 117.25Å 62.76Å 90.00° 90.08° 90.00°	Depositor
Resolution (Å)	34.98 – 2.24 34.98 – 2.24	Depositor EDS
% Data completeness (in resolution range)	94.9 (34.98-2.24) 91.1 (34.98-2.24)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.88 (at 2.24Å)	Xtriage
Refinement program	PHENIX 1.6_289	Depositor
R, R_{free}	0.199 , 0.236 (Not available) , 0.304	Depositor DCC
R_{free} test set	2021 reflections (7.28%)	wwPDB-VP
Wilson B-factor (Å ²)	33.8	Xtriage
Anisotropy	0.962	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 52.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.390 for h,-k,-l	Xtriage
Reported twinning fraction	0.382 for h,-k,-l	Depositor
Outliers	0 of 27767 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4337	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

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

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FUM, ALC, P4E, NH2, 08M, DAB

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	0.33	0/2109	0.80	8/2854 (0.3%)
1	B	0.33	0/2097	0.82	10/2837 (0.4%)
All	All	0.33	0/4206	0.81	18/5691 (0.3%)

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	264	ARG	NE-CZ-NH2	8.13	126.52	119.20
1	A	460	ARG	NE-CZ-NH2	7.83	126.25	119.20
1	B	264	ARG	NE-CZ-NH1	-7.63	113.87	121.50
1	B	385	ARG	NE-CZ-NH2	7.52	125.97	119.20
1	A	460	ARG	NE-CZ-NH1	-7.27	114.23	121.50
1	B	385	ARG	NE-CZ-NH1	-6.91	114.59	121.50
1	B	460	ARG	NE-CZ-NH2	-6.10	113.71	119.20
1	A	264	ARG	NE-CZ-NH2	-5.83	113.95	119.20
1	B	460	ARG	CD-NE-CZ	5.82	132.55	124.40
1	B	502	ASP	CA-C-N	5.72	125.19	119.24
1	B	502	ASP	C-N-CA	5.72	125.19	119.24
1	B	264	ARG	CD-NE-CZ	5.72	132.41	124.40
1	A	460	ARG	CD-NE-CZ	5.69	132.37	124.40
1	A	264	ARG	CD-NE-CZ	5.67	132.34	124.40
1	A	502	ASP	CA-C-N	5.55	125.01	119.24
1	A	502	ASP	C-N-CA	5.55	125.01	119.24
1	B	460	ARG	NE-CZ-NH1	5.17	126.67	121.50
1	A	385	ARG	NE-CZ-NH2	-5.16	114.55	119.20

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	2059	0	2046	59	0
1	B	2048	0	2038	55	0
2	C	54	0	35	9	0
2	D	54	0	36	8	0
3	A	59	0	0	3	0
3	B	61	0	0	2	0
3	C	2	0	0	0	0
All	All	4337	0	4155	118	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 14.

All (118) 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)
2:D:2:P4E:C	2:D:3:ALC:HD22	2.15	0.76
1:A:424:PHE:HA	2:C:2:P4E:H01	1.68	0.74
2:D:4:08M:O	2:D:5:DAB:HB3	1.87	0.74
1:B:281:VAL:HG23	1:B:295:LYS:HG2	1.70	0.73
1:B:278:PHE:HD2	1:B:301:THR:HB	1.54	0.72
2:D:2:P4E:O	2:D:3:ALC:HD22	1.88	0.72
1:A:281:VAL:HG23	1:A:295:LYS:HG2	1.70	0.72
1:B:384:HIS:O	1:B:385:ARG:HB2	1.92	0.70
1:A:384:HIS:O	1:A:385:ARG:HB2	1.92	0.70
1:A:278:PHE:HD2	1:A:301:THR:HB	1.55	0.70
1:A:323:VAL:HG21	1:A:393:LEU:HD12	1.78	0.66
1:B:329:VAL:HB	1:B:335:TYR:HB2	1.78	0.66
1:B:346:LEU:HD21	1:B:455:LEU:HD21	1.78	0.65
1:B:323:VAL:HG21	1:B:393:LEU:HD12	1.78	0.65
1:A:344:GLY:HA2	2:C:4:08M:H31	1.79	0.64
1:B:378:GLU:OE1	3:B:659:HOH:O	2.14	0.64
1:A:329:VAL:HB	1:A:335:TYR:HB2	1.78	0.64
1:A:346:LEU:HD21	1:A:455:LEU:HD21	1.78	0.64
1:A:347:LEU:HD23	2:C:6:NH2:N	2.13	0.64
1:A:273:LEU:HB2	1:A:281:VAL:CG1	2.29	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:279:GLY:HA3	1:B:296:THR:O	2.00	0.62
1:A:279:GLY:HA3	1:A:296:THR:O	2.00	0.61
1:A:262:ILE:CD1	1:A:267:LEU:HD11	2.31	0.61
1:B:262:ILE:CD1	1:B:267:LEU:HD11	2.30	0.61
1:B:273:LEU:HB2	1:B:281:VAL:CG1	2.30	0.61
1:B:305:GLU:O	1:B:308:LEU:HB3	2.00	0.60
1:A:275:GLN:HG3	1:A:280:GLU:HG2	1.85	0.59
1:A:305:GLU:O	1:A:308:LEU:HB3	2.03	0.59
1:A:273:LEU:HB2	1:A:281:VAL:HG12	1.84	0.59
1:A:262:ILE:HD12	1:A:267:LEU:HD11	1.85	0.59
1:B:273:LEU:HB2	1:B:281:VAL:HG12	1.85	0.58
1:B:261:GLU:HA	1:B:328:VAL:O	2.03	0.58
1:B:262:ILE:HD12	1:B:267:LEU:HD11	1.84	0.58
1:B:275:GLN:HG3	1:B:280:GLU:HG2	1.85	0.57
1:A:311:ALA:HA	1:A:314:MET:HE2	1.86	0.57
1:A:261:GLU:HA	1:A:328:VAL:O	2.04	0.57
1:A:278:PHE:CD2	1:A:301:THR:HB	2.38	0.56
1:B:323:VAL:HG21	1:B:403:ALA:HB2	1.87	0.56
1:A:295:LYS:HE2	2:C:4:08M:H29	1.87	0.56
1:B:311:ALA:HA	1:B:314:MET:HE2	1.86	0.56
1:A:323:VAL:HG21	1:A:403:ALA:HB2	1.87	0.55
1:B:278:PHE:CD2	1:B:301:THR:HB	2.38	0.55
1:A:278:PHE:C	1:A:298:LYS:HG2	2.32	0.55
1:B:363:LEU:HD23	1:B:366:MET:CE	2.36	0.55
1:A:281:VAL:CG2	2:C:4:08M:H27	2.37	0.55
1:A:363:LEU:HD23	1:A:366:MET:CE	2.36	0.55
1:B:278:PHE:C	1:B:298:LYS:HG2	2.32	0.54
1:A:378:GLU:HG3	1:A:441:ILE:HG12	1.91	0.52
1:A:438:ARG:NH1	3:A:616:HOH:O	2.42	0.52
1:B:375:ALA:O	1:B:379:ARG:HG3	2.10	0.52
1:B:378:GLU:HG3	1:B:441:ILE:HG12	1.91	0.52
1:A:424:PHE:HB2	3:A:652:HOH:O	2.09	0.52
1:A:375:ALA:O	1:A:379:ARG:HG3	2.09	0.51
1:B:278:PHE:CD1	2:D:2:P4E:H107	2.46	0.50
1:A:281:VAL:HG21	2:C:4:08M:H27	1.93	0.50
1:B:486:GLU:OE1	1:B:530:GLY:HA3	2.12	0.50
1:A:262:ILE:HD13	1:A:327:ALA:CB	2.42	0.50
1:A:486:GLU:OE1	1:A:530:GLY:HA3	2.12	0.50
1:A:333:PRO:HA	3:A:619:HOH:O	2.12	0.49
1:B:262:ILE:HD13	1:B:327:ALA:CB	2.42	0.49
1:B:264:ARG:NH1	1:B:333:PRO:O	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:CYS:O	1:A:298:LYS:HD3	2.13	0.48
1:B:277:CYS:O	1:B:298:LYS:HD3	2.13	0.48
1:B:526:GLN:HB2	3:B:643:HOH:O	2.13	0.47
1:A:297:LEU:HD13	2:C:3:ALC:HZ2	1.97	0.47
1:A:285:THR:HG22	1:A:286:TRP:N	2.29	0.47
1:B:493:ASP:O	1:B:497:GLN:HG3	2.15	0.47
1:B:285:THR:HG22	1:B:286:TRP:N	2.29	0.47
1:A:340:TYR:CE2	1:A:342:SER:HA	2.50	0.47
1:A:493:ASP:O	1:A:497:GLN:HG3	2.16	0.46
1:B:340:TYR:CE2	1:B:342:SER:HA	2.50	0.46
1:A:521:THR:HB	1:B:461:VAL:HG21	1.98	0.46
1:B:297:LEU:HD21	1:B:302:MET:HB2	1.97	0.46
2:D:4:08M:O	2:D:5:DAB:CB	2.60	0.46
1:B:281:VAL:CG2	1:B:295:LYS:HG2	2.44	0.45
2:C:1:FUM:O7	2:C:1:FUM:O	2.35	0.45
1:A:262:ILE:HD13	1:A:327:ALA:HB3	1.99	0.45
1:B:296:THR:HG22	1:B:335:TYR:CE2	2.52	0.45
1:A:296:THR:HG22	1:A:335:TYR:CE2	2.52	0.45
1:A:350:LEU:HD11	1:A:455:LEU:HD23	1.99	0.45
2:D:1:FUM:O7	2:D:2:P4E:C	2.65	0.45
1:A:501:LYS:O	1:A:503:PRO:HD3	2.18	0.44
1:A:278:PHE:O	2:C:3:ALC:HE22	2.17	0.44
1:A:297:LEU:HD21	1:A:302:MET:HB2	1.98	0.44
1:A:445:VAL:O	1:A:498:CYS:HB3	2.18	0.44
1:B:262:ILE:HD13	1:B:327:ALA:HB3	1.99	0.44
1:B:460:ARG:HD2	1:B:460:ARG:HA	1.75	0.44
1:A:518:ASP:OD2	1:B:460:ARG:HD2	2.17	0.44
1:B:445:VAL:O	1:B:498:CYS:HB3	2.18	0.44
1:A:283:MET:HG2	1:A:284:GLY:N	2.34	0.43
1:B:332:GLU:HA	1:B:333:PRO:C	2.43	0.43
1:B:350:LEU:HD11	1:B:455:LEU:HD23	2.00	0.43
1:B:520:PHE:O	1:B:525:PRO:HA	2.18	0.43
1:B:380:MET:O	1:B:382:TYR:CD1	2.72	0.43
2:D:2:P4E:O	2:D:3:ALC:O	2.37	0.43
1:A:380:MET:O	1:A:382:TYR:CD1	2.72	0.43
1:B:283:MET:HG2	1:B:284:GLY:N	2.34	0.43
1:A:332:GLU:HA	1:A:333:PRO:C	2.44	0.42
1:A:494:LEU:HD11	1:A:512:LEU:HD23	2.02	0.42
1:A:520:PHE:O	1:A:525:PRO:HA	2.19	0.42
1:B:501:LYS:O	1:B:503:PRO:HD3	2.19	0.42
1:A:281:VAL:CG2	1:A:295:LYS:HG2	2.44	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:494:LEU:HD11	1:B:512:LEU:HD23	2.01	0.41
1:B:383:VAL:HG13	1:B:385:ARG:HG3	2.02	0.41
1:A:312:GLN:HA	1:A:315:LYS:HD3	2.02	0.41
1:A:522:SER:O	2:D:6:NH2:N	2.53	0.41
1:A:405:PHE:O	1:A:406:GLY:C	2.64	0.41
1:A:446:TRP:HA	1:A:498:CYS:O	2.21	0.41
1:B:298:LYS:HA	1:B:299:PRO:HD3	1.91	0.41
1:B:457:THR:O	1:B:458:LYS:HB2	2.21	0.41
1:A:487:CYS:HA	1:A:488:PRO:HD3	1.88	0.41
1:A:518:ASP:CG	1:B:460:ARG:HH11	2.28	0.41
1:B:278:PHE:O	1:B:297:LEU:HD12	2.21	0.41
1:B:363:LEU:HD23	1:B:366:MET:HE1	2.03	0.41
1:A:384:HIS:O	1:A:385:ARG:CB	2.65	0.41
1:B:461:VAL:HA	1:B:462:PRO:HD3	1.92	0.40
1:B:312:GLN:HA	1:B:315:LYS:HD3	2.02	0.40
1:B:427:LYS:HG2	1:B:471:VAL:HG21	2.03	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	252/275 (92%)	242 (96%)	8 (3%)	2 (1%)	16	13
1	B	251/275 (91%)	242 (96%)	7 (3%)	2 (1%)	16	13
All	All	503/550 (92%)	484 (96%)	15 (3%)	4 (1%)	16	13

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	385	ARG
1	B	385	ARG

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Mol	Chain	Res	Type
1	A	404	ASP
1	B	404	ASP

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	223/237 (94%)	219 (98%)	4 (2%)	51	61
1	B	222/237 (94%)	216 (97%)	6 (3%)	39	47
All	All	445/474 (94%)	435 (98%)	10 (2%)	45	54

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	281	VAL
1	A	353	GLU
1	A	383	VAL
1	A	469	ARG
1	B	281	VAL
1	B	308	LEU
1	B	353	GLU
1	B	383	VAL
1	B	460	ARG
1	B	469	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

8 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	ALC	C	3	2	9,11,12	0.48	0	11,13,15	1.15	1 (9%)
2	ALC	D	3	2	9,11,12	0.49	0	11,13,15	1.42	2 (18%)
2	P4E	D	2	2	12,13,14	1.22	1 (8%)	10,15,17	1.44	2 (20%)
2	P4E	C	2	2	12,13,14	1.21	1 (8%)	10,15,17	1.72	2 (20%)
2	08M	D	4	2	15,16,17	1.49	1 (6%)	14,19,21	1.45	3 (21%)
2	DAB	D	5	2	5,6,7	0.25	0	1,6,8	0.05	0
2	08M	C	4	2	15,16,17	1.50	1 (6%)	14,19,21	1.62	3 (21%)
2	DAB	C	5	2	5,6,7	0.30	0	1,6,8	1.03	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ALC	C	3	2	-	2/5/14/16	0/1/1/1
2	ALC	D	3	2	-	4/5/14/16	0/1/1/1
2	P4E	D	2	2	-	5/7/8/10	0/1/1/1
2	P4E	C	2	2	-	6/7/8/10	0/1/1/1
2	08M	D	4	2	-	4/12/13/15	0/1/1/1
2	DAB	D	5	2	-	0/4/5/7	-
2	08M	C	4	2	-	6/12/13/15	0/1/1/1
2	DAB	C	5	2	-	1/4/5/7	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	4	08M	C35-N34	5.43	1.45	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	4	08M	C35-N34	5.34	1.45	1.33
2	C	2	P4E	C07-C08	2.77	1.40	1.31
2	D	2	P4E	C07-C08	2.70	1.40	1.31

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	P4E	C09-C08-C07	-4.32	118.74	124.31
2	C	4	08M	C37-C35-N34	3.63	120.61	115.56
2	D	2	P4E	C04-C07-C08	-3.19	119.17	126.99
2	D	3	ALC	CG-CB-CA	-2.91	110.61	114.52
2	C	3	ALC	CG-CB-CA	-2.88	110.65	114.52
2	D	4	08M	C37-C35-N34	2.77	119.41	115.56
2	C	2	P4E	C04-C07-C08	-2.76	120.22	126.99
2	D	2	P4E	C09-C08-C07	-2.72	120.80	124.31
2	D	3	ALC	CB-CA-N	2.59	116.14	110.48
2	C	4	08M	C39-N38-C37	2.24	119.82	116.93
2	C	4	08M	C35-C37-N38	2.23	120.03	117.42
2	D	4	08M	C35-C37-N38	2.17	119.95	117.42
2	D	4	08M	C39-N38-C37	2.17	119.72	116.93

There are no chirality outliers.

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	3	ALC	N-CA-CB-CG
2	C	3	ALC	C-CA-CB-CG
2	D	3	ALC	N-CA-CB-CG
2	C	2	P4E	C04-C07-C08-C09
2	C	2	P4E	C07-C08-C09-CA
2	C	2	P4E	C08-C09-CA-N
2	D	2	P4E	C04-C07-C08-C09
2	D	2	P4E	C08-C09-CA-C
2	D	2	P4E	C08-C09-CA-N
2	C	4	08M	C32-C31-CA-C
2	C	4	08M	C32-C31-CA-N
2	D	4	08M	O-C-CA-C31
2	D	4	08M	C32-C31-CA-N
2	D	2	P4E	C03-C04-C07-C08
2	C	2	P4E	C05-C04-C07-C08
2	C	2	P4E	C03-C04-C07-C08
2	D	2	P4E	C05-C04-C07-C08

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Mol	Chain	Res	Type	Atoms
2	C	5	DAB	C-CA-CB-CG
2	D	3	ALC	CA-CB-CG-CD2
2	D	4	08M	C32-C31-CA-C
2	C	2	P4E	C08-C09-CA-C
2	C	4	08M	O36-C35-C37-C42
2	D	3	ALC	C-CA-CB-CG
2	C	4	08M	O36-C35-C37-N38
2	D	3	ALC	CA-CB-CG-CD1
2	D	4	08M	CA-C31-C32-C33
2	C	4	08M	N34-C35-C37-N38
2	C	4	08M	N34-C35-C37-C42

There are no ring outliers.

7 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	3	ALC	2	0
2	D	3	ALC	3	0
2	D	2	P4E	5	0
2	C	2	P4E	1	0
2	D	4	08M	2	0
2	D	5	DAB	2	0
2	C	4	08M	4	0

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 ⓘ

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	256/275 (93%)	0.85	25 (9%) 13 12	24, 46, 93, 117	0
1	B	255/275 (92%)	0.84	35 (13%) 6 6	24, 45, 93, 117	0
2	C	0/6	-	-	-	-
2	D	0/6	-	-	-	-
All	All	511/562 (90%)	0.85	60 (11%) 9 8	24, 46, 93, 117	0

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	304	PRO	4.2
1	A	406	GLY	3.9
1	A	304	PRO	3.9
1	A	308	LEU	3.7
1	A	405	PHE	3.7
1	A	302	MET	3.5
1	B	313	VAL	3.3
1	B	302	MET	3.1
1	A	303	SER	3.1
1	B	307	PHE	3.0
1	A	504	GLU	3.0
1	B	405	PHE	3.0
1	A	262	ILE	2.9
1	A	301	THR	2.9
1	B	282	TRP	2.9
1	B	301	THR	2.9
1	A	266	SER	2.8
1	B	305	GLU	2.8
1	B	262	ILE	2.7
1	B	267	LEU	2.7
1	A	313	VAL	2.6
1	A	267	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	306	ALA	2.6
1	A	532	ASN	2.6
1	B	281	VAL	2.5
1	B	292	VAL	2.5
1	B	528	GLN	2.5
1	B	439	PHE	2.4
1	A	286	TRP	2.4
1	A	297	LEU	2.4
1	B	425	PRO	2.4
1	B	291	ARG	2.4
1	B	296	THR	2.3
1	A	307	PHE	2.3
1	B	276	GLY	2.3
1	B	335	TYR	2.3
1	B	404	ASP	2.2
1	A	261	GLU	2.2
1	B	286	TRP	2.2
1	B	334	ILE	2.2
1	A	340	TYR	2.2
1	B	287	ASN	2.2
1	B	299	PRO	2.2
1	B	269	LEU	2.2
1	B	297	LEU	2.2
1	B	312	GLN	2.2
1	B	330	SER	2.2
1	A	383	VAL	2.1
1	B	476	GLU	2.1
1	A	531	GLU	2.1
1	A	278	PHE	2.1
1	A	306	ALA	2.1
1	A	526	GLN	2.1
1	B	397	ASN	2.1
1	B	298	LYS	2.0
1	B	289	THR	2.0
1	B	532	ASN	2.0
1	A	288	GLY	2.0
1	A	287	ASN	2.0
1	B	263	PRO	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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	DAB	C	5	7/8	0.67	0.20	39,62,70,72	0
2	P4E	C	2	13/14	0.74	0.21	52,60,72,77	0
2	DAB	D	5	7/8	0.75	0.20	61,66,80,86	0
2	ALC	D	3	11/12	0.79	0.23	75,81,95,96	0
2	08M	D	4	16/17	0.82	0.17	49,59,98,111	0
2	P4E	D	2	13/14	0.84	0.14	50,60,72,74	0
2	ALC	C	3	11/12	0.85	0.15	57,63,79,82	0
2	08M	C	4	16/17	0.86	0.13	36,52,71,74	0

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.