



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 09:33 AM UTC

PDB ID : 8BOX / pdb_00008box
Title : LSD1-CoREST in complex with AW4 and SNAG peptide
Authors : Caroli, J.; Mattevi, A.
Deposited on : 2022-11-15
Resolution : 2.82 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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

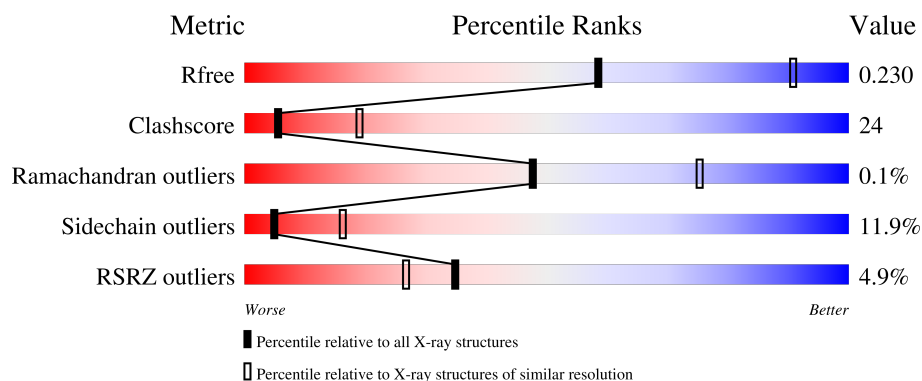
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.82 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	4591 (2.84-2.80)
Clashscore	190562	5010 (2.84-2.80)
Ramachandran outliers	187476	4916 (2.84-2.80)
Sidechain outliers	187428	4918 (2.84-2.80)
RSRZ outliers	180081	4594 (2.84-2.80)

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	871	3% 49% 23% • 24%
2	B	144	9% 48% 31% 13% • 8%
3	C	9	22% 33% 11% 56%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6403 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 Lysine-specific histone demethylase 1A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	666	Total	C	N	O	S	0	0	0
			5217	3324	906	967	20			

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	GLY	-	expression tag	UNP O60341
A	-17	SER	-	expression tag	UNP O60341
A	-16	SER	-	expression tag	UNP O60341
A	-15	HIS	-	expression tag	UNP O60341
A	-14	HIS	-	expression tag	UNP O60341
A	-13	HIS	-	expression tag	UNP O60341
A	-12	HIS	-	expression tag	UNP O60341
A	-11	HIS	-	expression tag	UNP O60341
A	-10	HIS	-	expression tag	UNP O60341
A	-9	SER	-	expression tag	UNP O60341
A	-8	SER	-	expression tag	UNP O60341
A	-7	GLY	-	expression tag	UNP O60341
A	-6	LEU	-	expression tag	UNP O60341
A	-5	VAL	-	expression tag	UNP O60341
A	-4	PRO	-	expression tag	UNP O60341
A	-3	ARG	-	expression tag	UNP O60341
A	-2	GLY	-	expression tag	UNP O60341
A	-1	SER	-	expression tag	UNP O60341
A	0	HIS	-	expression tag	UNP O60341

- Molecule 2 is a protein called REST corepressor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	133	Total	C	N	O	S	0	0	0
			1076	676	194	203	3			

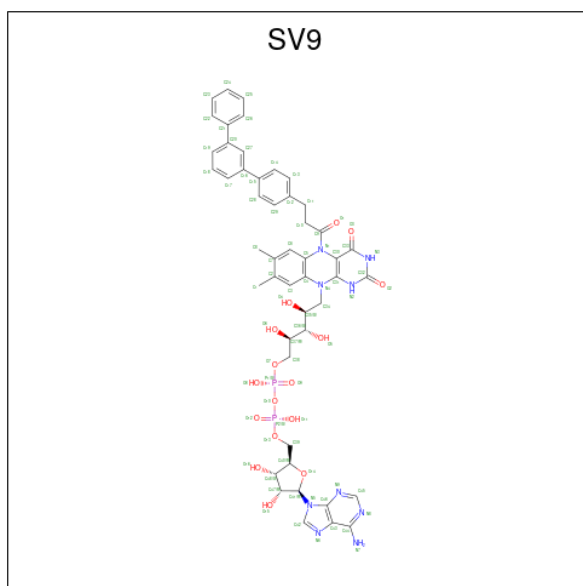
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	297	GLY	-	expression tag	UNP Q9UKL0
B	298	PRO	-	expression tag	UNP Q9UKL0
B	299	LEU	-	expression tag	UNP Q9UKL0
B	300	GLY	-	expression tag	UNP Q9UKL0
B	301	SER	-	expression tag	UNP Q9UKL0
B	302	PRO	-	expression tag	UNP Q9UKL0
B	303	GLU	-	expression tag	UNP Q9UKL0
B	304	PHE	-	expression tag	UNP Q9UKL0

- Molecule 3 is a protein called Zinc finger protein SNAI1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	4	Total	C	N	O	0	0	0
			35	23	7	5			

- Molecule 4 is [(2 {R},3 {S},4 {R},5 {R})-5-(6-aminopurin-9-yl)-3,4-bis(oxidanyl)oxolan-2-yl]methoxy-oxidanyl-phosphoryl [(2 {R},3 {S},4 {S})-5-[7,8-dimethyl-2,4-bis(oxidanylidene)-5-[3-[4-(3-phenylphenyl)phenyl]propanoyl]-1 {H}-benzo[g]pteridin-10-yl]-2,3,4-tris(oxidanyl)pentyl] hydrogen phosphate (CCD ID: SV9) (formula: C₄₈H₅₁N₉O₁₆P₂) (labeled as "Ligand of Interest" by depositor).

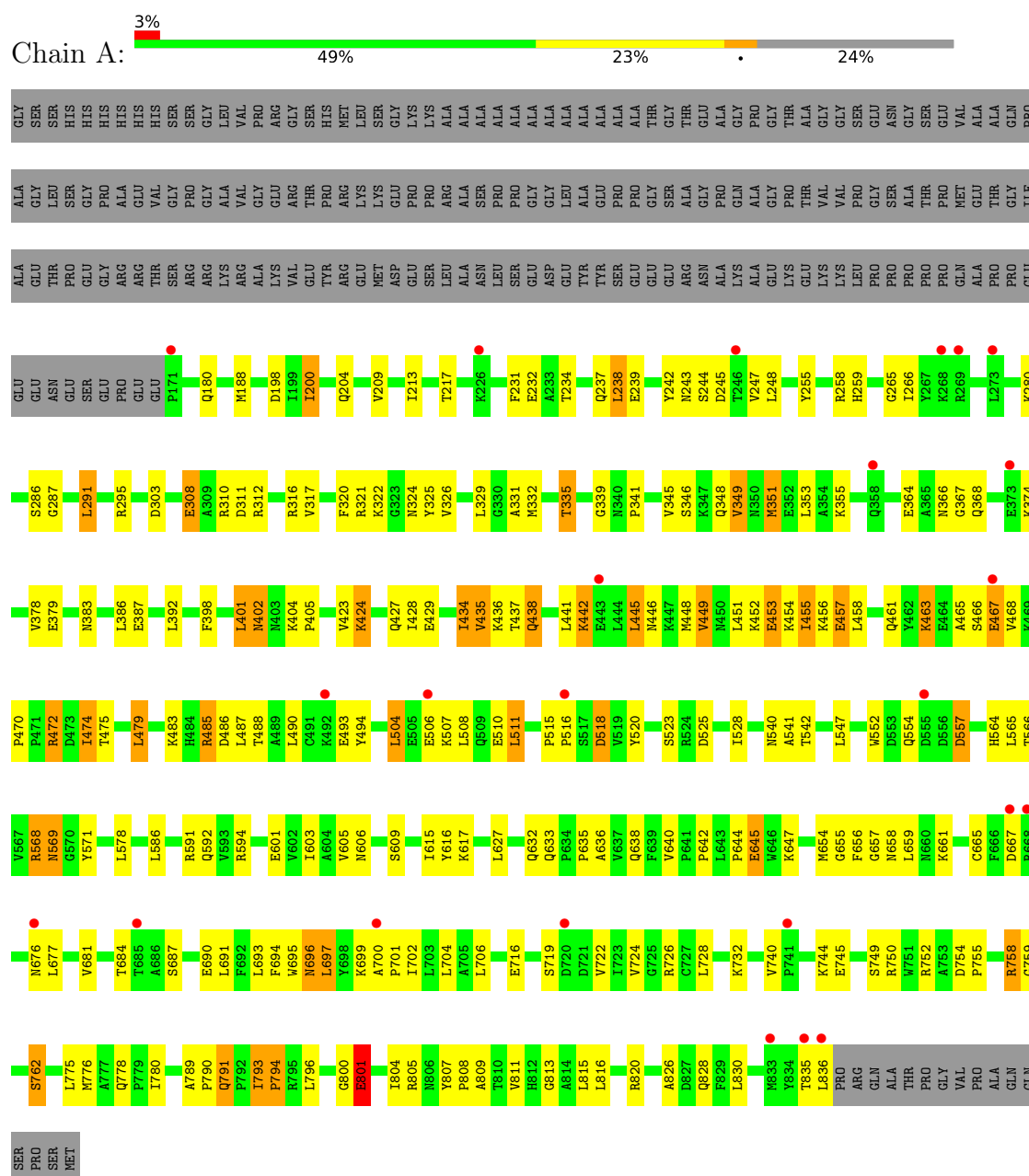


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			75	48	9	16	2		

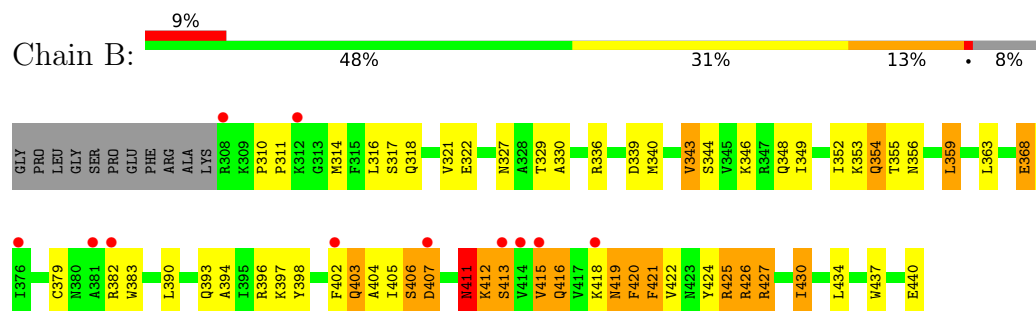
3 Residue-property plots

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.

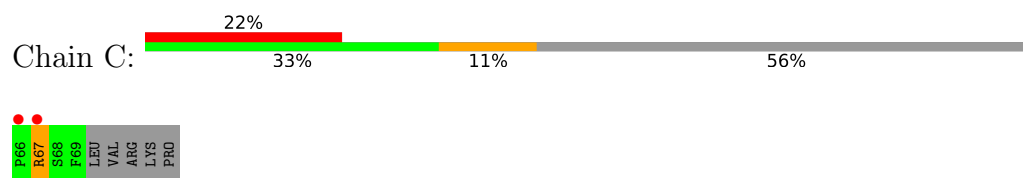
- Molecule 1: Lysine-specific histone demethylase 1A



- Molecule 2: REST corepressor 1



- Molecule 3: Zinc finger protein SNAI1



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	118.98Å 177.89Å 234.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.34 – 2.82 48.34 – 2.82	Depositor EDS
% Data completeness (in resolution range)	99.3 (48.34-2.82) 99.3 (48.34-2.82)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.26 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.18.2	Depositor
R, R_{free}	0.220 , 0.229 0.229 , 0.230	Depositor DCC
R_{free} test set	1176 reflections (1.96%)	wwPDB-VP
Wilson B-factor (Å ²)	92.8	Xtriage
Anisotropy	0.480	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 75.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6403	wwPDB-VP
Average B, all atoms (Å ²)	104.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.15% 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: SV9

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	0.88	6/5331 (0.1%)	1.10	11/7232 (0.2%)
2	B	0.76	1/1091 (0.1%)	1.15	2/1471 (0.1%)
3	C	0.91	0/36	1.71	0/46
All	All	0.86	7/6458 (0.1%)	1.12	13/8749 (0.1%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	808	PRO	C-O	-6.06	1.15	1.23
1	A	644	PRO	C-O	-5.77	1.17	1.23
1	A	405	PRO	C-O	-5.49	1.17	1.23
1	A	762	SER	CA-CB	-5.39	1.45	1.53
1	A	801	GLU	C-O	-5.33	1.17	1.24
2	B	406	SER	CA-CB	-5.28	1.47	1.53
1	A	794	PRO	C-O	-5.23	1.18	1.23

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	420	PHE	CB-CA-C	-8.67	93.64	110.46
1	A	642	PRO	CB-CA-C	-7.15	102.08	111.23
1	A	438	GLN	CB-CA-C	-6.53	100.62	110.88
1	A	475	THR	CA-CB-OG1	-6.21	100.29	109.60
1	A	437	THR	CB-CA-C	5.65	120.45	110.85
1	A	308	GLU	CB-CG-CD	-5.52	103.22	112.60
1	A	800	GLY	CA-C-O	-5.40	118.56	122.45
1	A	308	GLU	N-CA-CB	-5.21	102.52	110.65
2	B	411	ASN	CB-CA-C	5.11	117.99	109.56
1	A	402	ASN	CB-CA-C	5.07	119.09	111.89
1	A	775	LEU	N-CA-C	-5.05	105.90	111.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	457	GLU	CA-C-N	-5.00	112.03	120.58
1	A	457	GLU	C-N-CA	-5.00	112.03	120.58

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	5217	0	5252	240	1
2	B	1076	0	1091	89	1
3	C	35	0	34	1	0
4	A	75	0	0	8	0
All	All	6403	0	6377	301	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 24.

All (301) 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:654:MET:HE1	1:A:776:MET:CG	1.72	1.18
1:A:435:VAL:HG12	2:B:349:ILE:CD1	1.76	1.16
1:A:188:MET:HE3	1:A:200:ILE:HG12	1.29	1.13
1:A:654:MET:CE	1:A:776:MET:HG3	1.82	1.10
1:A:793:ILE:HD12	1:A:793:ILE:H	1.22	1.04
1:A:754:ASP:OD1	1:A:755:PRO:HD2	1.59	1.01
1:A:188:MET:HE3	1:A:200:ILE:CG1	1.95	0.95
1:A:654:MET:CE	1:A:776:MET:CG	2.41	0.95
1:A:485:ARG:NH1	2:B:407:ASP:OD2	2.01	0.92
1:A:435:VAL:HG12	2:B:349:ILE:HD11	1.53	0.91
1:A:457:GLU:O	1:A:461:GLN:HG3	1.71	0.91
2:B:403:GLN:O	2:B:406:SER:HB3	1.70	0.91
1:A:325:TYR:CE2	1:A:665:CYS:HB3	2.05	0.90
1:A:758:ARG:HG2	1:A:758:ARG:HH11	1.35	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:566:THR:HG21	1:A:697:LEU:HD22	1.55	0.88
2:B:311:PRO:HG2	2:B:314:MET:HG3	1.55	0.88
1:A:654:MET:HE1	1:A:776:MET:HG3	0.91	0.88
2:B:419:ASN:HD22	2:B:419:ASN:H	1.19	0.87
1:A:374:LYS:HD2	1:A:525:ASP:OD1	1.73	0.86
1:A:345:VAL:O	1:A:349:VAL:HG12	1.76	0.85
2:B:382:ARG:C	2:B:412:LYS:HZ3	1.84	0.85
1:A:427:GLN:NE2	1:A:518:ASP:HA	1.94	0.83
1:A:435:VAL:CG1	2:B:349:ILE:HD11	2.09	0.82
2:B:425:ARG:HA	2:B:430:ILE:HG13	1.61	0.82
1:A:325:TYR:HE2	1:A:665:CYS:HB3	1.42	0.81
1:A:518:ASP:OD1	1:A:518:ASP:N	2.12	0.81
1:A:465:ALA:CB	1:A:479:LEU:HD23	2.11	0.80
2:B:368:GLU:HA	2:B:368:GLU:OE1	1.82	0.80
1:A:485:ARG:HG2	1:A:485:ARG:HH11	1.47	0.79
1:A:569:ASN:OD1	1:A:569:ASN:N	2.13	0.78
1:A:465:ALA:HB2	1:A:479:LEU:HD23	1.67	0.77
1:A:346:SER:HA	1:A:351:MET:CE	2.14	0.77
1:A:468:VAL:O	1:A:472:ARG:NH1	2.16	0.77
1:A:346:SER:HA	1:A:351:MET:HE2	1.65	0.77
1:A:435:VAL:HG12	2:B:349:ILE:CG1	2.15	0.77
1:A:434:ILE:HG22	2:B:349:ILE:CD1	2.16	0.75
1:A:801:GLU:HG3	1:A:809:ALA:HA	1.69	0.74
1:A:815:LEU:C	1:A:815:LEU:HD23	2.13	0.74
1:A:435:VAL:HG12	2:B:349:ILE:HD13	1.70	0.74
1:A:700:ALA:HB1	1:A:701:PRO:HD2	1.70	0.73
1:A:487:LEU:C	1:A:487:LEU:HD23	2.13	0.72
1:A:754:ASP:OD1	1:A:755:PRO:CD	2.35	0.72
1:A:511:LEU:N	1:A:511:LEU:HD23	2.03	0.72
1:A:695:TRP:HE3	1:A:697:LEU:HD21	1.55	0.72
2:B:425:ARG:NH1	2:B:425:ARG:HG2	2.05	0.71
1:A:438:GLN:HB3	2:B:352:ILE:HG21	1.70	0.71
1:A:332:MET:SD	1:A:661:LYS:NZ	2.65	0.70
1:A:188:MET:CE	1:A:200:ILE:HG12	2.16	0.69
1:A:467:GLU:HA	1:A:467:GLU:OE1	1.91	0.69
2:B:379:CYS:HG	2:B:413:SER:HG	1.39	0.69
1:A:716:GLU:HG2	1:A:750:ARG:HG2	1.73	0.68
1:A:321:ARG:HG2	1:A:326:VAL:HG12	1.74	0.68
1:A:592:GLN:HG2	1:A:638:GLN:HB3	1.76	0.68
2:B:327:ASN:OD1	2:B:330:ALA:N	2.27	0.67
2:B:416:GLN:CD	2:B:416:GLN:H	2.00	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:427:GLN:HE22	1:A:518:ASP:HA	1.60	0.67
1:A:353:LEU:HB3	1:A:565:LEU:CD2	2.26	0.66
2:B:425:ARG:HG2	2:B:425:ARG:HH11	1.61	0.66
1:A:445:LEU:N	1:A:445:LEU:HD23	2.08	0.66
1:A:758:ARG:HH11	1:A:758:ARG:CG	2.08	0.66
1:A:435:VAL:HG12	2:B:349:ILE:HG12	1.78	0.66
1:A:485:ARG:HH11	1:A:485:ARG:CG	2.09	0.65
2:B:418:LYS:O	2:B:421:PHE:HB2	1.96	0.65
2:B:403:GLN:OE1	2:B:407:ASP:OD1	2.14	0.65
1:A:776:MET:CA	1:A:776:MET:HE3	2.26	0.65
1:A:601:GLU:HB3	1:A:617:LYS:HD3	1.78	0.64
1:A:455:ILE:HD11	1:A:490:LEU:CB	2.27	0.64
1:A:510:GLU:HG2	1:A:511:LEU:HD23	1.78	0.64
1:A:455:ILE:HD11	1:A:490:LEU:HB3	1.79	0.64
2:B:340:MET:O	2:B:343:VAL:HG23	1.98	0.63
1:A:266:ILE:HA	1:A:295:ARG:HH22	1.63	0.63
1:A:266:ILE:HD11	1:A:578:LEU:HD23	1.81	0.63
2:B:396:ARG:HD2	2:B:396:ARG:O	1.97	0.63
2:B:419:ASN:HD22	2:B:419:ASN:N	1.94	0.63
1:A:435:VAL:CG1	2:B:349:ILE:CD1	2.61	0.63
1:A:793:ILE:HD12	1:A:793:ILE:N	2.05	0.63
1:A:188:MET:CE	1:A:200:ILE:CG1	2.73	0.62
1:A:658:ASN:ND2	1:A:752:ARG:HB2	2.16	0.61
1:A:346:SER:CA	1:A:351:MET:CE	2.78	0.61
1:A:448:MET:HE3	2:B:363:LEU:HD13	1.82	0.61
2:B:402:PHE:HE2	2:B:421:PHE:CE2	2.19	0.60
1:A:346:SER:HB3	1:A:351:MET:HE3	1.84	0.60
1:A:442:LYS:CG	2:B:356:ASN:HD21	2.13	0.60
1:A:661:LYS:HD3	1:A:704:LEU:HD21	1.81	0.60
2:B:370:TYR:HD2	2:B:370:TYR:N	1.99	0.60
1:A:465:ALA:HB2	1:A:479:LEU:CD2	2.32	0.59
1:A:346:SER:HB3	1:A:351:MET:CE	2.32	0.59
1:A:835:THR:O	1:A:835:THR:HG22	2.03	0.59
2:B:426:ARG:HD3	2:B:427:ARG:HG2	1.83	0.59
1:A:804:ILE:HG23	1:A:804:ILE:O	2.01	0.59
1:A:820:ARG:NH1	1:A:820:ARG:HG2	2.16	0.59
1:A:325:TYR:CD2	1:A:665:CYS:SG	2.96	0.59
1:A:449:VAL:HA	2:B:363:LEU:HD21	1.85	0.58
1:A:434:ILE:CG2	2:B:349:ILE:HD12	2.33	0.58
1:A:820:ARG:HG2	1:A:820:ARG:HH11	1.68	0.58
1:A:665:CYS:HB2	1:A:745:GLU:O	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:424:TYR:HE2	2:B:427:ARG:NH2	2.01	0.58
1:A:355:LYS:HD3	1:A:355:LYS:H	1.69	0.57
1:A:654:MET:CE	1:A:776:MET:HG2	2.31	0.57
1:A:353:LEU:HB3	1:A:565:LEU:HD22	1.86	0.57
1:A:557:ASP:OD2	1:A:557:ASP:N	2.31	0.57
1:A:461:GLN:OE1	1:A:483:LYS:HE3	2.05	0.57
2:B:407:ASP:OD1	2:B:407:ASP:N	2.37	0.57
1:A:245:ASP:OD1	1:A:247:VAL:HG22	2.05	0.57
1:A:355:LYS:HD3	1:A:355:LYS:N	2.19	0.57
1:A:258:ARG:HD2	1:A:826:ALA:HB3	1.86	0.57
2:B:359:LEU:HD23	2:B:359:LEU:N	2.20	0.56
2:B:403:GLN:O	2:B:407:ASP:OD1	2.23	0.56
1:A:434:ILE:CG2	2:B:349:ILE:CD1	2.82	0.56
2:B:370:TYR:N	2:B:370:TYR:CD2	2.70	0.56
2:B:419:ASN:H	2:B:419:ASN:ND2	1.96	0.56
1:A:830:LEU:N	1:A:830:LEU:HD23	2.19	0.56
2:B:403:GLN:O	2:B:406:SER:CB	2.50	0.56
1:A:345:VAL:O	1:A:349:VAL:CG1	2.52	0.56
1:A:424:LYS:NZ	2:B:339:ASP:OD2	2.38	0.56
1:A:758:ARG:HG2	1:A:758:ARG:NH1	2.15	0.56
2:B:402:PHE:CE2	2:B:421:PHE:CE2	2.94	0.56
1:A:435:VAL:CG1	2:B:349:ILE:HG12	2.36	0.56
1:A:465:ALA:HB1	1:A:479:LEU:HD23	1.85	0.56
1:A:684:THR:HG23	1:A:687:SER:H	1.71	0.55
1:A:719:SER:HB3	1:A:722:VAL:HG12	1.87	0.55
1:A:655:GLY:O	1:A:762:SER:HB2	2.05	0.55
1:A:332:MET:HE2	1:A:661:LYS:HZ1	1.70	0.55
1:A:487:LEU:HD23	1:A:487:LEU:O	2.06	0.55
1:A:667:ASP:HB3	1:A:744:LYS:HE2	1.87	0.55
1:A:793:ILE:H	1:A:793:ILE:CD1	1.95	0.55
1:A:353:LEU:HB3	1:A:565:LEU:HD23	1.89	0.54
1:A:776:MET:HE3	1:A:776:MET:HA	1.89	0.54
1:A:695:TRP:HE1	1:A:706:LEU:HD13	1.72	0.54
1:A:504:LEU:N	1:A:504:LEU:HD23	2.21	0.54
1:A:451:LEU:HD21	1:A:493:GLU:HG2	1.87	0.54
1:A:676:ASN:HB2	1:A:677:LEU:HD22	1.89	0.54
1:A:286:SER:HB2	1:A:291:LEU:HD11	1.90	0.54
2:B:339:ASP:O	2:B:343:VAL:HG22	2.08	0.54
2:B:348:GLN:OE1	2:B:348:GLN:HA	2.08	0.54
2:B:382:ARG:O	2:B:412:LYS:NZ	2.33	0.54
1:A:308:GLU:HG3	1:A:310:ARG:O	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:LEU:HD22	1:A:239:GLU:H	1.73	0.53
1:A:325:TYR:HD2	1:A:665:CYS:SG	2.32	0.53
4:A:901:SV9:C11	4:A:901:SV9:C30	2.87	0.53
1:A:198:ASP:OD1	1:A:198:ASP:N	2.42	0.52
1:A:474:ILE:HG22	2:B:393:GLN:OE1	2.09	0.52
1:A:335:THR:O	1:A:335:THR:OG1	2.21	0.52
1:A:520:TYR:C	1:A:520:TYR:CD2	2.86	0.52
1:A:217:THR:HG22	1:A:234:THR:HG21	1.92	0.52
1:A:442:LYS:HG3	2:B:356:ASN:HD21	1.73	0.52
2:B:311:PRO:HG2	2:B:314:MET:CG	2.35	0.52
1:A:341:PRO:HG3	1:A:816:LEU:CD1	2.40	0.51
1:A:724:VAL:O	1:A:728:LEU:HG	2.10	0.51
2:B:317:SER:O	2:B:321:VAL:HG23	2.11	0.51
2:B:420:PHE:CD2	2:B:420:PHE:C	2.88	0.51
1:A:180:GLN:HA	1:A:339:GLY:HA2	1.93	0.51
1:A:434:ILE:HG21	2:B:349:ILE:HD12	1.92	0.51
1:A:801:GLU:HG3	1:A:809:ALA:CA	2.40	0.51
1:A:458:LEU:HD21	1:A:486:ASP:HB3	1.92	0.51
1:A:695:TRP:NE1	1:A:706:LEU:HD13	2.26	0.51
1:A:601:GLU:OE1	1:A:617:LYS:HE2	2.12	0.50
1:A:474:ILE:CG2	2:B:393:GLN:OE1	2.59	0.50
1:A:458:LEU:HD21	1:A:486:ASP:CB	2.41	0.50
1:A:374:LYS:CD	1:A:525:ASP:OD1	2.53	0.50
1:A:435:VAL:HG13	2:B:349:ILE:HD11	1.92	0.50
1:A:701:PRO:HG2	1:A:701:PRO:O	2.11	0.50
1:A:442:LYS:CB	2:B:356:ASN:HD21	2.25	0.50
1:A:485:ARG:NH2	2:B:404:ALA:HB2	2.27	0.50
2:B:415:VAL:O	2:B:419:ASN:ND2	2.44	0.50
2:B:425:ARG:HH11	2:B:425:ARG:CG	2.25	0.50
1:A:291:LEU:HD23	1:A:578:LEU:HB2	1.94	0.49
1:A:485:ARG:NH1	1:A:485:ARG:CG	2.72	0.49
1:A:594:ARG:HG2	1:A:640:VAL:HB	1.94	0.49
1:A:451:LEU:CD2	1:A:493:GLU:HG2	2.42	0.49
1:A:438:GLN:HA	1:A:438:GLN:OE1	2.11	0.49
1:A:286:SER:HB2	1:A:291:LEU:CD1	2.42	0.49
1:A:815:LEU:C	1:A:815:LEU:CD2	2.85	0.49
1:A:213:ILE:HD11	1:A:248:LEU:HD23	1.95	0.49
1:A:693:LEU:HD12	1:A:694:PHE:H	1.78	0.49
2:B:369:PRO:HB2	2:B:370:TYR:CD2	2.48	0.49
1:A:332:MET:CE	1:A:661:LYS:NZ	2.75	0.49
2:B:383:TRP:CZ2	2:B:420:PHE:HB2	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:438:GLN:O	1:A:441:LEU:HB3	2.13	0.48
1:A:446:ASN:ND2	2:B:359:LEU:HD11	2.27	0.48
1:A:455:ILE:HD11	1:A:490:LEU:HB2	1.94	0.48
1:A:540:ASN:O	1:A:542:THR:HG22	2.14	0.48
1:A:188:MET:HE3	1:A:200:ILE:HG13	1.91	0.48
1:A:487:LEU:C	1:A:487:LEU:CD2	2.85	0.48
1:A:392:LEU:HD23	1:A:398:PHE:CD1	2.49	0.48
1:A:632:GLN:NE2	1:A:636:ALA:HB2	2.29	0.47
1:A:676:ASN:O	1:A:696:ASN:N	2.33	0.47
2:B:340:MET:HA	2:B:343:VAL:CG2	2.44	0.47
1:A:329:LEU:HD12	1:A:749:SER:HB3	1.97	0.47
2:B:369:PRO:HB2	2:B:370:TYR:HD2	1.78	0.47
1:A:331:ALA:HB2	4:A:901:SV9:C31	2.44	0.47
1:A:346:SER:CB	1:A:351:MET:CE	2.92	0.47
1:A:346:SER:CB	1:A:351:MET:HE3	2.44	0.47
1:A:383:ASN:O	1:A:387:GLU:HG3	2.15	0.47
1:A:568:ARG:HH21	1:A:699:LYS:HA	1.80	0.47
1:A:789:ALA:HB1	1:A:790:PRO:HD2	1.96	0.47
2:B:318:GLN:O	2:B:322:GLU:HG3	2.15	0.47
2:B:394:ALA:O	2:B:398:TYR:HB2	2.14	0.47
2:B:394:ALA:O	2:B:398:TYR:N	2.48	0.47
1:A:280:LYS:HD2	1:A:303:ASP:O	2.15	0.47
1:A:308:GLU:HG2	1:A:586:LEU:HD22	1.96	0.46
1:A:320:PHE:CZ	1:A:322:LYS:HB2	2.50	0.46
1:A:378:VAL:HG11	1:A:528:ILE:HG21	1.96	0.46
1:A:601:GLU:HA	1:A:616:TYR:O	2.15	0.46
1:A:188:MET:HE1	1:A:200:ILE:HA	1.97	0.46
1:A:633:GLN:OE1	1:A:635:PRO:HD3	2.16	0.46
1:A:820:ARG:HH11	1:A:820:ARG:CG	2.28	0.46
2:B:404:ALA:C	2:B:406:SER:N	2.69	0.46
1:A:316:ARG:NH1	1:A:656:PHE:HZ	2.13	0.46
1:A:455:ILE:HG22	2:B:370:TYR:HD1	1.79	0.46
1:A:603:ILE:HG12	1:A:615:ILE:HD13	1.96	0.46
1:A:793:ILE:HG22	1:A:794:PRO:CD	2.46	0.46
1:A:232:GLU:OE1	1:A:232:GLU:N	2.45	0.46
1:A:209:VAL:O	1:A:213:ILE:HG12	2.14	0.46
1:A:456:LYS:HA	2:B:370:TYR:CE1	2.51	0.45
1:A:217:THR:HG22	1:A:234:THR:CG2	2.46	0.45
1:A:647:LYS:NZ	1:A:778:GLN:O	2.49	0.45
2:B:426:ARG:H	2:B:426:ARG:HG3	1.47	0.45
1:A:266:ILE:N	1:A:348:GLN:OE1	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:564:HIS:ND1	1:A:564:HIS:N	2.62	0.45
1:A:793:ILE:N	1:A:793:ILE:CD1	2.72	0.45
1:A:286:SER:O	1:A:291:LEU:CD1	2.65	0.45
1:A:325:TYR:CD2	1:A:665:CYS:HB3	2.50	0.45
1:A:451:LEU:HD23	1:A:494:TYR:HB2	1.98	0.45
1:A:286:SER:C	1:A:291:LEU:HD12	2.42	0.44
1:A:515:PRO:HA	1:A:516:PRO:HD3	1.82	0.44
1:A:520:TYR:CD2	1:A:520:TYR:O	2.70	0.44
1:A:317:VAL:HG13	1:A:571:TYR:HB3	1.98	0.44
2:B:336:ARG:O	2:B:340:MET:HG2	2.17	0.44
1:A:331:ALA:HA	4:A:901:SV9:C5	2.47	0.44
2:B:310:PRO:HB3	2:B:316:LEU:HD12	1.98	0.44
1:A:474:ILE:HD13	1:A:474:ILE:HA	1.56	0.44
1:A:591:ARG:HD2	1:A:605:VAL:HG13	1.99	0.44
2:B:430:ILE:HG22	2:B:434:LEU:HD12	1.99	0.44
1:A:255:TYR:CE1	1:A:259:HIS:HD2	2.36	0.44
2:B:421:PHE:HE1	2:B:434:LEU:HD11	1.82	0.44
1:A:627:LEU:HD21	1:A:654:MET:HB3	2.00	0.44
1:A:242:TYR:C	1:A:244:SER:H	2.26	0.44
1:A:379:GLU:O	1:A:383:ASN:ND2	2.50	0.44
1:A:470:PRO:HA	1:A:472:ARG:HG2	2.00	0.44
1:A:541:ALA:O	1:A:657:GLY:HA3	2.18	0.44
1:A:780:ILE:HB	1:A:796:LEU:HB3	1.99	0.44
1:A:815:LEU:HD23	1:A:815:LEU:O	2.17	0.44
1:A:265:GLY:O	1:A:295:ARG:NH2	2.51	0.43
2:B:379:CYS:SG	2:B:413:SER:OG	2.60	0.43
1:A:591:ARG:HD2	1:A:605:VAL:CG1	2.49	0.43
1:A:654:MET:HE2	1:A:776:MET:HG2	2.00	0.43
1:A:656:PHE:CE2	1:A:759:GLY:HA3	2.54	0.43
2:B:327:ASN:OD1	2:B:329:THR:N	2.51	0.43
1:A:291:LEU:CD2	1:A:578:LEU:HB2	2.48	0.43
1:A:645:GLU:C	1:A:645:GLU:CD	2.86	0.43
1:A:364:GLU:HA	1:A:681:VAL:HB	2.01	0.43
1:A:386:LEU:HD23	1:A:386:LEU:HA	1.84	0.43
1:A:401:LEU:HD12	1:A:402:ASN:N	2.34	0.43
1:A:434:ILE:HG22	2:B:349:ILE:HD11	1.99	0.43
1:A:547:LEU:HD22	1:A:552:TRP:HB2	1.99	0.43
1:A:828:GLN:HE21	1:A:828:GLN:HB2	1.63	0.43
1:A:287:GLY:HA3	4:A:901:SV9:O13	2.19	0.43
1:A:331:ALA:HA	4:A:901:SV9:N1	2.34	0.43
1:A:213:ILE:HG22	1:A:238:LEU:HD11	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:MET:HE1	1:A:200:ILE:CA	2.49	0.42
1:A:366:ASN:HD21	1:A:368:GLN:HB2	1.84	0.42
1:A:448:MET:HE3	2:B:363:LEU:CD1	2.47	0.42
1:A:791:GLN:HE21	1:A:791:GLN:HB2	1.41	0.42
2:B:419:ASN:N	2:B:419:ASN:ND2	2.59	0.42
1:A:378:VAL:HG11	1:A:528:ILE:CG2	2.50	0.42
1:A:435:VAL:CG1	2:B:349:ILE:CG1	2.90	0.42
1:A:690:GLU:OE1	1:A:726:ARG:NH1	2.44	0.42
1:A:448:MET:HB2	2:B:363:LEU:HD11	2.01	0.42
1:A:463:LYS:HD2	1:A:463:LYS:HA	1.77	0.42
1:A:696:ASN:ND2	1:A:696:ASN:C	2.73	0.42
1:A:510:GLU:HG2	1:A:511:LEU:CD2	2.46	0.42
1:A:691:LEU:HA	1:A:691:LEU:HD23	1.77	0.42
1:A:732:LYS:HG2	1:A:740:VAL:HG11	2.01	0.42
4:A:901:SV9:O3	4:A:901:SV9:C9	2.68	0.42
1:A:332:MET:CE	1:A:661:LYS:HZ1	2.31	0.42
1:A:807:TYR:O	1:A:813:GLY:HA3	2.20	0.42
1:A:312:ARG:NH1	1:A:312:ARG:HG3	2.35	0.41
1:A:606:ASN:HB3	1:A:609:SER:O	2.20	0.41
1:A:655:GLY:O	1:A:762:SER:CB	2.68	0.41
1:A:331:ALA:CB	4:A:901:SV9:C30	2.98	0.41
2:B:317:SER:O	2:B:318:GLN:C	2.61	0.41
2:B:368:GLU:N	2:B:369:PRO:CD	2.84	0.41
2:B:379:CYS:HA	2:B:411:ASN:O	2.20	0.41
1:A:458:LEU:HA	1:A:458:LEU:HD12	1.68	0.41
4:A:901:SV9:C22	3:C:67:ARG:H	2.33	0.41
1:A:311:ASP:OD2	1:A:311:ASP:N	2.49	0.41
1:A:455:ILE:HD12	1:A:455:ILE:HA	1.94	0.41
1:A:656:PHE:CD2	1:A:759:GLY:HA3	2.55	0.41
1:A:677:LEU:HA	1:A:694:PHE:O	2.20	0.41
2:B:418:LYS:O	2:B:421:PHE:CB	2.66	0.41
1:A:188:MET:CE	1:A:200:ILE:HA	2.51	0.41
2:B:390:LEU:HD23	2:B:390:LEU:HA	1.91	0.41
1:A:204:GLN:HE21	1:A:204:GLN:HB2	1.64	0.40
2:B:437:TRP:O	2:B:440:GLU:HG3	2.21	0.40
1:A:316:ARG:NH1	1:A:656:PHE:CZ	2.90	0.40
1:A:231:PHE:O	1:A:234:THR:HB	2.22	0.40
1:A:308:GLU:HG2	1:A:586:LEU:CD2	2.51	0.40
1:A:366:ASN:OD1	1:A:367:GLY:N	2.55	0.40
2:B:404:ALA:C	2:B:406:SER:H	2.27	0.40
1:A:453:GLU:N	1:A:453:GLU:OE1	2.54	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:324:ASN:ND2	2:B:354:GLN:OE1[8_455]	1.26	0.94

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	664/871 (76%)	631 (95%)	32 (5%)	1 (0%)	43	71
2	B	131/144 (91%)	121 (92%)	10 (8%)	0	100	100
3	C	2/9 (22%)	2 (100%)	0	0	100	100
All	All	797/1024 (78%)	754 (95%)	42 (5%)	1 (0%)	48	75

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	243	ASN

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	566/715 (79%)	512 (90%)	54 (10%)	8	25
2	B	117/125 (94%)	90 (77%)	27 (23%)	1	2
3	C	4/9 (44%)	3 (75%)	1 (25%)	0	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	687/849 (81%)	605 (88%)	82 (12%)	5 16

All (82) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	200	ILE
1	A	237	GLN
1	A	238	LEU
1	A	291	LEU
1	A	335	THR
1	A	349	VAL
1	A	351	MET
1	A	401	LEU
1	A	404	LYS
1	A	423	VAL
1	A	424	LYS
1	A	428	ILE
1	A	429	GLU
1	A	434	ILE
1	A	435	VAL
1	A	436	LYS
1	A	442	LYS
1	A	445	LEU
1	A	449	VAL
1	A	452	LYS
1	A	453	GLU
1	A	454	LYS
1	A	455	ILE
1	A	463	LYS
1	A	466	SER
1	A	467	GLU
1	A	472	ARG
1	A	474	ILE
1	A	479	LEU
1	A	485	ARG
1	A	488	THR
1	A	504	LEU
1	A	506	GLU
1	A	507	LYS
1	A	508	LEU
1	A	511	LEU
1	A	518	ASP

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Mol	Chain	Res	Type
1	A	523	SER
1	A	554	GLN
1	A	557	ASP
1	A	568	ARG
1	A	569	ASN
1	A	645	GLU
1	A	659	LEU
1	A	696	ASN
1	A	697	LEU
1	A	702	ILE
1	A	758	ARG
1	A	791	GLN
1	A	793	ILE
1	A	801	GLU
1	A	805	ARG
1	A	811	VAL
1	A	836	LEU
2	B	343	VAL
2	B	344	SER
2	B	346	LYS
2	B	353	LYS
2	B	354	GLN
2	B	355	THR
2	B	359	LEU
2	B	368	GLU
2	B	370	TYR
2	B	374	GLU
2	B	375	VAL
2	B	397	LYS
2	B	403	GLN
2	B	405	ILE
2	B	407	ASP
2	B	411	ASN
2	B	412	LYS
2	B	413	SER
2	B	415	VAL
2	B	416	GLN
2	B	419	ASN
2	B	421	PHE
2	B	422	VAL
2	B	425	ARG
2	B	426	ARG

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Mol	Chain	Res	Type
2	B	427	ARG
2	B	430	ILE
3	C	67	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	185	HIS
1	A	204	GLN
1	A	259	HIS
1	A	298	GLN
1	A	394	HIS
1	A	399	ASN
1	A	402	ASN
1	A	427	GLN
1	A	446	ASN
1	A	632	GLN
1	A	696	ASN
1	A	791	GLN
1	A	806	ASN
1	A	828	GLN
2	B	419	ASN
2	B	423	ASN
2	B	429	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

1 ligand is 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
4	SV9	A	901	-	82,83,83	1.32	7 (8%)	110,124,124	0.89	5 (4%)

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
4	SV9	A	901	-	-	28/51/67/67	0/9/9/9

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	901	SV9	C5-N1	-6.18	1.34	1.42
4	A	901	SV9	P2-O10	-3.62	1.55	1.59
4	A	901	SV9	C30-C33	-3.39	1.34	1.43
4	A	901	SV9	P1-O10	-3.12	1.56	1.59
4	A	901	SV9	O4-C35	-2.71	1.37	1.43
4	A	901	SV9	C6-C7	-2.48	1.36	1.39
4	A	901	SV9	O5-C36	-2.22	1.37	1.43

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	901	SV9	C30-C33-N3	3.41	116.94	110.94
4	A	901	SV9	C48-C47-C41	-2.78	96.20	101.46
4	A	901	SV9	O8-P1-O10	2.75	114.69	107.27
4	A	901	SV9	C6-C5-N1	-2.21	119.38	122.70
4	A	901	SV9	O16-C48-C47	-2.05	105.26	111.82

There are no chirality outliers.

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	901	SV9	C9-C10-C11-C12
4	A	901	SV9	C10-C9-N1-C5
4	A	901	SV9	C10-C9-N1-C30
4	A	901	SV9	O1-C9-N1-C5
4	A	901	SV9	O1-C9-N1-C30
4	A	901	SV9	O6-C37-C38-O7
4	A	901	SV9	C39-O13-P2-O12
4	A	901	SV9	C38-O7-P1-O10
4	A	901	SV9	C38-O7-P1-O9
4	A	901	SV9	C19-C20-C21-C22
4	A	901	SV9	C27-C20-C21-C22
4	A	901	SV9	C27-C20-C21-C26
4	A	901	SV9	C19-C20-C21-C26
4	A	901	SV9	C11-C10-C9-N1
4	A	901	SV9	C11-C10-C9-O1
4	A	901	SV9	C14-C15-C16-C27
4	A	901	SV9	C14-C15-C16-C17
4	A	901	SV9	C36-C37-C38-O7
4	A	901	SV9	C28-C15-C16-C17
4	A	901	SV9	C28-C15-C16-C27
4	A	901	SV9	P2-O10-P1-O7
4	A	901	SV9	O4-C35-C36-C37
4	A	901	SV9	C38-O7-P1-O8
4	A	901	SV9	P1-O10-P2-O11
4	A	901	SV9	P1-O10-P2-O12
4	A	901	SV9	C10-C11-C12-C13
4	A	901	SV9	C10-C11-C12-C29
4	A	901	SV9	O13-C39-C40-O14

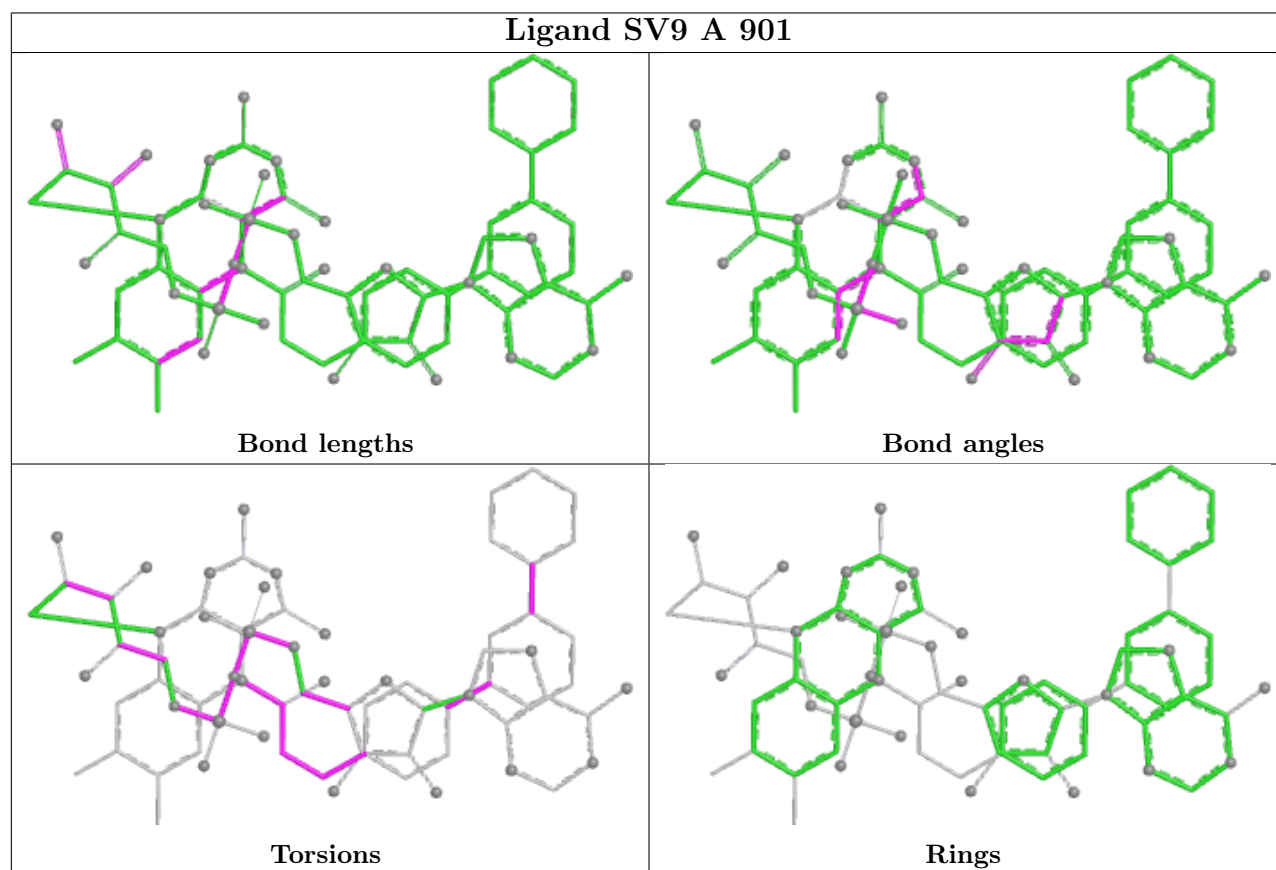
There are no ring outliers.

1 monomer is involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	901	SV9	8	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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(Å²)	Q<0.9
1	A	666/871 (76%)	0.46	24 (3%)	46	37	63, 98, 132, 147	0
2	B	133/144 (92%)	0.90	13 (9%)	13	9	95, 127, 148, 159	0
3	C	4/9 (44%)	3.09	2 (50%)	0	0	120, 125, 131, 137	0
All	All	803/1024 (78%)	0.55	39 (4%)	35	27	63, 105, 136, 159	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	836	LEU	6.9
3	C	66	PRO	5.9
2	B	414	VAL	5.1
1	A	171	PRO	4.2
1	A	467	GLU	4.1
1	A	835	THR	3.7
1	A	506	GLU	3.6
2	B	376	ILE	3.6
2	B	375	VAL	3.5
1	A	268	LYS	3.4
3	C	67	ARG	3.4
1	A	269	ARG	3.3
2	B	413	SER	3.3
1	A	555	ASP	3.0
2	B	382	ARG	3.0
1	A	833	MET	3.0
2	B	381	ALA	2.9
2	B	312	LYS	2.9
1	A	358	GLN	2.8
1	A	492	LYS	2.7
1	A	226	LYS	2.7
1	A	667	ASP	2.7
1	A	516	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
2	B	374	GLU	2.5
2	B	308	ARG	2.4
1	A	246	THR	2.4
1	A	443	GLU	2.4
1	A	373	GLU	2.3
2	B	418	LYS	2.3
2	B	415	VAL	2.2
1	A	273	LEU	2.2
1	A	720	ASP	2.2
2	B	407	ASP	2.2
1	A	700	ALA	2.1
1	A	676	ASN	2.1
1	A	741	PRO	2.1
1	A	685	THR	2.0
1	A	668	ARG	2.0
2	B	402	PHE	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](#)

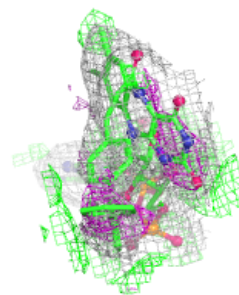
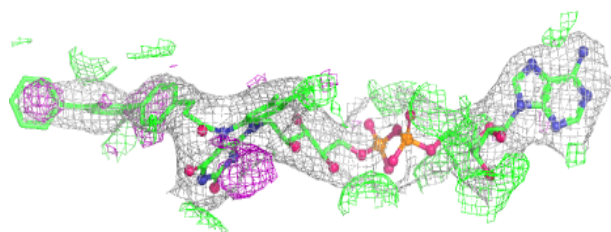
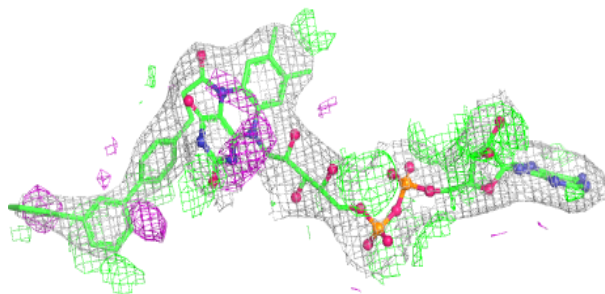
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	SV9	A	901	75/75	0.96	0.11	55,79,124,131	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around SV9 A 901:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.