



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 11:47 AM UTC

PDB ID : 4FD2 / pdb_00004fd2
Title : Crystal structure of the C-terminal domain of ClpB
Authors : Biter, A.B.; Lee, S.; Sung, N.; Tsai, F.T.F.
Deposited on : 2012-05-25
Resolution : 3.00 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

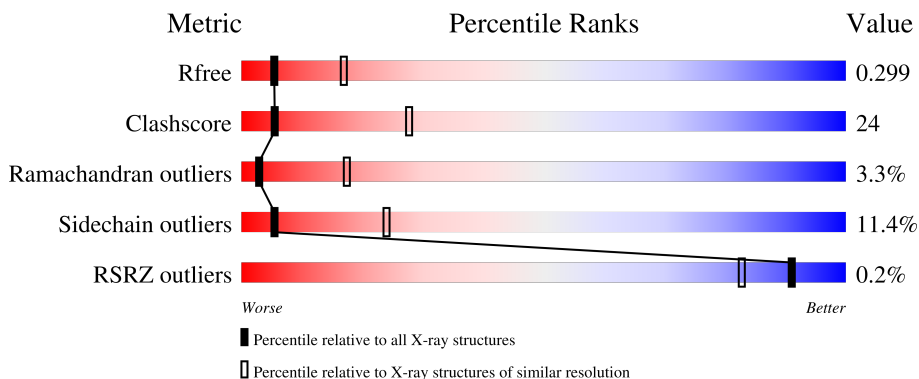
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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.

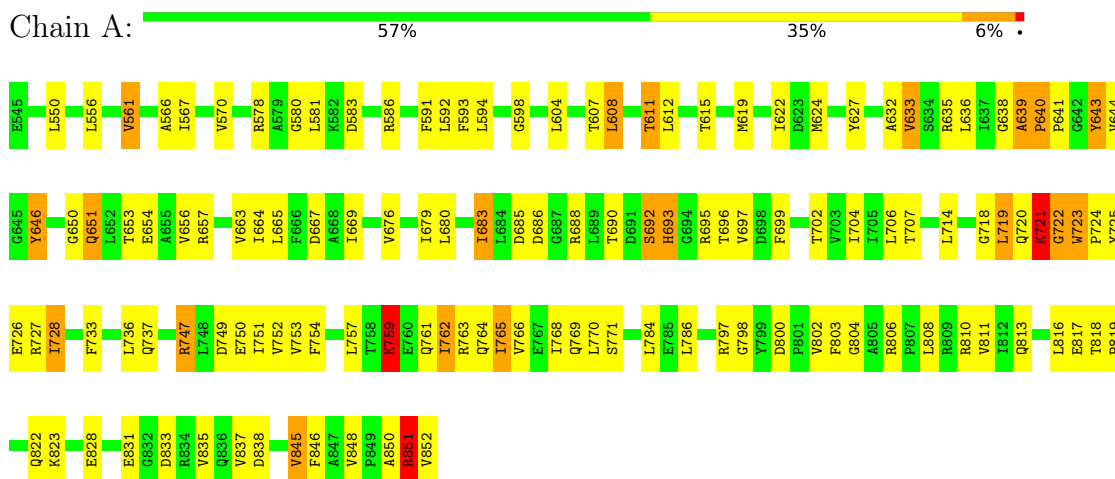
Mol	Chain	Length	Quality of chain
1	A	308	 57% 35% 6% •
1	B	308	 56% 36% 6% •
1	D	308	 56% 36% 7% •

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 27	C 10	N 5	O 10	P 2	0	0
2	B	1	Total 27	C 10	N 5	O 10	P 2	0	0
2	D	1	Total 27	C 10	N 5	O 10	P 2	0	0

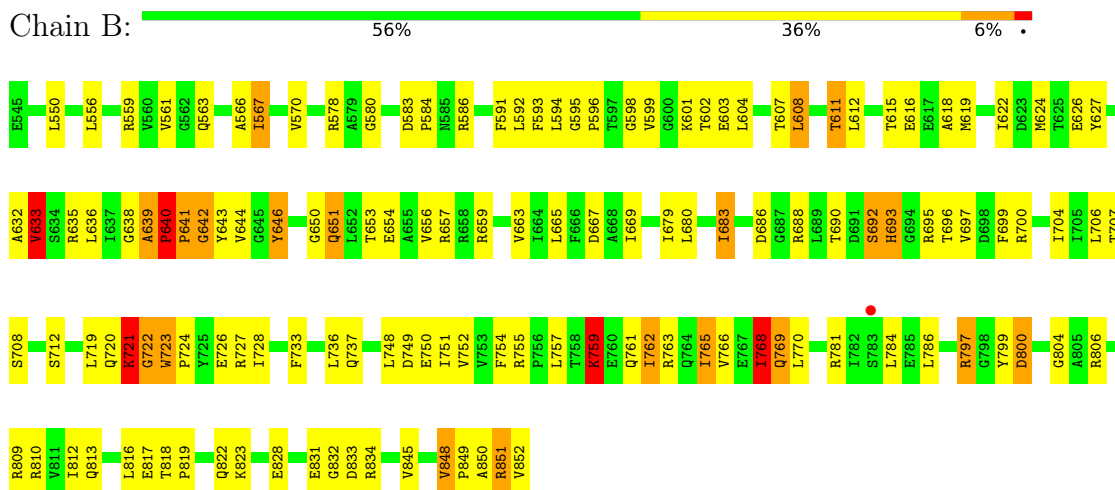
3 Residue-property plots [i](#)

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: Chaperone protein ClpB

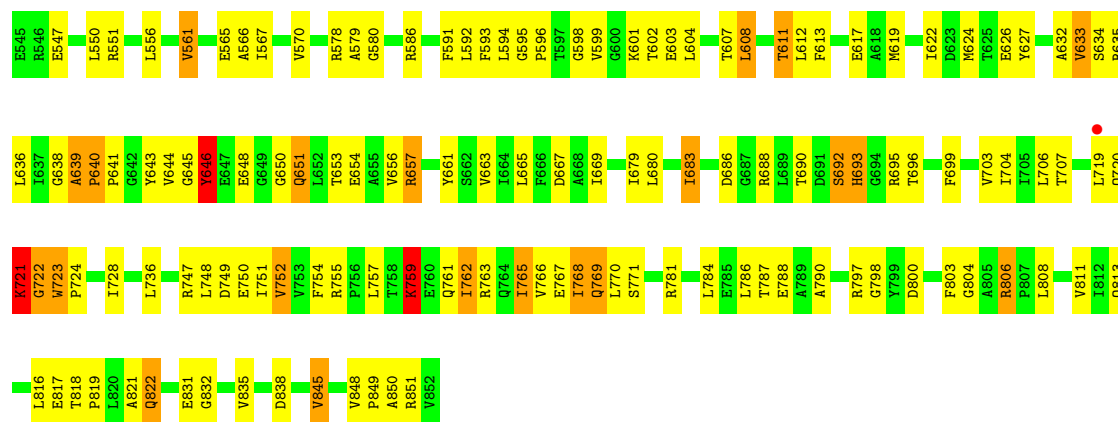


- Molecule 1: Chaperone protein ClpB



- Molecule 1: Chaperone protein ClpB





4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	129.78Å 129.78Å 129.40Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.48 – 3.00 42.48 – 3.00	Depositor EDS
% Data completeness (in resolution range)	98.8 (42.48-3.00) 99.0 (42.48-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.56 (at 2.86Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.278 , 0.298 0.271 , 0.299	Depositor DCC
R_{free} test set	1173 reflections (4.05%)	wwPDB-VP
Wilson B-factor (Å ²)	79.8	Xtrriage
Anisotropy	0.230	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 114.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.480 for h,-h-k,-l	Xtrriage
Reported twinning fraction	0.497 for H, K, L 0.503 for h+k,-k,-l	Depositor
Outliers	1 of 28928 reflections (0.003%)	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7467	wwPDB-VP
Average B, all atoms (Å ²)	109.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 53.05 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.4543e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: ADP

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	0.74	0/2504	1.02	5/3383 (0.1%)
1	B	0.78	1/2504 (0.0%)	1.01	6/3383 (0.2%)
1	D	0.76	0/2504	1.03	3/3383 (0.1%)
All	All	0.76	1/7512 (0.0%)	1.02	14/10149 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	768	ILE	CA-CB	5.02	1.60	1.54

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	728	ILE	N-CA-C	-9.72	102.43	111.67
1	A	765	ILE	CB-CA-C	-6.12	103.77	112.22
1	B	800	ASP	CA-C-N	5.99	126.42	119.47
1	B	800	ASP	C-N-CA	5.99	126.42	119.47
1	B	615	THR	N-CA-C	5.82	117.36	108.52
1	D	765	ILE	CB-CA-C	-5.68	104.58	112.02
1	B	640	PRO	N-CA-C	5.64	117.58	110.70
1	B	651	GLN	N-CA-C	5.59	117.45	111.36
1	A	615	THR	N-CA-C	5.58	116.88	108.46
1	B	765	ILE	CB-CA-C	-5.24	105.26	111.97
1	D	646	TYR	N-CA-C	-5.14	106.17	112.90
1	D	651	GLN	N-CA-C	5.08	116.90	111.36
1	A	747	ARG	N-CA-C	-5.08	107.22	113.41
1	A	651	GLN	N-CA-C	5.05	116.86	111.36

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	2462	0	2532	111	0
1	B	2462	0	2532	135	0
1	D	2462	0	2532	120	0
2	A	27	0	12	2	0
2	B	27	0	12	2	0
2	D	27	0	12	4	0
All	All	7467	0	7632	359	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 24.

All (359) 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:B:834:ARG:NH2	1:D:832:GLY:HA3	1.48	1.26
1:B:851:ARG:O	1:B:852:VAL:HG23	1.35	1.24
1:B:640:PRO:HB2	1:B:641:PRO:HA	1.30	1.13
1:B:851:ARG:CZ	1:B:851:ARG:HA	1.83	1.08
1:B:759:LYS:H	1:B:759:LYS:HD3	1.14	1.04
1:B:851:ARG:O	1:B:852:VAL:CG2	2.05	1.04
1:B:834:ARG:HH22	1:D:832:GLY:HA3	0.88	1.04
1:A:851:ARG:O	1:A:852:VAL:HG23	1.58	1.01
1:A:759:LYS:H	1:A:759:LYS:HD3	1.23	1.01
1:B:851:ARG:HA	1:B:851:ARG:NH1	1.76	1.00
1:D:759:LYS:HD3	1:D:759:LYS:H	1.25	0.99
1:A:598:GLY:HA3	1:A:804:GLY:HA3	1.47	0.96
1:A:640:PRO:HB2	1:A:641:PRO:HA	1.49	0.95
1:D:607:THR:O	1:D:611:THR:HG22	1.65	0.94
1:B:640:PRO:CB	1:B:641:PRO:HA	1.98	0.92
1:B:834:ARG:HH22	1:D:832:GLY:CA	1.81	0.91
1:B:834:ARG:NH2	1:D:832:GLY:CA	2.36	0.89
1:B:640:PRO:CB	1:B:641:PRO:CA	2.52	0.87
1:B:848:VAL:HG12	1:B:849:PRO:HD2	1.56	0.87
1:B:640:PRO:HB3	1:B:641:PRO:O	1.75	0.86
1:A:851:ARG:O	1:A:852:VAL:CG2	2.25	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:759:LYS:HA	1:B:762:ILE:HG13	1.60	0.83
1:D:624:MET:HA	1:D:624:MET:HE2	1.61	0.83
1:A:636:LEU:HA	1:A:651:GLN:HE22	1.43	0.83
1:D:636:LEU:HA	1:D:651:GLN:NE2	1.94	0.83
1:B:640:PRO:HB2	1:B:641:PRO:CA	2.08	0.82
1:D:680:LEU:O	1:D:683:ILE:HG22	1.80	0.81
1:D:640:PRO:HB2	1:D:641:PRO:HA	1.61	0.80
1:D:656:VAL:HG21	1:D:699:PHE:CE2	2.16	0.80
1:D:636:LEU:HA	1:D:651:GLN:HE22	1.48	0.79
1:A:640:PRO:HB2	1:A:641:PRO:CA	2.13	0.79
1:B:641:PRO:HB3	1:B:646:TYR:CE1	2.17	0.78
1:A:669:ILE:HG12	1:A:706:LEU:HD23	1.65	0.78
1:D:598:GLY:HA3	1:D:804:GLY:HA3	1.66	0.78
1:B:607:THR:O	1:B:611:THR:HG22	1.83	0.77
1:B:759:LYS:HD3	1:B:759:LYS:N	1.96	0.77
1:D:680:LEU:HD21	1:D:706:LEU:HD21	1.67	0.77
1:D:818:THR:HB	1:D:819:PRO:HD3	1.68	0.76
1:B:640:PRO:HB3	1:B:641:PRO:C	2.10	0.76
1:A:607:THR:O	1:A:611:THR:HG22	1.86	0.75
1:B:636:LEU:HA	1:B:651:GLN:HE22	1.49	0.75
1:B:850:ALA:O	1:B:851:ARG:NH1	2.20	0.75
1:B:704:ILE:HG22	1:B:706:LEU:HD11	1.70	0.74
1:B:593:PHE:HB2	1:B:707:THR:HG22	1.70	0.73
1:B:781:ARG:O	1:B:832:GLY:HA2	1.90	0.72
1:D:593:PHE:HB2	1:D:707:THR:HG22	1.71	0.72
1:A:636:LEU:HA	1:A:651:GLN:NE2	2.05	0.71
1:B:704:ILE:HG22	1:B:706:LEU:CD1	2.19	0.71
1:B:636:LEU:HA	1:B:651:GLN:NE2	2.07	0.70
1:A:680:LEU:HD21	1:A:706:LEU:HD21	1.73	0.69
1:A:593:PHE:HB2	1:A:707:THR:HG22	1.75	0.69
1:B:851:ARG:C	1:B:852:VAL:HG23	2.15	0.69
1:A:818:THR:HB	1:A:819:PRO:HD3	1.74	0.68
1:A:759:LYS:HA	1:A:762:ILE:HG13	1.74	0.68
1:B:596:PRO:HD2	1:B:599:VAL:HG21	1.75	0.67
1:B:680:LEU:HD21	1:B:706:LEU:HD21	1.76	0.67
1:D:849:PRO:O	1:D:851:ARG:N	2.21	0.67
1:A:723:TRP:CD1	1:A:723:TRP:N	2.63	0.66
1:B:656:VAL:HG21	1:B:699:PHE:CE2	2.30	0.66
1:A:851:ARG:HA	1:A:851:ARG:NE	2.10	0.66
1:B:641:PRO:O	1:B:643:TYR:N	2.28	0.66
1:B:624:MET:HE2	1:B:624:MET:HA	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:653:THR:O	1:B:657:ARG:HB2	1.96	0.65
1:D:723:TRP:N	1:D:723:TRP:CD1	2.64	0.64
1:A:640:PRO:HD2	1:A:646:TYR:HB2	1.80	0.64
1:A:683:ILE:HD11	1:A:699:PHE:CZ	2.32	0.64
1:A:656:VAL:HG21	1:A:699:PHE:CE2	2.32	0.64
1:D:848:VAL:HG12	1:D:849:PRO:HD2	1.80	0.64
1:B:848:VAL:CG1	1:B:849:PRO:HD2	2.26	0.63
1:D:640:PRO:HD2	1:D:646:TYR:HB2	1.80	0.63
1:A:759:LYS:HD3	1:A:759:LYS:N	2.05	0.63
1:B:638:GLY:C	1:B:640:PRO:HD2	2.24	0.63
1:D:683:ILE:HD11	1:D:699:PHE:CZ	2.34	0.62
1:B:639:ALA:N	1:B:640:PRO:CD	2.63	0.62
1:A:851:ARG:C	1:A:852:VAL:HG23	2.24	0.61
1:B:749:ASP:O	1:B:750:GLU:HG2	2.00	0.61
1:D:640:PRO:HB2	1:D:641:PRO:CA	2.29	0.61
1:D:704:ILE:HG22	1:D:706:LEU:HD11	1.82	0.61
1:A:726:GLU:O	1:A:727:ARG:HB3	2.00	0.61
1:A:720:GLN:O	1:A:722:GLY:N	2.35	0.60
1:D:592:LEU:HD23	1:D:751:ILE:HG12	1.81	0.60
1:D:720:GLN:O	1:D:722:GLY:N	2.34	0.60
1:D:759:LYS:HA	1:D:762:ILE:HG13	1.83	0.60
1:A:690:THR:HA	1:A:696:THR:HA	1.82	0.60
1:B:594:LEU:HD11	1:B:736:LEU:HD11	1.82	0.60
1:D:596:PRO:HD2	1:D:599:VAL:HG21	1.84	0.60
1:D:561:VAL:H	2:D:901:ADP:HN62	1.49	0.59
1:A:704:ILE:HG22	1:A:706:LEU:HD11	1.83	0.59
1:A:838:ASP:O	1:A:845:VAL:N	2.32	0.59
1:D:657:ARG:HH22	1:D:695:ARG:HH11	1.51	0.59
1:B:683:ILE:HD11	1:B:699:PHE:CZ	2.38	0.59
1:B:641:PRO:HB3	1:B:646:TYR:CZ	2.37	0.59
1:A:627:TYR:CE2	1:A:635:ARG:HB2	2.38	0.58
1:A:578:ARG:C	1:A:580:GLY:H	2.11	0.58
1:B:690:THR:HA	1:B:696:THR:HA	1.85	0.58
1:B:723:TRP:CD1	1:B:723:TRP:N	2.71	0.58
1:D:639:ALA:N	1:D:640:PRO:HD3	2.17	0.58
1:B:852:VAL:HG11	1:D:851:ARG:CG	2.33	0.58
1:D:690:THR:HA	1:D:696:THR:HA	1.86	0.57
1:A:639:ALA:N	1:A:640:PRO:HD3	2.19	0.57
1:B:818:THR:HB	1:B:819:PRO:HD3	1.86	0.57
1:B:759:LYS:H	1:B:759:LYS:CD	1.99	0.57
1:B:593:PHE:CB	1:B:707:THR:HG22	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:850:ALA:O	1:A:851:ARG:C	2.48	0.57
1:D:704:ILE:HG22	1:D:706:LEU:CD1	2.34	0.57
1:B:592:LEU:HB2	1:B:748:LEU:HD13	1.87	0.56
1:D:757:LEU:HA	1:D:761:GLN:OE1	2.04	0.56
1:A:667:ASP:HA	1:A:707:THR:OG1	2.05	0.56
1:B:578:ARG:C	1:B:580:GLY:H	2.13	0.56
1:D:570:VAL:HG13	1:D:591:PHE:CZ	2.41	0.56
1:A:566:ALA:HA	1:A:752:VAL:CG1	2.35	0.56
1:A:570:VAL:HG13	1:A:591:PHE:CZ	2.41	0.56
1:D:607:THR:O	1:D:611:THR:CG2	2.48	0.56
1:D:640:PRO:HG2	1:D:646:TYR:CB	2.36	0.55
1:A:641:PRO:HB3	1:A:646:TYR:CE1	2.41	0.55
1:B:583:ASP:HB3	1:B:586:ARG:HD3	1.88	0.55
1:B:669:ILE:HG12	1:B:706:LEU:HD23	1.88	0.55
1:A:598:GLY:H	2:A:901:ADP:PB	2.29	0.55
1:B:720:GLN:O	1:B:722:GLY:N	2.39	0.55
1:A:723:TRP:CE3	1:A:727:ARG:HG2	2.42	0.55
1:B:763:ARG:O	1:B:766:VAL:HB	2.06	0.55
1:B:852:VAL:CG1	1:D:851:ARG:HG3	2.37	0.55
1:A:680:LEU:O	1:A:683:ILE:HG22	2.07	0.55
1:A:640:PRO:HB3	1:A:643:TYR:HB2	1.89	0.55
1:A:851:ARG:NE	1:A:851:ARG:CA	2.69	0.55
1:D:634:SER:O	1:D:638:GLY:HA2	2.06	0.55
1:B:598:GLY:N	2:B:901:ADP:O2B	2.41	0.54
1:D:566:ALA:HA	1:D:752:VAL:CG1	2.37	0.54
1:D:593:PHE:CB	1:D:707:THR:HG22	2.37	0.54
1:B:566:ALA:HA	1:B:752:VAL:CG1	2.37	0.54
1:D:763:ARG:NH2	1:D:788:GLU:OE2	2.35	0.54
1:D:787:THR:O	1:D:790:ALA:HB3	2.08	0.54
1:A:594:LEU:HD11	1:A:736:LEU:HD11	1.90	0.54
1:D:594:LEU:HD11	1:D:736:LEU:HD11	1.90	0.53
1:D:763:ARG:O	1:D:766:VAL:HB	2.08	0.53
1:D:556:LEU:HD23	1:D:611:THR:HG21	1.90	0.53
1:D:627:TYR:HB3	1:D:632:ALA:HB1	1.91	0.53
1:A:800:ASP:OD2	1:A:803:PHE:HB2	2.07	0.53
1:D:638:GLY:O	1:D:692:SER:HB2	2.08	0.53
1:D:640:PRO:HG2	1:D:646:TYR:HB3	1.90	0.53
1:D:645:GLY:HA3	1:D:648:GLU:HG2	1.91	0.53
1:A:749:ASP:O	1:A:750:GLU:HG2	2.08	0.53
1:B:640:PRO:HB3	1:B:641:PRO:CA	2.35	0.53
1:D:838:ASP:O	1:D:845:VAL:N	2.31	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:653:THR:O	1:D:657:ARG:HB2	2.08	0.53
1:D:639:ALA:HA	1:D:692:SER:OG	2.09	0.52
1:D:638:GLY:C	1:D:640:PRO:HD3	2.34	0.52
1:A:583:ASP:HB3	1:A:586:ARG:HD3	1.91	0.52
1:D:749:ASP:O	1:D:750:GLU:HG2	2.08	0.52
1:A:640:PRO:CB	1:A:641:PRO:CA	2.85	0.52
1:A:556:LEU:HD23	1:A:611:THR:HG21	1.91	0.52
1:A:723:TRP:N	1:A:723:TRP:HD1	2.06	0.52
1:A:622:ILE:HG22	1:A:624:MET:CE	2.40	0.52
1:B:598:GLY:H	2:B:901:ADP:PB	2.32	0.52
1:A:704:ILE:HG22	1:A:706:LEU:CD1	2.40	0.52
1:B:641:PRO:O	1:B:642:GLY:C	2.52	0.52
1:D:690:THR:HG23	1:D:696:THR:HG22	1.92	0.51
1:B:627:TYR:CE2	1:B:635:ARG:HB2	2.44	0.51
1:B:640:PRO:HB2	1:B:646:TYR:CB	2.40	0.51
1:B:556:LEU:HD23	1:B:611:THR:HG21	1.91	0.51
1:A:761:GLN:O	1:A:762:ILE:C	2.53	0.51
1:A:640:PRO:CD	1:A:646:TYR:HB2	2.41	0.51
1:A:640:PRO:HG2	1:A:646:TYR:HB2	1.92	0.51
1:A:624:MET:HA	1:A:624:MET:HE2	1.91	0.51
1:A:638:GLY:O	1:A:692:SER:HB2	2.11	0.51
1:D:669:ILE:HG12	1:D:706:LEU:HD23	1.92	0.51
1:A:757:LEU:CD1	1:A:765:ILE:HD11	2.41	0.51
1:D:848:VAL:HG12	1:D:849:PRO:CD	2.41	0.50
1:A:640:PRO:HG2	1:A:646:TYR:CB	2.42	0.50
1:D:657:ARG:HH22	1:D:695:ARG:NH1	2.08	0.50
1:A:653:THR:O	1:A:657:ARG:HB2	2.11	0.50
1:A:851:ARG:C	1:A:851:ARG:HE	2.18	0.50
1:B:632:ALA:O	1:B:633:VAL:C	2.55	0.50
1:D:667:ASP:HA	1:D:707:THR:OG1	2.12	0.50
1:B:669:ILE:HG22	1:B:708:SER:HB2	1.93	0.50
1:D:586:ARG:NH2	1:D:747:ARG:O	2.35	0.50
1:B:618:ALA:HA	1:B:659:ARG:HD3	1.95	0.49
1:A:723:TRP:HE3	1:A:727:ARG:HG2	1.77	0.49
1:B:816:LEU:C	1:B:816:LEU:HD12	2.37	0.49
1:B:851:ARG:HA	1:B:851:ARG:NE	2.23	0.49
1:B:761:GLN:O	1:B:762:ILE:C	2.56	0.49
1:D:640:PRO:CB	1:D:641:PRO:CA	2.90	0.49
1:B:640:PRO:CB	1:B:641:PRO:C	2.80	0.49
1:D:650:GLY:O	1:D:654:GLU:HB2	2.12	0.49
1:A:640:PRO:CG	1:A:646:TYR:HB2	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:646:TYR:CE2	1:A:693:HIS:CE1	3.00	0.49
1:A:763:ARG:O	1:A:766:VAL:HB	2.13	0.49
1:B:583:ASP:OD1	1:B:584:PRO:HD2	2.12	0.49
1:B:833:ASP:OD2	1:B:848:VAL:HG11	2.13	0.49
1:B:800:ASP:O	1:B:804:GLY:N	2.46	0.49
1:A:586:ARG:NH2	1:A:747:ARG:O	2.39	0.49
1:A:706:LEU:N	1:A:706:LEU:HD12	2.27	0.49
1:B:639:ALA:N	1:B:640:PRO:HD3	2.26	0.49
1:B:640:PRO:CB	1:B:641:PRO:O	2.56	0.49
1:A:638:GLY:C	1:A:640:PRO:HD3	2.38	0.48
1:D:721:LYS:O	1:D:722:GLY:C	2.56	0.48
1:B:638:GLY:C	1:B:640:PRO:CD	2.86	0.48
1:B:704:ILE:CG2	1:B:706:LEU:HD11	2.43	0.48
1:B:757:LEU:CD1	1:B:765:ILE:HD11	2.43	0.48
1:B:641:PRO:C	1:B:643:TYR:N	2.72	0.48
1:D:640:PRO:HG3	1:D:643:TYR:HB2	1.95	0.48
1:D:759:LYS:HD3	1:D:759:LYS:N	2.09	0.48
1:D:759:LYS:H	1:D:759:LYS:CD	2.06	0.48
1:A:627:TYR:HE2	1:A:635:ARG:HB2	1.76	0.48
1:D:640:PRO:CD	1:D:646:TYR:HB2	2.43	0.48
1:A:816:LEU:HD12	1:A:816:LEU:O	2.13	0.48
1:A:784:LEU:HD12	1:A:835:VAL:HB	1.95	0.47
1:B:657:ARG:NH2	1:B:695:ARG:HD2	2.29	0.47
1:D:561:VAL:H	2:D:901:ADP:N6	2.11	0.47
1:D:800:ASP:O	1:D:804:GLY:N	2.47	0.47
1:A:798:GLY:HA2	1:A:811:VAL:HG21	1.95	0.47
1:A:800:ASP:O	1:A:804:GLY:N	2.47	0.47
1:B:667:ASP:HA	1:B:707:THR:OG1	2.14	0.47
1:B:852:VAL:HG11	1:D:851:ARG:HG2	1.96	0.47
1:D:770:LEU:O	1:D:771:SER:C	2.58	0.47
1:D:798:GLY:HA2	1:D:811:VAL:HG21	1.96	0.47
1:D:578:ARG:O	1:D:579:ALA:HB3	2.14	0.47
1:D:688:ARG:HB2	1:D:688:ARG:CZ	2.44	0.47
1:D:626:GLU:HG3	1:D:627:TYR:CE1	2.49	0.47
1:B:627:TYR:HB3	1:B:632:ALA:HB1	1.96	0.47
1:B:650:GLY:O	1:B:654:GLU:HB2	2.14	0.47
1:D:627:TYR:CE2	1:D:635:ARG:HB2	2.49	0.47
1:D:849:PRO:C	1:D:851:ARG:H	2.18	0.47
1:B:665:LEU:HG	1:B:667:ASP:OD2	2.15	0.47
1:B:851:ARG:C	1:B:852:VAL:CG2	2.81	0.47
1:D:665:LEU:HG	1:D:667:ASP:OD2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:723:TRP:N	1:D:723:TRP:HD1	2.12	0.47
1:B:680:LEU:O	1:B:683:ILE:HG22	2.15	0.47
1:B:770:LEU:HD21	1:B:812:ILE:HD13	1.97	0.47
1:D:566:ALA:HA	1:D:752:VAL:HG12	1.97	0.46
1:A:653:THR:HB	1:A:697:VAL:HG21	1.97	0.46
1:B:640:PRO:HG2	1:B:646:TYR:HB2	1.96	0.46
1:B:641:PRO:HB3	1:B:646:TYR:CD1	2.50	0.46
1:B:733:PHE:HE2	1:B:737:GLN:NE2	2.14	0.46
1:A:846:PHE:N	1:A:846:PHE:CD1	2.84	0.46
1:B:640:PRO:HG2	1:B:646:TYR:CB	2.46	0.46
1:A:640:PRO:HG3	1:A:643:TYR:HB2	1.97	0.46
1:D:797:ARG:NH1	1:D:797:ARG:HB3	2.31	0.46
1:A:757:LEU:HA	1:A:761:GLN:OE1	2.15	0.46
1:B:816:LEU:HD12	1:B:816:LEU:O	2.15	0.46
1:D:683:ILE:HD11	1:D:699:PHE:CE2	2.50	0.46
1:B:608:LEU:O	1:B:612:LEU:HB2	2.16	0.46
1:D:578:ARG:C	1:D:580:GLY:H	2.23	0.46
1:D:608:LEU:O	1:D:612:LEU:HB2	2.15	0.46
1:A:813:GLN:HG3	1:A:817:GLU:OE1	2.15	0.46
1:D:657:ARG:NH2	1:D:695:ARG:HD2	2.31	0.46
1:B:653:THR:HB	1:B:697:VAL:HG21	1.98	0.46
1:D:632:ALA:O	1:D:633:VAL:C	2.59	0.46
1:A:770:LEU:O	1:A:771:SER:C	2.58	0.45
1:A:833:ASP:OD2	1:A:848:VAL:HG11	2.15	0.45
1:D:808:LEU:O	1:D:811:VAL:HB	2.17	0.45
1:B:595:GLY:O	1:B:712:SER:OG	2.33	0.45
1:B:797:ARG:NH1	1:B:797:ARG:HB3	2.31	0.45
1:A:665:LEU:HG	1:A:667:ASP:OD2	2.16	0.45
1:B:690:THR:HG23	1:B:696:THR:HG22	1.98	0.45
1:A:688:ARG:HB2	1:A:688:ARG:CZ	2.46	0.45
1:D:767:GLU:O	1:D:768:ILE:C	2.60	0.45
1:A:632:ALA:O	1:A:633:VAL:C	2.60	0.45
1:B:640:PRO:HG3	1:B:643:TYR:HB2	1.98	0.45
1:A:693:HIS:CD2	1:A:693:HIS:N	2.85	0.45
1:D:598:GLY:H	2:D:901:ADP:PB	2.40	0.45
1:A:604:LEU:HD23	1:A:754:PHE:HZ	1.81	0.45
1:A:608:LEU:O	1:A:612:LEU:HB2	2.17	0.45
1:D:640:PRO:HB3	1:D:643:TYR:HB2	1.99	0.45
1:B:799:TYR:CD2	1:B:799:TYR:O	2.69	0.44
1:A:813:GLN:HA	1:A:817:GLU:HB2	1.99	0.44
1:D:613:PHE:CD2	1:D:661:TYR:HB3	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:638:GLY:O	1:D:692:SER:CB	2.64	0.44
1:A:578:ARG:C	1:A:580:GLY:N	2.75	0.44
1:D:757:LEU:CD1	1:D:765:ILE:HD11	2.48	0.44
1:A:580:GLY:C	1:A:581:LEU:HD12	2.42	0.44
1:B:578:ARG:C	1:B:580:GLY:N	2.76	0.44
1:B:592:LEU:HD23	1:B:751:ILE:HG12	2.00	0.44
1:B:766:VAL:O	1:B:770:LEU:HG	2.18	0.44
1:B:823:LYS:HA	1:B:828:GLU:HB2	2.00	0.44
1:D:595:GLY:HA3	1:D:754:PHE:HB2	2.00	0.44
1:D:604:LEU:HD23	1:D:754:PHE:HZ	1.82	0.44
1:D:781:ARG:O	1:D:832:GLY:HA2	2.17	0.44
1:D:592:LEU:HB2	1:D:748:LEU:HD13	1.99	0.44
1:D:784:LEU:HD12	1:D:835:VAL:HB	1.99	0.44
1:B:721:LYS:O	1:B:722:GLY:C	2.60	0.44
1:A:797:ARG:HB3	1:A:797:ARG:NH1	2.33	0.44
1:B:593:PHE:HB3	1:B:601:LYS:HG2	2.00	0.44
1:B:816:LEU:O	1:B:819:PRO:HD2	2.17	0.44
1:D:640:PRO:HG2	1:D:646:TYR:HB2	2.00	0.44
1:A:762:ILE:H	1:A:762:ILE:HG12	1.39	0.43
1:A:837:VAL:HG22	1:A:846:PHE:CD2	2.53	0.43
1:D:813:GLN:HG3	1:D:817:GLU:OE1	2.17	0.43
1:D:593:PHE:HB3	1:D:601:LYS:HG2	2.00	0.43
1:D:636:LEU:CA	1:D:651:GLN:HE22	2.25	0.43
1:D:561:VAL:N	2:D:901:ADP:HN62	2.14	0.43
1:B:626:GLU:HG3	1:B:627:TYR:CE1	2.52	0.43
1:A:664:ILE:HD11	1:A:702:THR:HG21	2.01	0.43
1:B:693:HIS:CD2	1:B:693:HIS:N	2.86	0.43
1:B:683:ILE:HD11	1:B:699:PHE:CE2	2.53	0.43
1:D:622:ILE:HG22	1:D:624:MET:CE	2.49	0.43
1:A:638:GLY:O	1:A:692:SER:CB	2.67	0.43
1:B:770:LEU:CD2	1:B:812:ILE:HD13	2.49	0.43
1:A:685:ASP:OD1	1:A:747:ARG:CZ	2.67	0.43
1:D:547:GLU:O	1:D:551:ARG:HB2	2.19	0.43
1:A:592:LEU:HD23	1:A:751:ILE:HG12	2.00	0.43
1:B:849:PRO:O	1:B:850:ALA:C	2.62	0.43
1:A:657:ARG:NH2	1:A:695:ARG:HD2	2.34	0.43
1:A:759:LYS:H	1:A:759:LYS:CD	2.08	0.43
1:A:808:LEU:O	1:A:811:VAL:HB	2.18	0.43
1:D:656:VAL:HG21	1:D:699:PHE:HE2	1.78	0.43
1:D:761:GLN:O	1:D:762:ILE:C	2.61	0.43
1:A:816:LEU:HD12	1:A:816:LEU:C	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:570:VAL:HG13	1:B:591:PHE:CZ	2.53	0.42
1:B:688:ARG:HH12	1:B:700:ARG:NE	2.17	0.42
1:B:809:ARG:O	1:B:812:ILE:HB	2.18	0.42
1:D:816:LEU:HD12	1:D:816:LEU:O	2.18	0.42
1:A:690:THR:HG23	1:A:696:THR:HG22	2.01	0.42
1:A:561:VAL:N	2:A:901:ADP:N1	2.61	0.42
1:A:627:TYR:HH	1:A:651:GLN:CD	2.27	0.42
1:B:602:THR:O	1:B:603:GLU:C	2.60	0.42
1:B:813:GLN:HA	1:B:817:GLU:HB2	2.01	0.42
1:B:851:ARG:O	1:B:852:VAL:HG22	2.11	0.42
1:D:645:GLY:CA	1:D:648:GLU:HG2	2.49	0.42
1:D:693:HIS:CD2	1:D:693:HIS:N	2.87	0.42
1:D:762:ILE:H	1:D:762:ILE:HG12	1.38	0.42
1:A:627:TYR:HB3	1:A:632:ALA:HB1	2.00	0.42
1:B:768:ILE:HG13	1:B:769:GLN:N	2.33	0.42
1:B:784:LEU:HD12	1:B:784:LEU:HA	1.81	0.42
1:D:803:PHE:O	1:D:806:ARG:HB2	2.20	0.42
1:A:718:GLY:O	1:A:719:LEU:C	2.63	0.42
1:A:721:LYS:O	1:A:722:GLY:C	2.63	0.42
1:B:721:LYS:O	1:B:723:TRP:N	2.52	0.42
1:A:650:GLY:O	1:A:654:GLU:HB2	2.20	0.42
1:B:563:GLN:HB3	1:B:566:ALA:HB3	2.02	0.42
1:B:640:PRO:CG	1:B:646:TYR:HB2	2.49	0.42
1:A:733:PHE:HE2	1:A:737:GLN:NE2	2.18	0.42
1:B:567:ILE:HD12	1:B:604:LEU:HD22	2.02	0.42
1:B:619:MET:HA	1:B:663:VAL:O	2.20	0.42
1:A:823:LYS:HB3	1:A:828:GLU:HB2	2.02	0.41
1:B:638:GLY:O	1:B:692:SER:HB2	2.19	0.41
1:D:663:VAL:HG22	1:D:703:VAL:HB	2.01	0.41
1:A:619:MET:HA	1:A:663:VAL:O	2.19	0.41
1:B:726:GLU:O	1:B:727:ARG:C	2.63	0.41
1:B:641:PRO:HB2	1:B:642:GLY:H	1.69	0.41
1:A:640:PRO:CB	1:A:643:TYR:HB2	2.51	0.41
1:A:683:ILE:HD11	1:A:699:PHE:CE2	2.54	0.41
1:B:596:PRO:HD3	1:B:754:PHE:O	2.20	0.41
1:B:641:PRO:HA	1:B:646:TYR:CG	2.56	0.41
1:A:693:HIS:CD2	1:A:693:HIS:H	2.39	0.41
1:A:761:GLN:O	1:A:764:GLN:N	2.53	0.41
1:D:768:ILE:HG13	1:D:769:GLN:N	2.34	0.41
1:A:639:ALA:HA	1:A:692:SER:OG	2.20	0.41
1:D:604:LEU:O	1:D:608:LEU:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:762:ILE:H	1:B:762:ILE:HG12	1.41	0.41
1:B:797:ARG:HB3	1:B:797:ARG:HH11	1.85	0.41
1:D:693:HIS:CD2	1:D:693:HIS:H	2.39	0.41
1:B:596:PRO:O	1:B:601:LYS:HE3	2.20	0.40
1:B:683:ILE:HG21	1:B:683:ILE:HD13	1.89	0.40
1:D:821:ALA:O	1:D:822:GLN:C	2.64	0.40
1:B:559:ARG:NH1	1:B:616:GLU:OE2	2.49	0.40
1:D:602:THR:O	1:D:603:GLU:C	2.64	0.40
1:D:617:GLU:C	1:D:619:MET:H	2.28	0.40
1:B:799:TYR:O	1:B:799:TYR:HD2	2.05	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	306/308 (99%)	268 (88%)	27 (9%)	11 (4%)	2	16
1	B	306/308 (99%)	269 (88%)	27 (9%)	10 (3%)	3	17
1	D	306/308 (99%)	270 (88%)	27 (9%)	9 (3%)	3	20
All	All	918/924 (99%)	807 (88%)	81 (9%)	30 (3%)	3	17

All (30) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	721	LYS
1	A	851	ARG
1	B	640	PRO
1	B	721	LYS
1	D	721	LYS
1	D	850	ALA
1	A	633	VAL

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Mol	Chain	Res	Type
1	A	640	PRO
1	A	643	TYR
1	A	644	VAL
1	A	722	GLY
1	A	724	PRO
1	A	759	LYS
1	B	633	VAL
1	B	642	GLY
1	B	644	VAL
1	B	722	GLY
1	B	724	PRO
1	B	759	LYS
1	D	633	VAL
1	D	644	VAL
1	D	722	GLY
1	D	724	PRO
1	A	725	TYR
1	D	640	PRO
1	D	759	LYS
1	D	639	ALA
1	A	639	ALA
1	B	639	ALA
1	B	641	PRO

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	260/260 (100%)	230 (88%)	30 (12%)	5 24
1	B	260/260 (100%)	229 (88%)	31 (12%)	5 22
1	D	260/260 (100%)	232 (89%)	28 (11%)	6 26
All	All	780/780 (100%)	691 (89%)	89 (11%)	5 24

All (89) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	550	LEU
1	A	561	VAL
1	A	567	ILE
1	A	608	LEU
1	A	611	THR
1	A	646	TYR
1	A	676	VAL
1	A	679	ILE
1	A	683	ILE
1	A	686	ASP
1	A	692	SER
1	A	693	HIS
1	A	714	LEU
1	A	719	LEU
1	A	721	LYS
1	A	723	TRP
1	A	728	ILE
1	A	753	VAL
1	A	759	LYS
1	A	762	ILE
1	A	768	ILE
1	A	769	GLN
1	A	786	LEU
1	A	802	VAL
1	A	806	ARG
1	A	810	ARG
1	A	822	GLN
1	A	831	GLU
1	A	845	VAL
1	A	851	ARG
1	B	550	LEU
1	B	561	VAL
1	B	567	ILE
1	B	608	LEU
1	B	611	THR
1	B	622	ILE
1	B	633	VAL
1	B	646	TYR
1	B	679	ILE
1	B	683	ILE
1	B	686	ASP
1	B	692	SER
1	B	693	HIS

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Mol	Chain	Res	Type
1	B	719	LEU
1	B	721	LYS
1	B	723	TRP
1	B	728	ILE
1	B	755	ARG
1	B	759	LYS
1	B	762	ILE
1	B	768	ILE
1	B	769	GLN
1	B	786	LEU
1	B	797	ARG
1	B	806	ARG
1	B	810	ARG
1	B	822	GLN
1	B	831	GLU
1	B	845	VAL
1	B	848	VAL
1	B	851	ARG
1	D	550	LEU
1	D	561	VAL
1	D	565	GLU
1	D	567	ILE
1	D	608	LEU
1	D	611	THR
1	D	646	TYR
1	D	657	ARG
1	D	679	ILE
1	D	683	ILE
1	D	686	ASP
1	D	692	SER
1	D	693	HIS
1	D	719	LEU
1	D	721	LYS
1	D	723	TRP
1	D	728	ILE
1	D	752	VAL
1	D	755	ARG
1	D	759	LYS
1	D	762	ILE
1	D	768	ILE
1	D	769	GLN
1	D	786	LEU

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Mol	Chain	Res	Type
1	D	806	ARG
1	D	822	GLN
1	D	831	GLU
1	D	845	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	557	HIS
1	A	585	ASN
1	A	631	HIS
1	A	651	GLN
1	A	682	GLN
1	A	693	HIS
1	A	746	ASN
1	A	836	GLN
1	B	557	HIS
1	B	585	ASN
1	B	651	GLN
1	B	682	GLN
1	B	693	HIS
1	B	746	ASN
1	B	764	GLN
1	B	769	GLN
1	B	836	GLN
1	D	557	HIS
1	D	585	ASN
1	D	693	HIS
1	D	746	ASN
1	D	836	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 ligands 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	ADP	A	901	-	28,29,29	1.42	4 (14%)	43,45,45	1.88	9 (20%)
2	ADP	D	901	-	28,29,29	1.50	5 (17%)	43,45,45	1.87	7 (16%)
2	ADP	B	901	-	28,29,29	1.44	5 (17%)	43,45,45	1.88	7 (16%)

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	ADP	A	901	-	-	6/16/32/32	0/3/3/3
2	ADP	D	901	-	-	9/16/32/32	0/3/3/3
2	ADP	B	901	-	-	1/16/32/32	0/3/3/3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	901	ADP	C5-C4	4.94	1.47	1.39
2	B	901	ADP	C5-C4	4.76	1.47	1.39
2	A	901	ADP	C5-C4	4.67	1.47	1.39
2	D	901	ADP	C5-N7	-2.98	1.33	1.39
2	A	901	ADP	C5-C6	2.78	1.48	1.41
2	B	901	ADP	C5-C6	2.63	1.48	1.41
2	D	901	ADP	C5-C6	2.58	1.48	1.41
2	A	901	ADP	C5-N7	-2.57	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	901	ADP	C5-N7	-2.57	1.34	1.39
2	B	901	ADP	PA-O3A	2.32	1.62	1.59
2	D	901	ADP	PA-O3A	2.25	1.61	1.59
2	B	901	ADP	C8-N7	2.19	1.35	1.31
2	A	901	ADP	C8-N7	2.17	1.35	1.31
2	D	901	ADP	C8-N7	2.14	1.35	1.31

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	901	ADP	C5-C4-N3	-6.33	118.00	126.72
2	A	901	ADP	C5-C4-N3	-6.14	118.26	126.72
2	D	901	ADP	C5-C4-N3	-6.04	118.40	126.72
2	B	901	ADP	N3-C4-N9	4.86	135.43	127.17
2	D	901	ADP	N3-C4-N9	4.77	135.27	127.17
2	A	901	ADP	N3-C4-N9	4.69	135.15	127.17
2	A	901	ADP	C2-N3-C4	3.82	121.16	111.83
2	B	901	ADP	C2-N3-C4	3.76	121.02	111.83
2	A	901	ADP	C4-C5-N7	-3.72	106.33	110.58
2	D	901	ADP	C2-N3-C4	3.61	120.64	111.83
2	B	901	ADP	C4-C5-N7	-3.54	106.53	110.58
2	D	901	ADP	C4-C5-N7	-3.34	106.76	110.58
2	A	901	ADP	N3-C2-N1	-3.33	123.54	128.58
2	D	901	ADP	N3-C2-N1	-3.20	123.73	128.58
2	B	901	ADP	N3-C2-N1	-3.17	123.79	128.58
2	D	901	ADP	C3'-C2'-C1'	2.76	106.69	101.46
2	A	901	ADP	C3'-C2'-C1'	2.73	106.63	101.46
2	A	901	ADP	C5-N7-C8	2.70	107.70	103.45
2	B	901	ADP	C3'-C2'-C1'	2.66	106.50	101.46
2	B	901	ADP	C5-N7-C8	2.56	107.47	103.45
2	D	901	ADP	C5-N7-C8	2.48	107.34	103.45
2	A	901	ADP	C6-C5-N7	2.10	136.13	132.09
2	A	901	ADP	C4-N9-C8	2.09	107.94	105.74

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	901	ADP	PA-O3A-PB-O2B
2	A	901	ADP	C5'-O5'-PA-O2A
2	A	901	ADP	C5'-O5'-PA-O3A
2	D	901	ADP	C5'-O5'-PA-O1A

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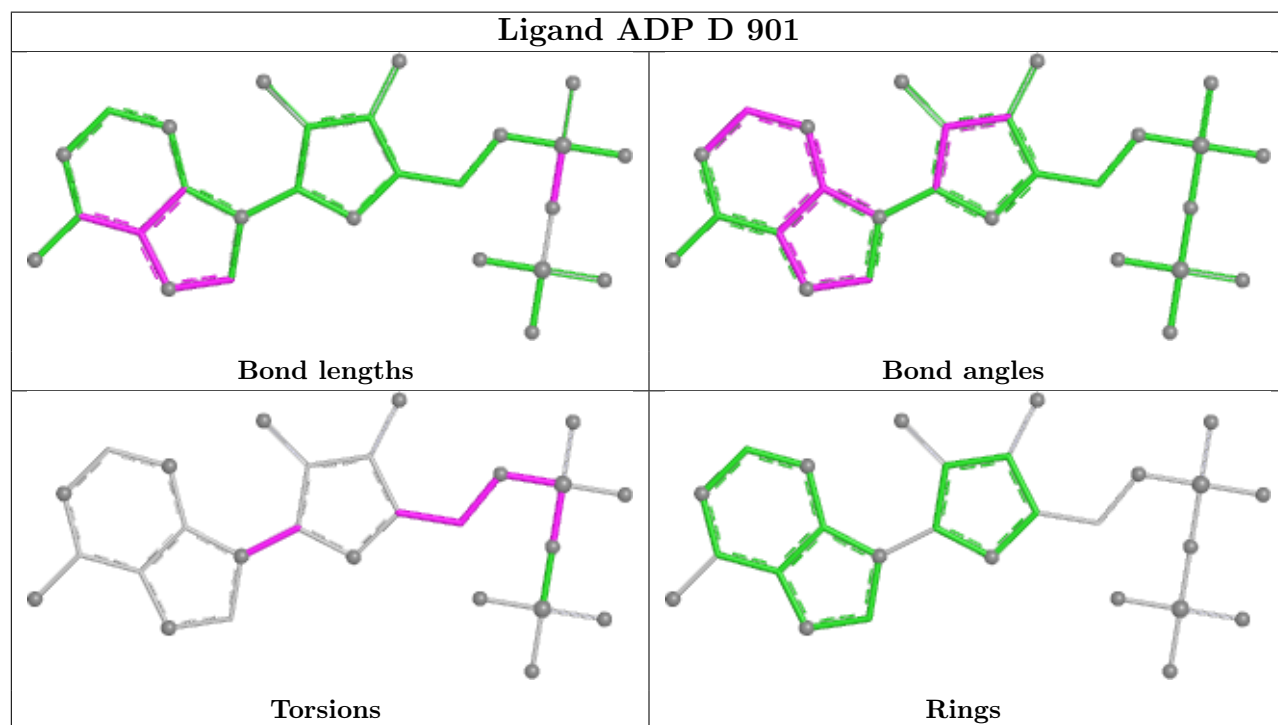
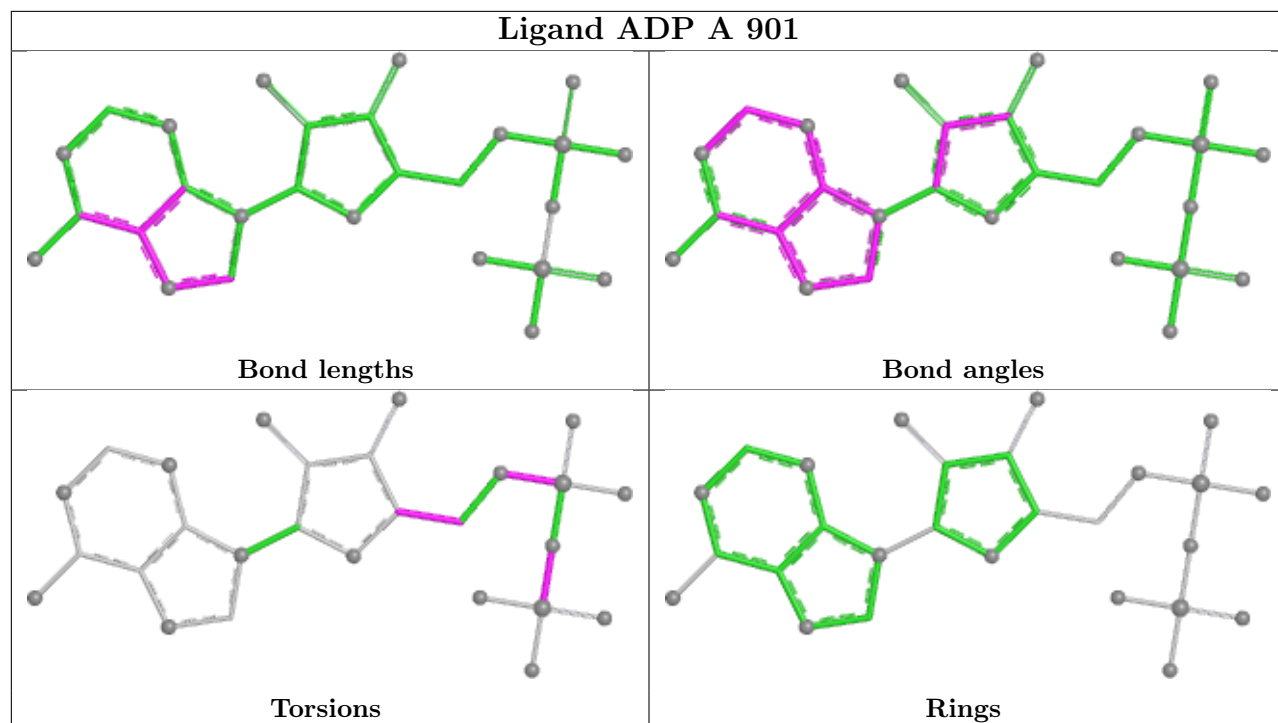
Mol	Chain	Res	Type	Atoms
2	D	901	ADP	C5'-O5'-PA-O2A
2	D	901	ADP	C5'-O5'-PA-O3A
2	D	901	ADP	O4'-C4'-C5'-O5'
2	D	901	ADP	C3'-C4'-C5'-O5'
2	A	901	ADP	O4'-C4'-C5'-O5'
2	A	901	ADP	C5'-O5'-PA-O1A
2	D	901	ADP	C4'-C5'-O5'-PA
2	D	901	ADP	C2'-C1'-N9-C8
2	D	901	ADP	C2'-C1'-N9-C4
2	A	901	ADP	C3'-C4'-C5'-O5'
2	B	901	ADP	PB-O3A-PA-O2A
2	D	901	ADP	PB-O3A-PA-O2A

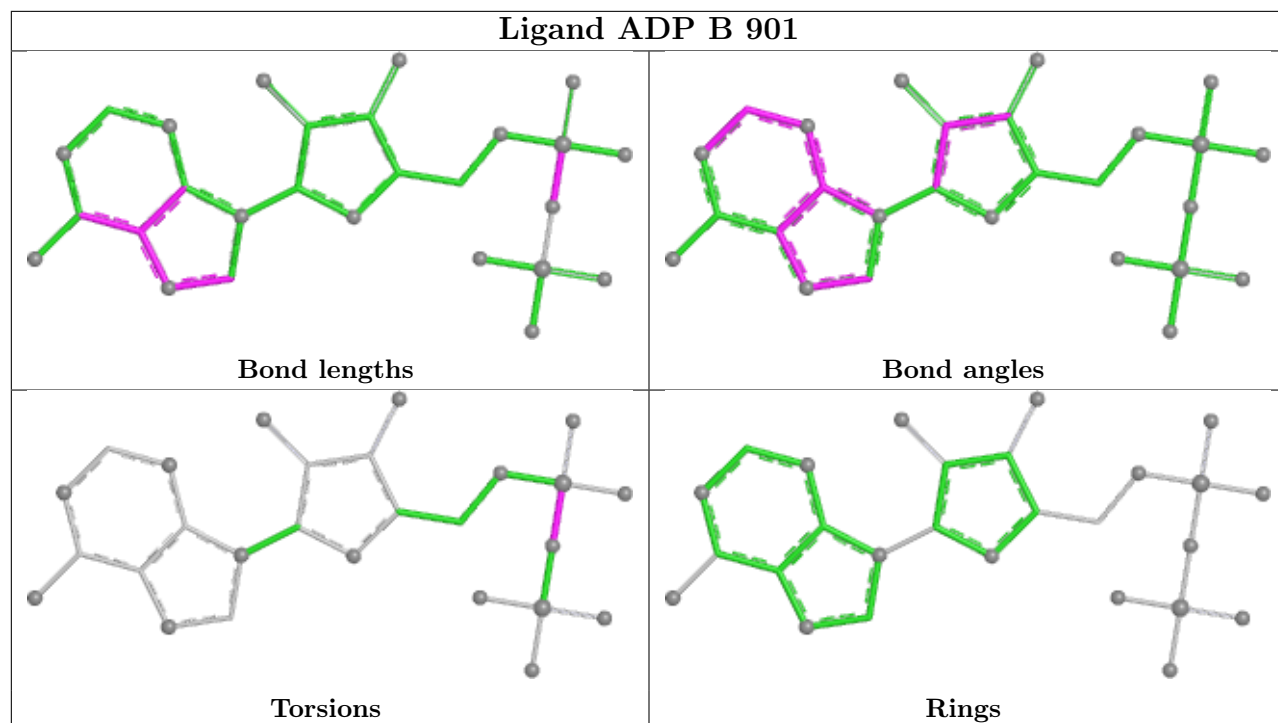
There are no ring outliers.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	901	ADP	2	0
2	D	901	ADP	4	0
2	B	901	ADP	2	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 [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	308/308 (100%)	-0.66	0 100 100	56, 88, 203, 295	0
1	B	308/308 (100%)	-0.38	1 (0%) 90 79	73, 104, 194, 231	0
1	D	308/308 (100%)	-0.65	1 (0%) 90 79	52, 89, 189, 222	0
All	All	924/924 (100%)	-0.56	2 (0%) 91 83	52, 94, 194, 295	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	719	LEU	2.4
1	B	783	SER	2.2

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.

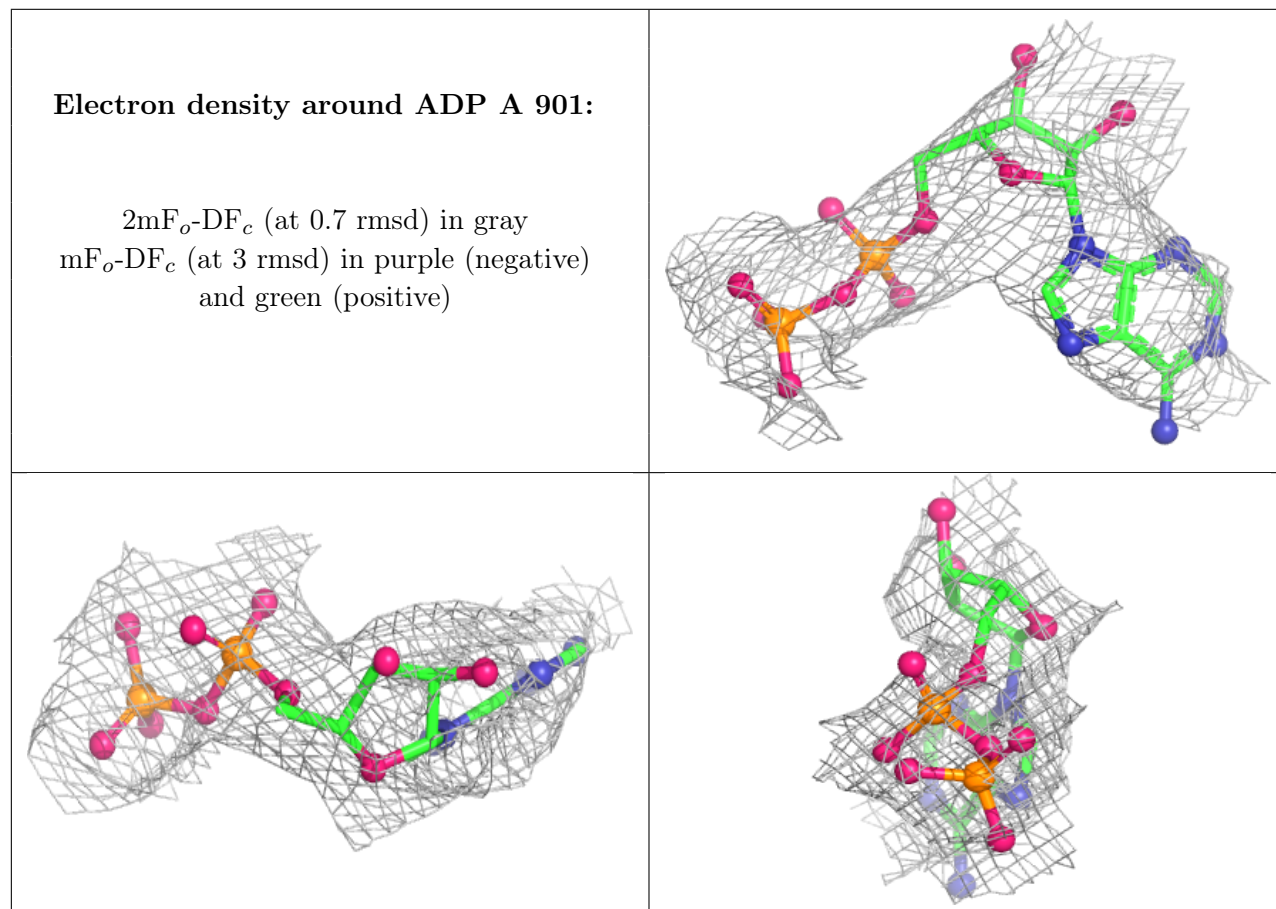
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	ADP	A	901	27/27	0.98	0.08	152,152,153,153	0

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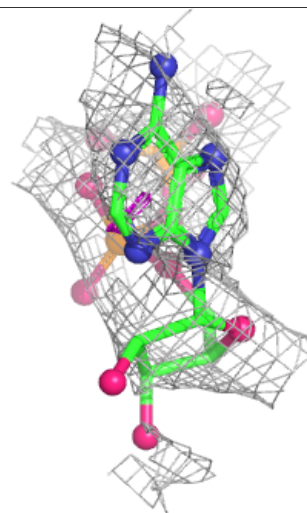
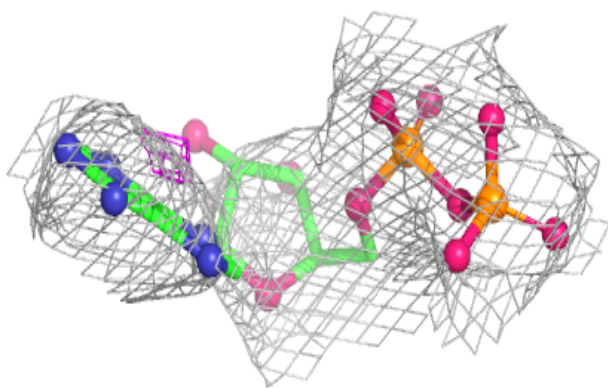
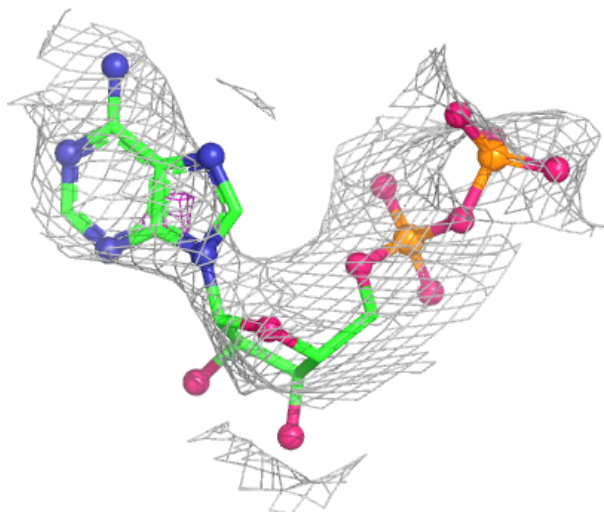
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	ADP	B	901	27/27	0.98	0.07	152,152,154,154	0
2	ADP	D	901	27/27	0.98	0.09	152,152,153,154	0

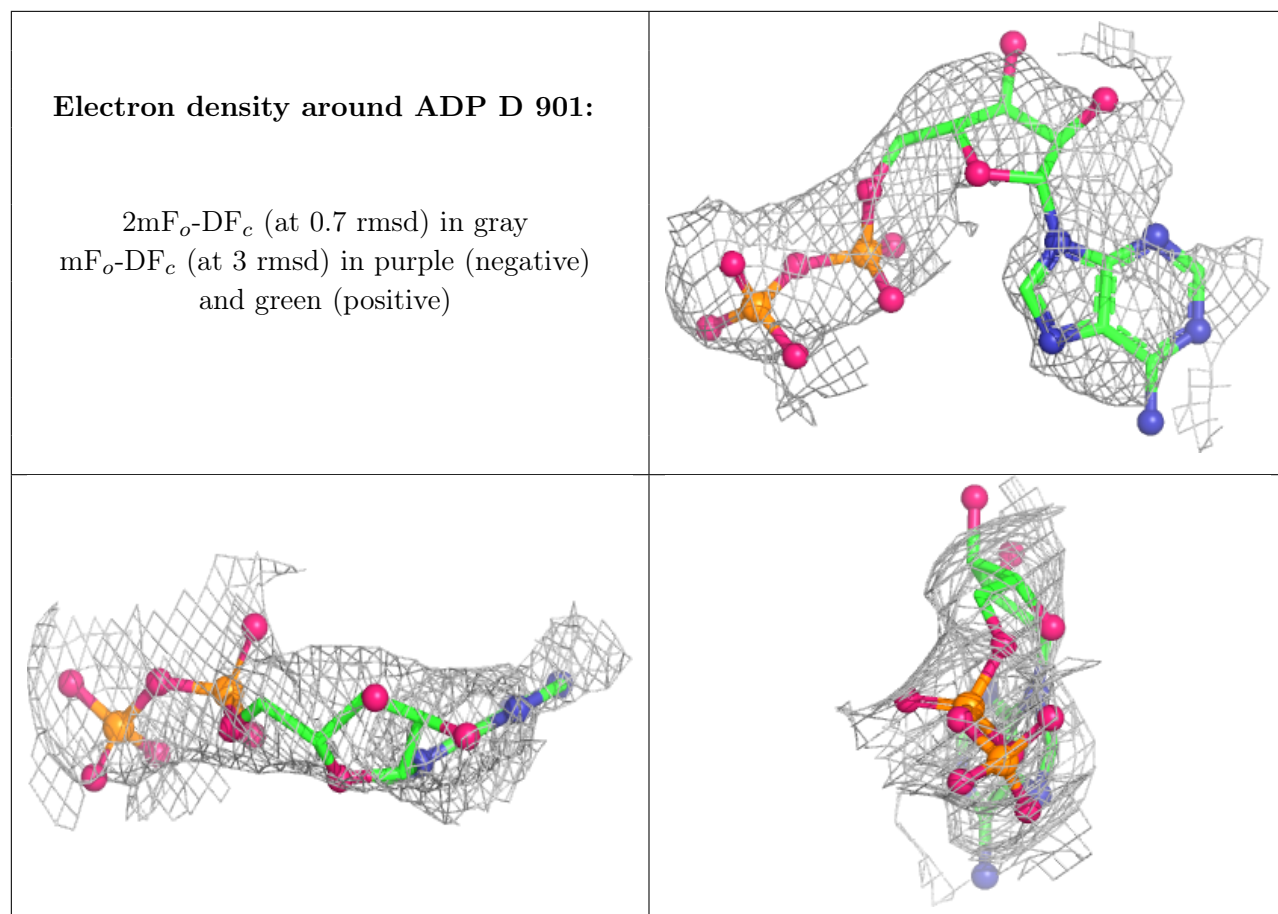
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



Electron density around ADP B 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.