



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:33 PM GMT

PDB ID : 4FD2
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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

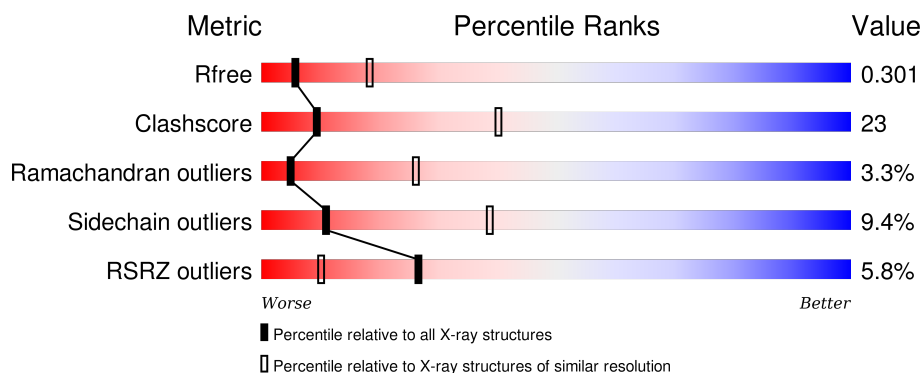
1 Overall quality at a glance

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}	91344	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	<div> <div>6%</div> <div> <div></div> <div>61%</div> <div>33%</div> <div>6%</div> </div> </div>
1	B	308	<div> <div>8%</div> <div> <div></div> <div>59%</div> <div>34%</div> <div>6%</div> </div> </div>
1	D	308	<div> <div>4%</div> <div> <div></div> <div>59%</div> <div>34%</div> <div>6%</div> </div> </div>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 7467 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.

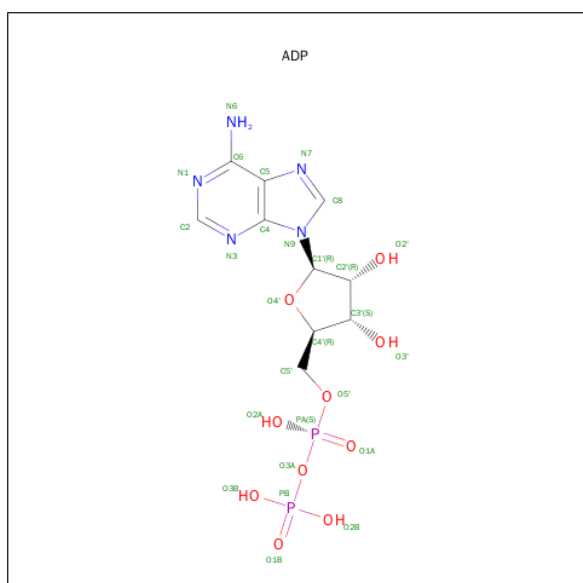
- Molecule 1 is a protein called Chaperone protein ClpB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	308	Total	C	N	O	S	0	0	0
			2462	1565	446	448	3			
1	B	308	Total	C	N	O	S	0	0	0
			2462	1565	446	448	3			
1	D	308	Total	C	N	O	S	0	0	0
			2462	1565	446	448	3			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	668	ALA	GLU	ENGINEERED MUTATION	UNP Q9RA63
B	668	ALA	GLU	ENGINEERED MUTATION	UNP Q9RA63
D	668	ALA	GLU	ENGINEERED MUTATION	UNP Q9RA63

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).

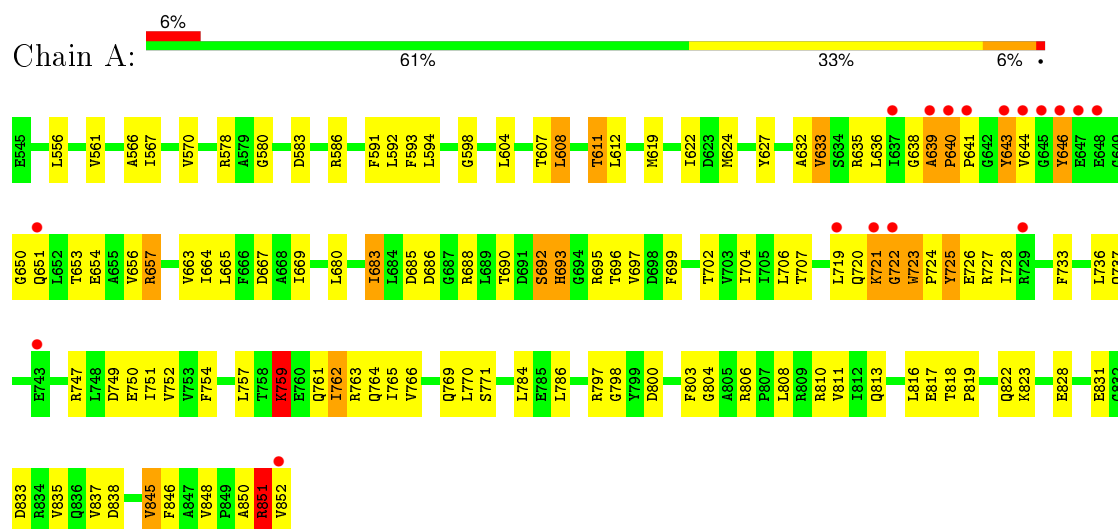


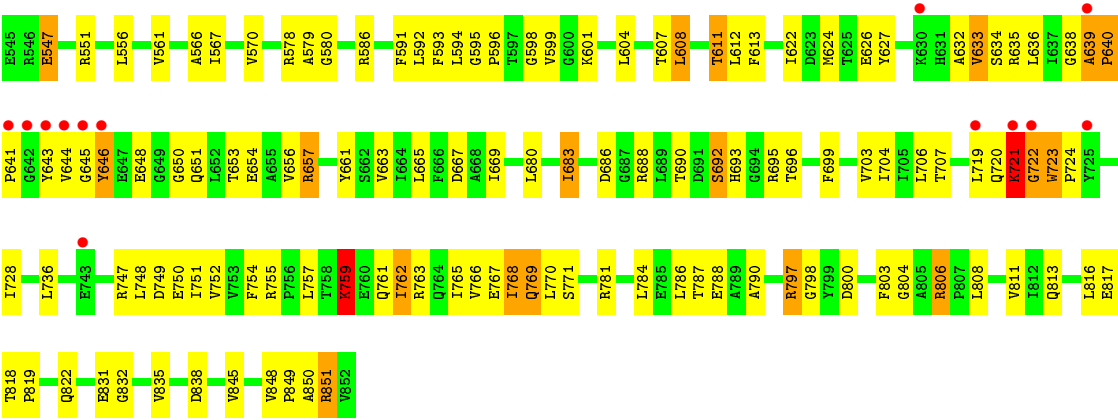
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	D	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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





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 – 2.84	Depositor EDS
% Data completeness (in resolution range)	98.8 (42.48-3.00) 99.1 (42.48-2.84)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.56 (at 2.86Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.278 , 0.298 0.272 , 0.301	Depositor DCC
R_{free} test set	999 reflections (4.24%)	DCC
Wilson B-factor (Å ²)	79.8	Xtriage
Anisotropy	0.230	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
Estimated twinning fraction	0.497 for H, K, L 0.503 for H+K, -K, -L 0.480 for h,-h-k,-l	Xtriage
Reported twinning fraction	0.497 for H, K, L 0.503 for H+K, -K, -L	Depositor
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 28928 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	7467	wwPDB-VP
Average B, all atoms (Å ²)	109.0	wwPDB-VP

Xtriage'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.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.61	0/2504	0.73	0/3383
1	B	0.65	0/2504	0.72	0/3383
1	D	0.63	1/2504 (0.0%)	0.72	0/3383
All	All	0.63	1/7512 (0.0%)	0.72	0/10149

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	547	GLU	CD-OE1	5.76	1.31	1.25

There are no bond angle outliers.

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	105	0
1	B	2462	0	2532	127	0
1	D	2462	0	2532	118	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	343	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 23.

All (343) 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:HA	1:B:851:ARG:CZ	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:NH1	1:B:851:ARG:HA	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
1:B:759:LYS:HA	1:B:762:ILE:HG13	1.60	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:656:VAL:HG21	1:D:699:PHE:CE2	2.16	0.80
1:D:640:PRO:HB2	1:D:641:PRO:HA	1.61	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:N	1:B:759:LYS:HD3	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:640:PRO:HB3	1:B:641:PRO:C	2.10	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: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:D:849:PRO:O	1:D:851:ARG:N	2.21	0.67
1:B:680:LEU:HD21	1:B:706:LEU:HD21	1.76	0.67
1:B:656:VAL:HG21	1:B:699:PHE:CE2	2.30	0.66
1:A:723:TRP:CD1	1:A:723:TRP:N	2.63	0.66
1:A:851:ARG:NE	1:A:851:ARG:HA	2.10	0.66
1:B:641:PRO:O	1:B:643:TYR:N	2.28	0.66
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:B:851:ARG:C	1:B:852:VAL:HG23	2.15	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:N	1:A:759:LYS:HD3	2.05	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: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:D:592:LEU:HD23	1:D:751:ILE:HG12	1.81	0.60
1:A:720:GLN:O	1:A:722:GLY:N	2.35	0.60
1:D:720:GLN:O	1:D:722:GLY:N	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:D:624:MET:HE2	1:D:624:MET:HA	1.85	0.59
1:A:627:TYR:CE2	1:A:635:ARG:HB2	2.38	0.58
1:B:690:THR:HA	1:B:696:THR:HA	1.85	0.58
1:B:638:GLY:C	1:B:640:PRO:HD2	2.24	0.58
1:D:639:ALA:N	1:D:640:PRO:HD3	2.17	0.58
1:B:723:TRP:CD1	1:B:723:TRP:N	2.71	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:CD	1:B:759:LYS:H	1.99	0.57
1:B:593:PHE:CB	1:B:707:THR:HG22	2.35	0.57
1:D:704:ILE:HG22	1:D:706:LEU:CD1	2.34	0.57
1:A:851:ARG:C	1:A:852:VAL:HG23	2.24	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: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:D:607:THR:O	1:D:611:THR:CG2	2.48	0.56
1:A:570:VAL:HG13	1:A:591:PHE:CZ	2.41	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:669:ILE:HG12	1:B:706:LEU:HD23	1.88	0.55
1:B:583:ASP:HB3	1:B:586:ARG:HD3	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:593:PHE:CB	1:D:707:THR:HG22	2.37	0.54
1:D:566:ALA:HA	1:D:752:VAL:CG1	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:622:ILE:CG2	1:A:624:MET:HE1	2.38	0.54
1:A:594:LEU:HD11	1:A:736:LEU:HD11	1.90	0.54
1:D:763:ARG:O	1:D:766:VAL:HB	2.08	0.53
1:D:594:LEU:HD11	1:D:736:LEU:HD11	1.90	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:640:PRO:HG2	1:D:646:TYR:HB3	1.90	0.53
1:D:638:GLY:O	1:D:692:SER:HB2	2.08	0.53
1:A:578:ARG:C	1:A:580:GLY:H	2.11	0.53
1:D:645:GLY:HA3	1:D:648:GLU:HG2	1.91	0.53
1:B:640:PRO:HB3	1:B:641:PRO:CA	2.35	0.53
1:A:749:ASP:O	1:A:750:GLU:HG2	2.08	0.53
1:D:838:ASP:O	1:D:845:VAL:N	2.31	0.53
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:749:ASP:O	1:D:750:GLU:HG2	2.08	0.52
1:A:583:ASP:HB3	1:A:586:ARG:HD3	1.91	0.52
1:A:850:ALA:O	1:A:851:ARG:C	2.48	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:B:578:ARG:C	1:B:580:GLY:H	2.13	0.52
1:B:598:GLY:H	2:B:901:ADP:PB	2.32	0.52
1:A:622:ILE:HG22	1:A:624:MET:CE	2.40	0.52
1:A:704:ILE:HG22	1:A:706:LEU:CD1	2.40	0.52
1:D:690:THR:HG23	1:D:696:THR:HG22	1.92	0.51
1:B:640:PRO:HB2	1:B:646:TYR:CB	2.40	0.51
1:B:627:TYR:CE2	1:B:635:ARG:HB2	2.44	0.51
1:B:556:LEU:HD23	1:B:611:THR:HG21	1.91	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:D:624:MET:HA	1:D:624:MET:CE	2.41	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: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:851:ARG:HA	1:B:851:ARG:NE	2.23	0.49
1:D:640:PRO:CB	1:D:641:PRO:CA	2.90	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
1:A:646:TYR:CE2	1:A:693:HIS:CE1	3.00	0.49
1:B:833:ASP:OD2	1:B:848:VAL:HG11	2.13	0.49
1:B:583:ASP:OD1	1:B:584:PRO:HD2	2.12	0.49
1:A:763:ARG:O	1:A:766:VAL:HB	2.13	0.49
1:B:800:ASP:O	1:B:804:GLY:N	2.46	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:706:LEU:N	1:A:706:LEU:HD12	2.27	0.49
1:A:586:ARG:NH2	1:A:747:ARG:O	2.39	0.49
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: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:CD	1:D:759:LYS:H	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:O	1:A:816:LEU:HD12	2.13	0.48
1:D:800:ASP:O	1:D:804:GLY:N	2.47	0.47
1:D:561:VAL:H	2:D:901:ADP:N6	2.11	0.47
1:B:657:ARG:NH2	1:B:695:ARG:HD2	2.29	0.47
1:A:784:LEU:HD12	1:A:835:VAL:HB	1.95	0.47
1:A:800:ASP:O	1:A:804:GLY:N	2.47	0.47
1:D:638:GLY:C	1:D:640:PRO:HD3	2.34	0.47
1:B:667:ASP:HA	1:B:707:THR:OG1	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:798:GLY:HA2	1:A:811:VAL:HG21	1.95	0.47
1:B:852:VAL:HG11	1:D:851:ARG:HG2	1.96	0.47
1:D:798:GLY:HA2	1:D:811:VAL:HG21	1.96	0.47
1:D:688:ARG:HB2	1:D:688:ARG:CZ	2.44	0.47
1:D:578:ARG:O	1:D:579:ALA:HB3	2.14	0.47
1:D:626:GLU:HG3	1:D:627:TYR:CE1	2.49	0.47
1:B:641:PRO:O	1:B:642:GLY:C	2.52	0.47
1:D:627:TYR:CE2	1:D:635:ARG:HB2	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:B:665:LEU:HG	1:B:667:ASP:OD2	2.15	0.47
1:D:665:LEU:HG	1:D:667:ASP:OD2	2.14	0.47
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:B:641:PRO:HB3	1:B:646:TYR:CD1	2.50	0.46
1:B:640:PRO:HG2	1:B:646:TYR:HB2	1.96	0.46
1:A:653:THR:HB	1:A:697:VAL:HG21	1.97	0.46
1:A:761:GLN:O	1:A:762:ILE:C	2.53	0.46
1:B:733:PHE:HE2	1:B:737:GLN:NE2	2.14	0.46
1:B:640:PRO:HG2	1:B:646:TYR:CB	2.46	0.46
1:A:846:PHE:CD1	1:A:846:PHE:N	2.84	0.46
1:A:640:PRO:HG3	1:A:643:TYR:HB2	1.97	0.46
1:D:797:ARG:HB3	1:D:797:ARG:NH1	2.31	0.46
1:A:757:LEU:HA	1:A:761:GLN:OE1	2.15	0.46
1:D:683:ILE:HD11	1:D:699:PHE:CE2	2.50	0.46
1:B:816:LEU:HD12	1:B:816:LEU:O	2.15	0.46
1:B:816:LEU:HD12	1:B:816:LEU:C	2.37	0.46
1:B:608:LEU:O	1:B:612:LEU:HB2	2.16	0.46
1:D:608:LEU:O	1:D:612:LEU:HB2	2.15	0.46
1:D:657:ARG:NH2	1:D:695:ARG:HD2	2.31	0.46
1:A:813:GLN:HG3	1:A:817:GLU:OE1	2.15	0.46
1:B:653:THR:HB	1:B:697:VAL:HG21	1.98	0.46
1:A:851:ARG:C	1:A:851:ARG:HE	2.18	0.45
1:D:808:LEU:O	1:D:811:VAL:HB	2.17	0.45
1:A:833:ASP:OD2	1:A:848:VAL:HG11	2.15	0.45
1:B:632:ALA:O	1:B:633:VAL:C	2.55	0.45
1:B:797:ARG:NH1	1:B:797:ARG:HB3	2.31	0.45
1:B:595:GLY:O	1:B:712:SER:OG	2.33	0.45
1:A:665:LEU:HG	1:A:667:ASP:OD2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:690:THR:HG23	1:B:696:THR:HG22	1.98	0.45
1:A:688:ARG:CZ	1:A:688:ARG:HB2	2.46	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:D:640:PRO:HB3	1:D:643:TYR:HB2	1.99	0.45
1:D:721:LYS:O	1:D:722:GLY:C	2.56	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:B:799:TYR:CD2	1:B:799:TYR:O	2.69	0.44
1:B:761:GLN:O	1:B:762:ILE:C	2.56	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
1:D:638:GLY:O	1:D:692:SER:CB	2.64	0.44
1:D:757:LEU:CD1	1:D:765:ILE:HD11	2.48	0.44
1:D:781:ARG:O	1:D:832:GLY:HA2	2.17	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: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:B:823:LYS:HA	1:B:828:GLU:HB2	2.00	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:A:638:GLY:C	1:A:640:PRO:HD3	2.38	0.44
1:D:640:PRO:HG2	1:D:646:TYR:HB2	2.00	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:A:797:ARG:NH1	1:A:797:ARG:HB3	2.33	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:B:638:GLY:C	1:B:640:PRO:CD	2.86	0.43
1:B:641:PRO:C	1:B:643:TYR:N	2.72	0.43
1:D:636:LEU:CA	1:D:651:GLN:HE22	2.25	0.43
1:D:593:PHE:HB3	1:D:601:LYS:HG2	2.00	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:N	1:B:693:HIS:CD2	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:A:759:LYS:H	1:A:759:LYS:CD	2.08	0.43
1:D:656:VAL:HG21	1:D:699:PHE:HE2	1.78	0.43
1:A:657:ARG:NH2	1:A:695:ARG:HD2	2.34	0.43
1:A:808:LEU:O	1:A:811:VAL:HB	2.18	0.43
1:D:770:LEU:O	1:D:771:SER:C	2.58	0.43
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:B:688:ARG:HH12	1:B:700:ARG:NE	2.17	0.42
1:B:570:VAL:HG13	1:B:591:PHE:CZ	2.53	0.42
1:A:690:THR:HG23	1:A:696:THR:HG22	2.01	0.42
1:B:851:ARG:O	1:B:852:VAL:HG22	2.11	0.42
1:A:561:VAL:N	2:A:901:ADP:N1	2.61	0.42
1:D:645:GLY:CA	1:D:648:GLU:HG2	2.49	0.42
1:D:693:HIS:N	1:D:693:HIS:CD2	2.87	0.42
1:B:813:GLN:HA	1:B:817:GLU:HB2	2.01	0.42
1:B:768:ILE:HG13	1:B:769:GLN:N	2.33	0.42
1:D:849:PRO:C	1:D:851:ARG:H	2.18	0.42
1:D:762:ILE:HG12	1:D:762:ILE:H	1.38	0.42
1:A:627:TYR:HB3	1:A:632:ALA:HB1	2.00	0.42
1:D:803:PHE:O	1:D:806:ARG:HB2	2.20	0.42
1:B:784:LEU:HA	1:B:784:LEU:HD12	1.81	0.42
1:B:721:LYS:O	1:B:723:TRP:N	2.52	0.42
1:B:640:PRO:CG	1:B:646:TYR:HB2	2.49	0.42
1:B:563:GLN:HB3	1:B:566:ALA:HB3	2.02	0.42
1:A:650:GLY:O	1:A:654:GLU:HB2	2.20	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:733:PHE:HE2	1:A:737:GLN:NE2	2.18	0.42
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:823:LYS:HB3	1:A:828:GLU:HB2	2.02	0.41
1:A:619:MET:HA	1:A:663:VAL:O	2.19	0.41
1:B:641:PRO:HB2	1:B:642:GLY:H	1.69	0.41
1:B:641:PRO:HA	1:B:646:TYR:CG	2.56	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:596:PRO:HD3	1:B:754:PHE:O	2.20	0.41
1:D:768:ILE:HG13	1:D:769:GLN:N	2.34	0.41
1:A:761:GLN:O	1:A:764:GLN:N	2.53	0.41
1:A:693:HIS:H	1:A:693:HIS:CD2	2.39	0.41
1:D:578:ARG:C	1:D:580:GLY:H	2.23	0.41
1:A:639:ALA:HA	1:A:692:SER:OG	2.20	0.41
1:D:632:ALA:O	1:D:633:VAL:C	2.59	0.41
1:D:604:LEU:O	1:D:608:LEU:HB2	2.20	0.41
1:A:770:LEU:O	1:A:771:SER:C	2.58	0.41
1:B:762:ILE:H	1:B:762:ILE:HG12	1.41	0.41
1:B:797:ARG:HH11	1:B:797:ARG:HB3	1.85	0.41
1:D:693:HIS:H	1:D:693:HIS:CD2	2.39	0.41
1:B:596:PRO:O	1:B:601:LYS:HE3	2.20	0.40
1:B:683:ILE:HD13	1:B:683:ILE:HG21	1.89	0.40
1:B:559:ARG:NH1	1:B:616:GLU:OE2	2.49	0.40
1:D:622:ILE:CG2	1:D:624:MET:HE1	2.51	0.40
1:A:632:ALA:O	1:A:633:VAL:C	2.60	0.40
1:D:767:GLU:O	1:D:768:ILE:C	2.60	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

5.3.1 Protein backbone

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%)	4	24
1	B	306/308 (99%)	269 (88%)	27 (9%)	10 (3%)	5	26
1	D	306/308 (99%)	270 (88%)	27 (9%)	9 (3%)	6	29
All	All	918/924 (99%)	807 (88%)	81 (9%)	30 (3%)	5	26

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
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 ⓘ

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%)	236 (91%)	24 (9%)	11	40
1	B	260/260 (100%)	234 (90%)	26 (10%)	9	34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	260/260 (100%)	237 (91%)	23 (9%)	12	42
All	All	780/780 (100%)	707 (91%)	73 (9%)	11	39

All (73) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	567	ILE
1	A	608	LEU
1	A	611	THR
1	A	646	TYR
1	A	657	ARG
1	A	683	ILE
1	A	686	ASP
1	A	692	SER
1	A	693	HIS
1	A	719	LEU
1	A	721	LYS
1	A	723	TRP
1	A	725	TYR
1	A	728	ILE
1	A	759	LYS
1	A	762	ILE
1	A	769	GLN
1	A	786	LEU
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	561	VAL
1	B	567	ILE
1	B	608	LEU
1	B	611	THR
1	B	622	ILE
1	B	646	TYR
1	B	657	ARG
1	B	683	ILE
1	B	686	ASP
1	B	692	SER
1	B	693	HIS
1	B	721	LYS

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Mol	Chain	Res	Type
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	851	ARG
1	D	567	ILE
1	D	608	LEU
1	D	611	THR
1	D	646	TYR
1	D	657	ARG
1	D	683	ILE
1	D	686	ASP
1	D	692	SER
1	D	719	LEU
1	D	721	LYS
1	D	723	TRP
1	D	728	ILE
1	D	755	ARG
1	D	759	LYS
1	D	762	ILE
1	D	768	ILE
1	D	769	GLN
1	D	786	LEU
1	D	797	ARG
1	D	806	ARG
1	D	822	GLN
1	D	831	GLU
1	D	851	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	631	HIS

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Mol	Chain	Res	Type
1	A	682	GLN
1	A	693	HIS
1	A	737	GLN
1	A	746	ASN
1	B	651	GLN
1	B	682	GLN
1	B	693	HIS
1	B	737	GLN
1	B	746	ASN
1	D	651	GLN
1	D	682	GLN
1	D	693	HIS
1	D	746	ASN

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 carbohydrates 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	-	22,29,29	1.02	2 (9%)	27,45,45	1.92	4 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	ADP	B	901	-	22,29,29	1.02	2 (9%)	27,45,45	1.87	5 (18%)
2	ADP	D	901	-	22,29,29	1.08	2 (9%)	27,45,45	1.85	4 (14%)

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	-	-	0/12/32/32	0/3/3/3
2	ADP	B	901	-	-	0/12/32/32	0/3/3/3
2	ADP	D	901	-	-	0/12/32/32	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	901	ADP	O4'-C1'	2.06	1.43	1.41
2	D	901	ADP	O4'-C1'	2.10	1.43	1.41
2	A	901	ADP	O4'-C1'	2.14	1.43	1.41
2	A	901	ADP	C5-C4	3.07	1.47	1.40
2	B	901	ADP	C5-C4	3.14	1.47	1.40
2	D	901	ADP	C5-C4	3.28	1.47	1.40

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	901	ADP	N3-C2-N1	-6.99	123.54	128.89
2	D	901	ADP	N3-C2-N1	-6.74	123.73	128.89
2	B	901	ADP	N3-C2-N1	-6.67	123.79	128.89
2	A	901	ADP	C4-C5-N7	-3.42	106.33	109.48
2	B	901	ADP	C4-C5-N7	-3.21	106.53	109.48
2	A	901	ADP	PA-O3A-PB	-3.15	122.12	132.67
2	D	901	ADP	C4-C5-N7	-2.96	106.76	109.48
2	B	901	ADP	PA-O3A-PB	-2.81	123.23	132.67
2	D	901	ADP	C2'-C1'-N9	-2.58	110.35	114.29
2	A	901	ADP	C2'-C1'-N9	-2.44	110.57	114.29
2	D	901	ADP	PA-O3A-PB	-2.31	124.91	132.67
2	B	901	ADP	C2'-C1'-N9	-2.22	110.91	114.29
2	B	901	ADP	C4'-O4'-C1'	2.43	112.39	109.72

There are no chirality outliers.

There are no torsion outliers.

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	B	901	ADP	2	0
2	D	901	ADP	4	0

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	308/308 (100%)	0.16	17 (5%)	29 11	56, 88, 203, 295	0
1	B	308/308 (100%)	0.49	24 (7%)	16 6	73, 104, 194, 231	0
1	D	308/308 (100%)	0.15	13 (4%)	40 16	52, 89, 189, 222	0
All	All	924/924 (100%)	0.27	54 (5%)	26 10	52, 94, 194, 295	0

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	645	GLY	13.7
1	A	641	PRO	9.9
1	B	639	ALA	9.8
1	A	644	VAL	8.2
1	B	642	GLY	6.4
1	A	646	TYR	6.3
1	B	643	TYR	6.2
1	D	641	PRO	5.7
1	A	639	ALA	5.6
1	D	645	GLY	5.4
1	D	644	VAL	5.4
1	D	719	LEU	4.6
1	A	719	LEU	4.5
1	D	725	TYR	4.4
1	B	647	GLU	4.4
1	B	646	TYR	4.2
1	A	647	GLU	4.2
1	A	640	PRO	4.1
1	D	722	GLY	3.9
1	B	644	VAL	3.7
1	B	641	PRO	3.7
1	D	642	GLY	3.7
1	B	723	TRP	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	630	LYS	3.5
1	B	719	LEU	3.3
1	A	852	VAL	3.3
1	B	709	ASN	3.2
1	B	640	PRO	3.1
1	A	651	GLN	3.0
1	D	639	ALA	2.9
1	B	634	SER	2.9
1	D	643	TYR	2.7
1	B	852	VAL	2.6
1	D	743	GLU	2.6
1	B	629	GLU	2.6
1	B	638	GLY	2.4
1	B	792	ASP	2.4
1	D	630	LYS	2.4
1	D	721	LYS	2.4
1	A	648	GLU	2.4
1	A	722	GLY	2.3
1	B	724	PRO	2.3
1	A	743	GLU	2.3
1	B	738	GLN	2.2
1	B	725	TYR	2.2
1	B	799	TYR	2.2
1	A	643	TYR	2.1
1	B	713	PRO	2.1
1	D	646	TYR	2.1
1	B	645	GLY	2.1
1	A	637	ILE	2.0
1	A	729	ARG	2.0
1	A	721	LYS	2.0
1	B	694	GLY	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	ADP	D	901	27/27	0.89	0.28	1.56	152,152,153,154	0
2	ADP	A	901	27/27	0.88	0.28	1.55	152,152,153,153	0
2	ADP	B	901	27/27	0.92	0.28	1.06	152,152,154,154	0

6.5 Other polymers [i](#)

There are no such residues in this entry.