



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:22 PM UTC

PDB ID : 6KBD / pdb_00006kbd
Title : fused To-MtbCsm1 with 2dATP
Authors : Li, T.; Huo, Y.; Jiang, T.
Deposited on : 2019-06-24
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

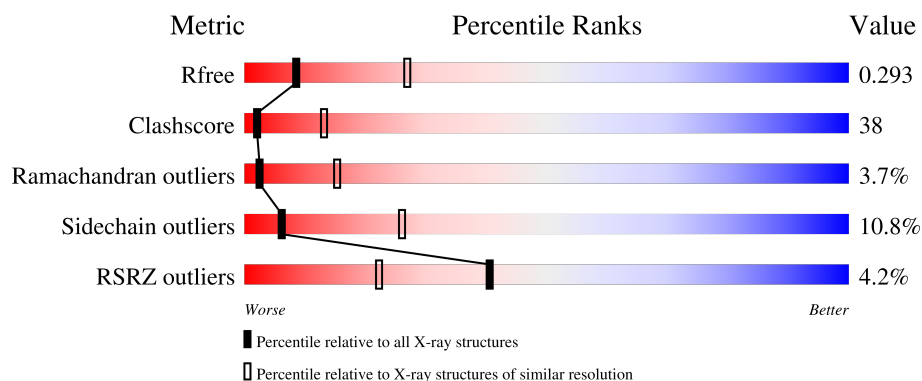
1 Overall quality at a glance

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	784	 3% 38% 33% 6% 21%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4986 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.

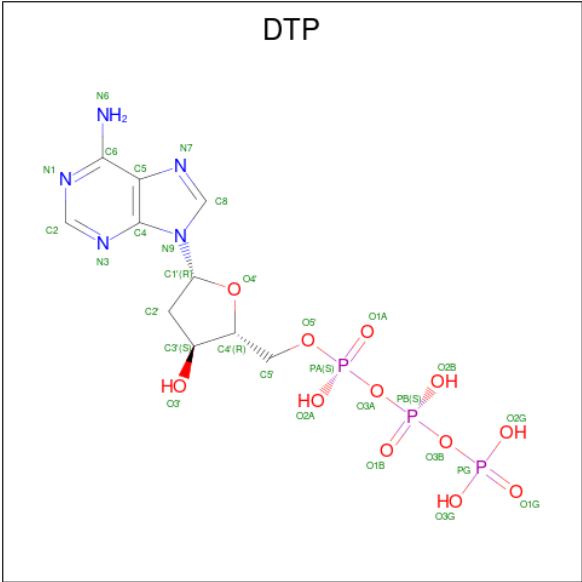
- Molecule 1 is a protein called CRISPR system single-strand-specific deoxyribonuclease Cas10/Csm1 (subtype III-A), CRISPR system single-strand-specific deoxyribonuclease Cas10/Csm1 (subtype III-A).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	616	Total	C	N	O	S	0	0	0
			4924	3168	853	890	13			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	810	HIS	-	expression tag	UNP P71629
A	811	HIS	-	expression tag	UNP P71629
A	812	HIS	-	expression tag	UNP P71629
A	813	HIS	-	expression tag	UNP P71629
A	814	HIS	-	expression tag	UNP P71629
A	815	HIS	-	expression tag	UNP P71629
A	816	HIS	-	expression tag	UNP P71629
A	817	HIS	-	expression tag	UNP P71629

- Molecule 2 is 2'-DEOXYADENOSINE 5'-TRIPHOSPHATE (CCD ID: DTP) (formula: C₁₀H₁₆N₅O₁₂P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			30	10	5	12	3		
2	A	1	Total	C	N	O	P	0	0
			30	10	5	12	3		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Mg	0	0
			2	2		

PHE	GLN	GLN	PHE	ALA	ASN	ARG	LEU	HIS	GLN	TRP	PHE	GLN	ASP	P786	K790	Q791	L792	K793	T794	H797	L798	Y799	I800	Y801	R802	T803	R804	K805	GLU	GLU	SER	GLU	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	57.80Å 53.32Å 124.13Å 90.00° 97.78° 90.00°	Depositor
Resolution (Å)	41.00 – 3.00 41.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.1 (41.00-3.00) 99.3 (41.00-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.70 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.237 , 0.283 0.249 , 0.293	Depositor DCC
R_{free} test set	735 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å ²)	85.1	Xtriage
Anisotropy	0.139	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 67.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	4986	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.10% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, DTP

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	1.08	3/5023 (0.1%)	1.17	16/6771 (0.2%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	325	PHE	N-CA	5.79	1.52	1.46
1	A	625	GLY	C-O	-5.46	1.18	1.24
1	A	157	LEU	CA-C	-5.25	1.46	1.52

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	129	TYR	CA-C-N	10.58	131.42	119.99
1	A	129	TYR	C-N-CA	10.58	131.42	119.99
1	A	556	VAL	CB-CA-C	-7.03	99.76	111.29
1	A	652	PHE	N-CA-C	6.33	124.28	110.80
1	A	652	PHE	CB-CA-C	-6.12	98.23	110.42
1	A	327	SER	CB-CA-C	5.95	120.23	110.17
1	A	207	ALA	N-CA-C	-5.95	104.71	111.07
1	A	136	PHE	CB-CA-C	5.80	120.20	109.70
1	A	351	LEU	N-CA-C	5.60	118.15	111.71
1	A	804	ARG	CB-CA-C	5.58	116.67	109.80
1	A	600	LEU	N-CA-C	5.46	117.31	111.36
1	A	243	ILE	CB-CA-C	-5.42	104.92	112.02
1	A	136	PHE	N-CA-C	-5.08	100.17	108.76
1	A	251	SER	CA-C-O	5.07	120.88	117.94
1	A	450	GLY	N-CA-C	-5.04	105.00	113.02
1	A	228	ARG	N-CA-C	5.01	119.67	113.50

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	4924	0	4955	375	0
2	A	60	0	24	5	0
3	A	2	0	0	0	0
All	All	4986	0	4979	375	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 38.

All (375) 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:134:LEU:HD12	1:A:140:LEU:CD2	1.33	1.56
1:A:698:PHE:CE2	1:A:797:HIS:HB3	1.41	1.55
1:A:698:PHE:CZ	1:A:797:HIS:HB3	1.41	1.54
1:A:698:PHE:CE2	1:A:797:HIS:CB	1.93	1.48
1:A:702:PHE:CA	1:A:790:LYS:HE3	1.53	1.38
1:A:134:LEU:CD1	1:A:140:LEU:CD2	2.00	1.36
1:A:612:ASP:HB3	1:A:613:PRO:CD	1.63	1.28
1:A:646:ARG:HG3	1:A:706:TRP:CE2	1.68	1.27
1:A:646:ARG:HG3	1:A:706:TRP:NE1	1.52	1.22
1:A:702:PHE:HA	1:A:790:LYS:CE	1.72	1.19
1:A:698:PHE:HE2	1:A:797:HIS:CB	1.42	1.18
1:A:698:PHE:HE2	1:A:797:HIS:HB2	1.06	1.16
1:A:736:ILE:HG22	1:A:800:ILE:HD11	1.18	1.15
1:A:612:ASP:HB3	1:A:613:PRO:HD3	1.29	1.12
1:A:134:LEU:HD12	1:A:140:LEU:HD23	1.19	1.11
1:A:698:PHE:CZ	1:A:797:HIS:CB	2.23	1.11
1:A:134:LEU:HD12	1:A:140:LEU:HD21	1.26	1.10
1:A:140:LEU:H	1:A:141:PRO:HD3	1.01	1.09
1:A:639:ILE:HG23	1:A:697:LEU:HD11	1.33	1.08
1:A:134:LEU:HD22	1:A:184:THR:OG1	1.52	1.07
1:A:612:ASP:CB	1:A:613:PRO:CD	2.31	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:564:THR:O	1:A:576:ASN:OD1	1.71	1.06
1:A:257:LYS:O	1:A:423:GLY:HA3	1.56	1.05
1:A:698:PHE:CE1	1:A:801:TYR:HE2	1.74	1.04
1:A:134:LEU:CD1	1:A:140:LEU:HD22	1.85	1.03
1:A:478:GLU:O	1:A:480:ALA:N	1.91	1.03
1:A:612:ASP:CB	1:A:613:PRO:HD2	1.88	1.02
1:A:698:PHE:HZ	1:A:797:HIS:HB3	1.24	1.00
1:A:140:LEU:H	1:A:141:PRO:CD	1.74	1.00
1:A:646:ARG:HG3	1:A:706:TRP:CD1	1.98	0.99
1:A:663:ILE:HB	1:A:697:LEU:HG	1.41	0.99
1:A:698:PHE:CB	1:A:702:PHE:CZ	2.47	0.97
1:A:134:LEU:CD1	1:A:140:LEU:HD21	1.84	0.95
1:A:702:PHE:HA	1:A:790:LYS:HE3	0.96	0.95
1:A:698:PHE:HB3	1:A:702:PHE:CZ	2.01	0.95
1:A:736:ILE:CG2	1:A:800:ILE:HD11	1.97	0.94
1:A:134:LEU:HA	1:A:140:LEU:HD23	1.48	0.94
1:A:257:LYS:HG2	1:A:423:GLY:O	1.68	0.94
1:A:140:LEU:N	1:A:141:PRO:HD3	1.82	0.93
1:A:670:TYR:CD2	1:A:671:PRO:HD2	2.04	0.93
1:A:671:PRO:HB2	1:A:674:VAL:HG23	1.51	0.93
1:A:334:GLU:HG2	1:A:366:ARG:HD2	1.51	0.92
1:A:698:PHE:CZ	1:A:797:HIS:CG	2.57	0.92
1:A:646:ARG:NE	1:A:706:TRP:CD1	2.38	0.92
1:A:698:PHE:CE2	1:A:797:HIS:CG	2.58	0.92
1:A:698:PHE:CB	1:A:702:PHE:CE1	2.53	0.91
1:A:698:PHE:HB2	1:A:702:PHE:CE1	2.05	0.91
1:A:646:ARG:HD2	1:A:706:TRP:CG	2.05	0.91
1:A:646:ARG:CD	1:A:706:TRP:CG	2.53	0.91
1:A:134:LEU:HD13	1:A:140:LEU:HD22	1.52	0.91
1:A:140:LEU:N	1:A:141:PRO:CD	2.35	0.89
1:A:702:PHE:CA	1:A:790:LYS:CE	2.42	0.89
1:A:257:LYS:HG2	1:A:423:GLY:C	1.98	0.88
1:A:646:ARG:CG	1:A:706:TRP:CE2	2.56	0.88
1:A:704:PHE:CE2	1:A:790:LYS:HG2	2.10	0.87
1:A:658:THR:HG21	1:A:693:ASN:HD21	1.38	0.86
1:A:698:PHE:CE2	1:A:797:HIS:HB2	1.86	0.85
1:A:682:LEU:HD21	1:A:699:ASP:HA	1.58	0.85
1:A:698:PHE:CZ	1:A:801:TYR:HE2	1.94	0.85
1:A:129:TYR:HB3	1:A:130:PRO:HD2	1.58	0.85
1:A:658:THR:HB	1:A:693:ASN:OD1	1.77	0.84
1:A:134:LEU:CD2	1:A:184:THR:OG1	2.24	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:639:ILE:HG23	1:A:697:LEU:CD1	2.07	0.84
1:A:702:PHE:CB	1:A:790:LYS:HE3	2.09	0.83
1:A:134:LEU:HD22	1:A:184:THR:CB	2.08	0.83
1:A:698:PHE:CB	1:A:702:PHE:HZ	1.90	0.83
1:A:612:ASP:HB2	1:A:613:PRO:HD2	1.58	0.83
1:A:658:THR:CG2	1:A:693:ASN:HD21	1.92	0.82
1:A:736:ILE:HG22	1:A:800:ILE:CD1	2.07	0.82
1:A:658:THR:HG21	1:A:693:ASN:ND2	1.95	0.82
1:A:195:ILE:HD11	1:A:580:ARG:HG2	1.60	0.81
1:A:129:TYR:CB	1:A:130:PRO:HD2	2.11	0.81
1:A:138:LYS:HE2	1:A:138:LYS:HA	1.62	0.80
1:A:670:TYR:CG	1:A:671:PRO:HD2	2.17	0.80
1:A:698:PHE:HE1	1:A:801:TYR:HE2	1.29	0.80
1:A:702:PHE:HB2	1:A:790:LYS:HG3	1.63	0.80
1:A:700:ARG:HH21	1:A:700:ARG:HG3	1.48	0.79
1:A:702:PHE:HB3	1:A:790:LYS:HZ2	1.47	0.79
1:A:646:ARG:CG	1:A:706:TRP:CD1	2.66	0.79
1:A:646:ARG:HG3	1:A:706:TRP:CD2	2.18	0.78
1:A:698:PHE:HB3	1:A:702:PHE:CE1	2.17	0.78
1:A:558:ASN:OD1	1:A:692:LYS:NZ	2.17	0.77
1:A:702:PHE:CB	1:A:790:LYS:CE	2.63	0.77
1:A:698:PHE:CZ	1:A:801:TYR:CE2	2.73	0.76
1:A:702:PHE:HB3	1:A:790:LYS:NZ	2.01	0.75
1:A:698:PHE:HD2	1:A:794:THR:HG23	1.52	0.75
1:A:334:GLU:CG	1:A:366:ARG:HD2	2.17	0.75
1:A:698:PHE:CD2	1:A:794:THR:HG23	2.20	0.75
1:A:144:GLY:O	1:A:145:ASP:O	2.04	0.75
1:A:698:PHE:CE1	1:A:801:TYR:CE2	2.67	0.74
1:A:702:PHE:CB	1:A:790:LYS:NZ	2.51	0.74
1:A:256:LEU:O	1:A:260:ARG:HG3	1.89	0.73
1:A:671:PRO:HB2	1:A:674:VAL:CG2	2.18	0.73
1:A:249:ARG:O	1:A:249:ARG:HG2	1.87	0.73
1:A:646:ARG:NH2	1:A:706:TRP:HB3	2.03	0.73
1:A:698:PHE:HB2	1:A:702:PHE:CZ	2.22	0.73
1:A:15:ASP:OD2	1:A:18:LYS:NZ	2.22	0.72
1:A:50:TYR:CE1	1:A:170:LEU:HD21	2.24	0.72
1:A:140:LEU:HD22	1:A:185:PHE:CE2	2.24	0.72
1:A:646:ARG:CD	1:A:706:TRP:CD1	2.73	0.71
1:A:490:TYR:HB3	1:A:600:LEU:HD13	1.73	0.71
1:A:140:LEU:HB2	1:A:185:PHE:CE2	2.26	0.70
1:A:171:ARG:HD2	1:A:173:ASP:OD1	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:131:TRP:CE2	1:A:157:LEU:HD13	2.27	0.70
1:A:601:ALA:HA	1:A:616:PRO:HB3	1.70	0.70
1:A:460:PRO:HB2	1:A:465:ILE:HD13	1.72	0.70
1:A:557:ASP:OD2	1:A:692:LYS:HB3	1.91	0.70
1:A:702:PHE:C	1:A:790:LYS:HE3	2.17	0.70
1:A:123:PHE:CE2	1:A:652:PHE:O	2.45	0.69
1:A:702:PHE:CB	1:A:790:LYS:HZ2	2.04	0.69
1:A:700:ARG:HG3	1:A:700:ARG:NH2	2.06	0.69
1:A:244:GLN:OE1	1:A:553:ARG:NH2	2.27	0.68
1:A:696:ALA:CB	1:A:703:THR:HG22	2.24	0.68
1:A:646:ARG:NE	1:A:706:TRP:CG	2.62	0.68
1:A:704:PHE:HE2	1:A:790:LYS:HG2	1.57	0.68
1:A:208:ILE:HG22	1:A:212:MET:CE	2.23	0.67
1:A:554:LEU:HD11	1:A:659:VAL:HG21	1.76	0.67
1:A:473:PRO:O	1:A:476:ILE:HG23	1.95	0.66
1:A:138:LYS:HA	1:A:138:LYS:CE	2.25	0.66
1:A:663:ILE:O	1:A:697:LEU:O	2.13	0.66
1:A:604:LYS:N	1:A:644:GLU:OE1	2.22	0.66
1:A:435:THR:OG1	1:A:436:ALA:N	2.29	0.66
1:A:698:PHE:CB	1:A:702:PHE:HE1	2.05	0.66
1:A:138:LYS:O	1:A:598:TYR:CE2	2.50	0.65
1:A:636:ASP:HA	1:A:639:ILE:HD12	1.78	0.65
1:A:702:PHE:HB2	1:A:790:LYS:CG	2.26	0.65
1:A:736:ILE:CG2	1:A:800:ILE:CD1	2.69	0.65
1:A:140:LEU:HD13	1:A:185:PHE:HZ	1.61	0.64
1:A:52:LEU:HD12	1:A:52:LEU:O	1.98	0.64
1:A:454:TYR:CE1	1:A:460:PRO:HD3	2.32	0.64
1:A:646:ARG:CG	1:A:706:TRP:NE1	2.46	0.64
1:A:646:ARG:CZ	1:A:706:TRP:CB	2.75	0.64
1:A:695:VAL:O	1:A:703:THR:HB	1.98	0.64
1:A:646:ARG:CG	1:A:706:TRP:CD2	2.79	0.64
1:A:284:THR:HG22	1:A:286:ALA:H	1.63	0.64
1:A:52:LEU:HD12	1:A:55:LEU:HD12	1.81	0.63
1:A:646:ARG:HG3	1:A:706:TRP:CG	2.34	0.63
1:A:646:ARG:NH2	1:A:706:TRP:CB	2.62	0.62
1:A:671:PRO:O	1:A:674:VAL:N	2.32	0.62
1:A:704:PHE:HB3	1:A:708:GLU:HG2	1.82	0.62
1:A:564:THR:O	1:A:576:ASN:CG	2.43	0.61
1:A:129:TYR:CB	1:A:130:PRO:CD	2.78	0.61
1:A:617:ARG:NH1	1:A:637:ASP:OD1	2.33	0.61
1:A:698:PHE:HB3	1:A:702:PHE:HZ	1.52	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:698:PHE:CG	1:A:702:PHE:HZ	2.18	0.61
1:A:140:LEU:HD22	1:A:185:PHE:HE2	1.63	0.61
1:A:234:LEU:HG	1:A:302:ASN:HA	1.83	0.61
1:A:659:VAL:HG23	1:A:706:TRP:CZ2	2.35	0.61
1:A:698:PHE:HB2	1:A:702:PHE:HE1	1.59	0.60
1:A:119:LEU:HD13	1:A:197:SER:HA	1.83	0.60
1:A:658:THR:CG2	1:A:693:ASN:ND2	2.59	0.60
1:A:698:PHE:HE1	1:A:801:TYR:CE2	2.11	0.59
1:A:666:PHE:O	1:A:667:PRO:O	2.20	0.59
1:A:705:GLY:H	1:A:708:GLU:HB3	1.68	0.59
1:A:134:LEU:HD11	1:A:140:LEU:HD21	1.83	0.59
1:A:696:ALA:HB2	1:A:703:THR:CG2	2.33	0.59
1:A:138:LYS:HD3	1:A:598:TYR:CE2	2.38	0.58
1:A:142:VAL:HG23	1:A:142:VAL:O	2.02	0.58
1:A:260:ARG:HH22	1:A:489:ASP:HB2	1.67	0.58
1:A:299:ILE:HD11	1:A:578:ILE:HG12	1.86	0.58
1:A:646:ARG:CZ	1:A:706:TRP:HB2	2.34	0.58
1:A:130:PRO:HA	1:A:149:ILE:HD11	1.85	0.58
1:A:140:LEU:HB2	1:A:185:PHE:HE2	1.67	0.58
1:A:646:ARG:CG	1:A:706:TRP:CG	2.86	0.58
1:A:659:VAL:HG23	1:A:706:TRP:HZ2	1.69	0.58
1:A:9:LEU:HD13	1:A:170:LEU:HD22	1.85	0.58
1:A:702:PHE:HB2	1:A:790:LYS:CE	2.34	0.58
1:A:160:ARG:O	1:A:161:LEU:C	2.47	0.58
1:A:58:GLU:OE2	1:A:74:ARG:HG2	2.04	0.58
1:A:556:VAL:HG22	1:A:649:PHE:CZ	2.39	0.57
1:A:160:ARG:O	1:A:163:GLU:N	2.37	0.57
1:A:144:GLY:HA3	1:A:147:PHE:CE2	2.40	0.57
1:A:704:PHE:HZ	1:A:794:THR:HG1	1.52	0.57
1:A:646:ARG:HD2	1:A:706:TRP:HB3	1.87	0.57
1:A:803:THR:O	1:A:804:ARG:C	2.48	0.57
1:A:555:ASP:OD2	1:A:628:ASP:OD2	2.22	0.56
1:A:646:ARG:HD2	1:A:706:TRP:CB	2.34	0.56
1:A:490:TYR:CD2	1:A:600:LEU:HB3	2.41	0.56
1:A:646:ARG:HD2	1:A:706:TRP:CD2	2.41	0.56
1:A:687:LYS:HD3	1:A:692:LYS:HD3	1.88	0.56
1:A:489:ASP:OD1	1:A:489:ASP:N	2.37	0.55
1:A:682:LEU:HD13	1:A:697:LEU:O	2.06	0.55
1:A:354:GLU:O	1:A:357:LYS:N	2.39	0.55
1:A:479:SER:O	1:A:479:SER:OG	2.22	0.55
1:A:144:GLY:CA	1:A:147:PHE:CE2	2.90	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:413:CYS:HA	1:A:416:CYS:SG	2.47	0.55
1:A:367:LYS:HB3	1:A:367:LYS:HZ1	1.72	0.55
1:A:367:LYS:HB3	1:A:367:LYS:NZ	2.22	0.55
1:A:670:TYR:CG	1:A:671:PRO:CD	2.89	0.55
1:A:478:GLU:C	1:A:480:ALA:N	2.63	0.54
1:A:241:SER:O	1:A:329:LEU:HD12	2.08	0.54
1:A:601:ALA:HA	1:A:616:PRO:CB	2.36	0.54
1:A:663:ILE:CB	1:A:697:LEU:HG	2.28	0.54
1:A:203:ARG:HG3	1:A:204:MET:N	2.21	0.54
1:A:237:GLU:HG2	1:A:363:LEU:HD11	1.90	0.54
1:A:696:ALA:HB2	1:A:703:THR:HG21	1.89	0.54
1:A:169:LYS:HE2	1:A:478:GLU:HG2	1.90	0.54
1:A:243:ILE:HG21	2:A:901:DTP:C8	2.38	0.54
1:A:565:HIS:CD2	1:A:565:HIS:N	2.76	0.54
1:A:257:LYS:CG	1:A:423:GLY:O	2.51	0.53
1:A:682:LEU:HD13	1:A:696:ALA:O	2.08	0.53
1:A:646:ARG:HB2	1:A:706:TRP:CZ2	2.43	0.53
1:A:689:LEU:HD11	1:A:703:THR:OG1	2.08	0.53
1:A:671:PRO:O	1:A:672:ILE:C	2.51	0.53
1:A:698:PHE:O	1:A:700:ARG:N	2.42	0.53
1:A:365:VAL:HG12	1:A:365:VAL:O	2.09	0.53
1:A:646:ARG:HH21	1:A:706:TRP:HB3	1.72	0.53
1:A:38:LEU:HD12	1:A:54:SER:HA	1.90	0.53
1:A:698:PHE:HZ	1:A:801:TYR:CE2	2.24	0.53
1:A:671:PRO:CB	1:A:674:VAL:HG23	2.32	0.53
1:A:696:ALA:CB	1:A:703:THR:CG2	2.87	0.53
1:A:140:LEU:HD13	1:A:185:PHE:CZ	2.43	0.53
1:A:203:ARG:CG	1:A:204:MET:N	2.71	0.53
1:A:460:PRO:CB	1:A:465:ILE:HD13	2.37	0.52
1:A:368:LEU:HD12	1:A:368:LEU:O	2.10	0.52
1:A:144:GLY:O	1:A:145:ASP:C	2.52	0.52
1:A:208:ILE:HG22	1:A:212:MET:HE3	1.91	0.52
1:A:459:ARG:O	1:A:461:VAL:HG23	2.10	0.52
1:A:646:ARG:HE	1:A:706:TRP:CD1	2.23	0.52
1:A:21:GLN:HA	1:A:33:GLN:NE2	2.24	0.52
1:A:183:LEU:HD22	1:A:198:LEU:HD23	1.92	0.52
1:A:131:TRP:CD2	1:A:131:TRP:C	2.87	0.52
1:A:641:PHE:CZ	1:A:645:LEU:HD22	2.45	0.52
1:A:663:ILE:HD12	1:A:697:LEU:CD1	2.40	0.52
1:A:701:GLU:HA	1:A:701:GLU:OE1	2.08	0.52
1:A:548:ARG:HB2	1:A:665:MET:HE3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:144:GLY:C	1:A:145:ASP:O	2.53	0.51
1:A:790:LYS:HA	1:A:793:LYS:HD2	1.92	0.51
1:A:212:MET:HG2	1:A:217:CYS:SG	2.50	0.51
1:A:586:ARG:O	1:A:590:LEU:HD13	2.10	0.51
1:A:290:PHE:CB	1:A:585:SER:OG	2.59	0.51
1:A:551:VAL:HG22	1:A:632:VAL:HG12	1.92	0.51
1:A:609:THR:HG22	1:A:636:ASP:OD2	2.10	0.51
1:A:698:PHE:C	1:A:700:ARG:N	2.69	0.51
1:A:487:VAL:HG12	1:A:593:ARG:NH1	2.26	0.50
1:A:38:LEU:HB2	1:A:54:SER:CB	2.41	0.50
1:A:322:TYR:O	1:A:326:GLU:N	2.44	0.50
1:A:334:GLU:CD	1:A:366:ARG:HD2	2.36	0.50
1:A:134:LEU:HD23	1:A:180:GLU:HG2	1.93	0.50
1:A:257:LYS:O	1:A:423:GLY:CA	2.45	0.50
1:A:210:LEU:O	1:A:214:ARG:HG2	2.11	0.50
1:A:717:LYS:HB3	1:A:792:LEU:HD12	1.93	0.50
1:A:211:ALA:O	1:A:212:MET:C	2.55	0.49
1:A:435:THR:HG21	1:A:439:ASP:HB3	1.93	0.49
1:A:230:GLU:OE1	1:A:232:ARG:NH2	2.45	0.49
1:A:14:HIS:CE1	1:A:205:THR:HG21	2.48	0.49
1:A:172:SER:O	1:A:173:ASP:C	2.55	0.49
1:A:612:ASP:HB3	1:A:613:PRO:HD2	1.50	0.49
1:A:218:THR:O	1:A:222:VAL:HG23	2.13	0.49
1:A:276:GLU:HG2	1:A:448:PHE:CG	2.48	0.49
1:A:203:ARG:NH2	1:A:582:ALA:HB1	2.28	0.48
1:A:174:ARG:NH2	1:A:476:ILE:HD11	2.28	0.48
1:A:15:ASP:O	1:A:18:LYS:HG2	2.13	0.48
1:A:417:ASN:HA	1:A:420:VAL:HG23	1.96	0.48
1:A:38:LEU:HB2	1:A:54:SER:HB3	1.94	0.48
1:A:646:ARG:CD	1:A:706:TRP:CD2	2.96	0.48
1:A:134:LEU:CD1	1:A:140:LEU:HD23	2.05	0.48
1:A:658:THR:CB	1:A:693:ASN:OD1	2.55	0.48
1:A:670:TYR:CE2	1:A:671:PRO:HD2	2.47	0.48
1:A:265:TYR:OH	1:A:445:GLU:O	2.25	0.48
1:A:313:ILE:HG23	1:A:448:PHE:CZ	2.49	0.48
1:A:602:ARG:N	1:A:603:PRO:HD3	2.29	0.48
1:A:144:GLY:HA3	1:A:147:PHE:CZ	2.49	0.47
1:A:469:ASN:O	1:A:470:THR:HB	2.12	0.47
1:A:548:ARG:HD3	1:A:665:MET:HE3	1.97	0.47
1:A:464:GLN:HG3	1:A:481:GLN:HB2	1.96	0.47
1:A:229:LYS:HB2	1:A:341:ARG:HH12	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:367:LYS:NZ	1:A:367:LYS:CB	2.77	0.47
1:A:648:ARG:HA	1:A:648:ARG:HD3	1.50	0.47
1:A:48:ALA:O	1:A:51:GLU:N	2.45	0.47
1:A:696:ALA:HA	1:A:703:THR:HG22	1.95	0.47
1:A:663:ILE:HD12	1:A:697:LEU:HD11	1.97	0.47
1:A:702:PHE:C	1:A:702:PHE:CD1	2.92	0.47
1:A:53:LEU:O	1:A:56:PHE:HD1	1.98	0.47
1:A:184:THR:O	1:A:197:SER:HB2	2.15	0.47
1:A:557:ASP:HB2	1:A:658:THR:OG1	2.14	0.47
1:A:670:TYR:HE2	1:A:674:VAL:CG1	2.29	0.46
1:A:682:LEU:O	1:A:685:ALA:HB3	2.15	0.46
1:A:314:ARG:HH11	1:A:366:ARG:HD3	1.80	0.46
1:A:651:GLU:O	1:A:654:GLN:N	2.38	0.46
1:A:675:MET:O	1:A:679:VAL:HG23	2.16	0.46
1:A:739:LEU:O	1:A:742:LEU:O	2.32	0.46
1:A:180:GLU:OE2	1:A:586:ARG:NH1	2.48	0.46
1:A:7:THR:CG2	1:A:209:ALA:HB1	2.46	0.46
1:A:211:ALA:O	1:A:215:ALA:N	2.46	0.46
1:A:646:ARG:CB	1:A:706:TRP:CE2	2.99	0.46
1:A:738:LYS:O	1:A:741:GLU:HG2	2.16	0.46
1:A:354:GLU:O	1:A:357:LYS:HB2	2.16	0.46
1:A:556:VAL:HB	1:A:627:ASP:HB2	1.98	0.46
1:A:424:GLY:O	1:A:427:PRO:HD2	2.17	0.45
1:A:704:PHE:HZ	1:A:794:THR:OG1	1.98	0.45
1:A:261:ALA:HB1	1:A:422:LEU:HD23	1.97	0.45
1:A:682:LEU:CD1	1:A:697:LEU:O	2.64	0.45
1:A:290:PHE:HB3	1:A:585:SER:OG	2.17	0.45
1:A:429:LEU:HD11	1:A:432:PHE:CZ	2.51	0.45
1:A:682:LEU:HB3	1:A:696:ALA:O	2.17	0.45
1:A:591:PHE:HB2	1:A:652:PHE:CE2	2.51	0.45
1:A:203:ARG:O	1:A:207:ALA:N	2.42	0.45
1:A:663:ILE:O	1:A:682:LEU:CD1	2.64	0.45
1:A:74:ARG:O	1:A:78:LEU:HD13	2.17	0.45
1:A:243:ILE:N	2:A:901:DTP:O1A	2.50	0.45
1:A:442:VAL:HA	1:A:451:PHE:O	2.17	0.45
1:A:428:LYS:O	1:A:456:GLN:HB2	2.16	0.45
1:A:131:TRP:O	1:A:131:TRP:CE3	2.70	0.45
1:A:291:ASN:OD1	1:A:296:PHE:HB3	2.17	0.44
1:A:321:LEU:HD22	1:A:329:LEU:HD23	1.99	0.44
1:A:636:ASP:O	1:A:640:GLU:HG3	2.17	0.44
1:A:658:THR:HG22	1:A:693:ASN:HD21	1.78	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:246:PHE:O	1:A:262:ARG:NH2	2.47	0.44
1:A:413:CYS:HA	1:A:416:CYS:HB2	1.99	0.44
1:A:266:LEU:O	1:A:267:GLU:C	2.60	0.44
1:A:116:SER:O	1:A:148:SER:HB3	2.18	0.44
1:A:123:PHE:CD2	1:A:653:THR:HA	2.53	0.44
1:A:144:GLY:C	1:A:147:PHE:CE2	2.96	0.44
1:A:203:ARG:HG3	1:A:204:MET:HE2	1.99	0.44
1:A:123:PHE:CE1	1:A:653:THR:HG22	2.53	0.44
1:A:290:PHE:CD1	1:A:290:PHE:C	2.95	0.44
1:A:698:PHE:CD2	1:A:702:PHE:HZ	2.34	0.44
1:A:554:LEU:HD11	1:A:659:VAL:CG2	2.47	0.43
1:A:98:TYR:O	1:A:101:ASP:HB3	2.17	0.43
1:A:490:TYR:N	1:A:597:ASN:OD1	2.51	0.43
1:A:491:PHE:O	1:A:491:PHE:CG	2.71	0.43
1:A:557:ASP:OD2	1:A:692:LYS:HD2	2.19	0.43
1:A:559:LEU:N	2:A:902:DTP:O1B	2.51	0.43
1:A:99:GLU:O	1:A:103:LEU:HG	2.18	0.43
1:A:120:TYR:N	1:A:194:ASN:O	2.49	0.43
1:A:79:SER:O	1:A:82:ARG:HG2	2.19	0.43
1:A:80:PRO:HB3	1:A:90:VAL:HG21	2.00	0.43
1:A:18:LYS:N	1:A:19:PRO:HD2	2.33	0.43
1:A:247:ILE:HG21	2:A:901:DTP:H2	2.01	0.43
1:A:463:GLU:O	1:A:480:ALA:HA	2.19	0.42
1:A:4:ASP:OD1	1:A:5:GLU:N	2.53	0.42
1:A:237:GLU:HG2	1:A:363:LEU:CD1	2.48	0.42
1:A:702:PHE:CD1	1:A:702:PHE:O	2.72	0.42
1:A:705:GLY:N	1:A:708:GLU:HB3	2.32	0.42
1:A:4:ASP:HA	1:A:213:LEU:CD2	2.49	0.42
1:A:23:ALA:O	1:A:155:ARG:NH2	2.52	0.42
1:A:189:VAL:HG12	1:A:191:SER:H	1.84	0.42
1:A:698:PHE:C	1:A:700:ARG:H	2.27	0.42
1:A:600:LEU:CD1	1:A:621:ILE:HD11	2.49	0.42
1:A:91:LEU:O	1:A:95:TRP:HD1	2.03	0.42
1:A:556:VAL:CG1	1:A:559:LEU:HB2	2.50	0.42
1:A:253:LYS:HD2	1:A:253:LYS:HA	1.69	0.42
1:A:718:TYR:HE1	1:A:799:TYR:HA	1.84	0.42
1:A:492:LYS:HD2	1:A:492:LYS:HA	1.73	0.41
1:A:698:PHE:CD2	1:A:702:PHE:CZ	3.09	0.41
1:A:276:GLU:O	1:A:277:ILE:C	2.62	0.41
1:A:663:ILE:O	1:A:682:LEU:HD12	2.21	0.41
1:A:660:SER:HA	1:A:694:GLY:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:31:SER:HB3	1:A:57:SER:O	2.21	0.41
1:A:119:LEU:HD11	1:A:195:ILE:O	2.21	0.41
1:A:184:THR:OG1	1:A:586:ARG:NH2	2.54	0.41
1:A:120:TYR:CD2	1:A:128:ALA:HB2	2.55	0.41
1:A:623:TYR:HB2	2:A:901:DTP:C2	2.51	0.41
1:A:702:PHE:CD1	1:A:702:PHE:N	2.86	0.41
1:A:52:LEU:O	1:A:55:LEU:HD12	2.21	0.41
1:A:120:TYR:HE2	1:A:146:VAL:HG22	1.85	0.41
1:A:131:TRP:NE1	1:A:157:LEU:HD13	2.35	0.41
1:A:301:GLN:O	1:A:301:GLN:HG2	2.20	0.41
1:A:435:THR:CG2	1:A:439:ASP:HB3	2.51	0.41
1:A:454:TYR:CD1	1:A:460:PRO:HD3	2.55	0.41
1:A:685:ALA:O	1:A:686:ALA:C	2.64	0.41
1:A:137:GLU:O	1:A:138:LYS:CB	2.67	0.41
1:A:712:LYS:CB	1:A:791:GLN:OE1	2.68	0.41
1:A:160:ARG:O	1:A:162:TRP:N	2.54	0.40
1:A:441:GLY:C	1:A:452:VAL:HG13	2.46	0.40
1:A:7:THR:HG22	1:A:209:ALA:HB1	2.04	0.40
1:A:556:VAL:CG2	1:A:627:ASP:HB2	2.51	0.40
1:A:670:TYR:CD2	1:A:671:PRO:CD	2.91	0.40
1:A:670:TYR:HE2	1:A:674:VAL:HG11	1.86	0.40
1:A:686:ALA:O	1:A:689:LEU:HB2	2.21	0.40
1:A:698:PHE:O	1:A:699:ASP:C	2.62	0.40
1:A:645:LEU:O	1:A:646:ARG:C	2.63	0.40
1:A:682:LEU:O	1:A:683:GLU:C	2.64	0.40
1:A:696:ALA:CA	1:A:703:THR:HG22	2.51	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	596/784 (76%)	504 (85%)	70 (12%)	22 (4%)	2	15

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	140	LEU
1	A	141	PRO
1	A	145	ASP
1	A	479	SER
1	A	612	ASP
1	A	652	PHE
1	A	667	PRO
1	A	326	GLU
1	A	699	ASP
1	A	470	THR
1	A	556	VAL
1	A	614	ALA
1	A	77	GLU
1	A	118	PRO
1	A	249	ARG
1	A	697	LEU
1	A	161	LEU
1	A	671	PRO
1	A	146	VAL
1	A	84	GLY
1	A	254	GLY
1	A	461	VAL

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	519/659 (79%)	463 (89%)	56 (11%)	6	26

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	HIS
1	A	16	ILE
1	A	29	ASP
1	A	51	GLU
1	A	52	LEU
1	A	72	ILE
1	A	86	THR
1	A	99	GLU
1	A	129	TYR
1	A	135	ASP
1	A	137	GLU
1	A	138	LYS
1	A	140	LEU
1	A	176	LEU
1	A	187	SER
1	A	189	VAL
1	A	203	ARG
1	A	218	THR
1	A	222	VAL
1	A	229	LYS
1	A	249	ARG
1	A	250	VAL
1	A	253	LYS
1	A	257	LYS
1	A	297	MET
1	A	327	SER
1	A	363	LEU
1	A	368	LEU
1	A	369	LYS
1	A	415	THR
1	A	418	ARG
1	A	421	SER
1	A	454	TYR
1	A	463	GLU
1	A	478	GLU
1	A	487	VAL
1	A	565	HIS
1	A	589	SER
1	A	611	ASP
1	A	615	ARG
1	A	628	ASP
1	A	648	ARG
1	A	663	ILE

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Mol	Chain	Res	Type
1	A	669	LYS
1	A	688	SER
1	A	692	LYS
1	A	695	VAL
1	A	697	LEU
1	A	698	PHE
1	A	700	ARG
1	A	702	PHE
1	A	704	PHE
1	A	707	ASP
1	A	736	ILE
1	A	739	LEU
1	A	803	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	102	ASN
1	A	469	ASN
1	A	565	HIS
1	A	576	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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	DTP	A	902	3	31,32,32	1.64	5 (16%)	46,50,50	1.84	12 (26%)
2	DTP	A	901	-	31,32,32	1.95	8 (25%)	46,50,50	2.27	13 (28%)

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	DTP	A	902	3	-	7/22/34/34	0/3/3/3
2	DTP	A	901	-	-	9/22/34/34	0/3/3/3

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	901	DTP	C5-C4	5.36	1.48	1.39
2	A	902	DTP	C5-C4	4.66	1.47	1.39
2	A	901	DTP	PB-O3B	4.64	1.64	1.59
2	A	902	DTP	PA-O3A	3.48	1.63	1.59
2	A	901	DTP	C5-N7	-3.40	1.32	1.39
2	A	901	DTP	PA-O3A	3.22	1.63	1.59
2	A	902	DTP	C5-C6	2.73	1.48	1.41
2	A	901	DTP	PB-O3A	2.70	1.62	1.59
2	A	901	DTP	C1'-N9	2.67	1.51	1.46
2	A	901	DTP	C4-N3	2.66	1.39	1.34
2	A	902	DTP	C5-N7	-2.59	1.34	1.39
2	A	902	DTP	C8-N7	2.34	1.36	1.31
2	A	901	DTP	C2-N3	2.31	1.38	1.33

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	901	DTP	N3-C4-N9	8.04	140.84	127.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	901	DTP	C5-C4-N3	-7.17	116.84	126.72
2	A	902	DTP	C5-C4-N3	-5.11	119.67	126.72
2	A	902	DTP	N3-C4-N9	4.47	134.76	127.17
2	A	901	DTP	C2-N3-C4	3.59	120.60	111.83
2	A	902	DTP	C4-N9-C8	3.55	109.47	105.74
2	A	902	DTP	C2-N3-C4	3.38	120.09	111.83
2	A	902	DTP	C4-C5-N7	-3.37	106.73	110.58
2	A	901	DTP	C5-C4-N9	-3.22	102.31	105.81
2	A	901	DTP	C4-N9-C8	3.19	109.09	105.74
2	A	901	DTP	N3-C2-N1	-3.18	123.77	128.58
2	A	902	DTP	N3-C2-N1	-3.06	123.95	128.58
2	A	901	DTP	C1'-N9-C8	-2.96	116.61	126.95
2	A	902	DTP	C2'-C3'-C4'	2.92	108.73	102.80
2	A	902	DTP	C5-N7-C8	2.82	107.89	103.45
2	A	901	DTP	N6-C6-N1	2.65	124.29	118.38
2	A	901	DTP	C5-C6-N6	-2.61	116.81	123.29
2	A	902	DTP	N9-C8-N7	-2.53	110.35	113.94
2	A	902	DTP	O2B-PB-O3A	2.43	113.85	107.27
2	A	901	DTP	C2'-C3'-C4'	2.26	107.39	102.80
2	A	901	DTP	O4'-C4'-C5'	2.16	116.27	109.33
2	A	902	DTP	O4'-C1'-C2'	2.13	110.22	106.25
2	A	901	DTP	O3A-PA-O1A	-2.05	104.53	110.70
2	A	901	DTP	O2A-PA-O1A	2.05	121.97	112.44
2	A	902	DTP	O2B-PB-O3B	2.03	112.75	107.27

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	901	DTP	C5'-O5'-PA-O1A
2	A	901	DTP	C5'-O5'-PA-O2A
2	A	901	DTP	C5'-O5'-PA-O3A
2	A	902	DTP	PB-O3A-PA-O5'
2	A	902	DTP	C5'-O5'-PA-O1A
2	A	902	DTP	C5'-O5'-PA-O2A
2	A	902	DTP	C5'-O5'-PA-O3A
2	A	901	DTP	C3'-C4'-C5'-O5'
2	A	901	DTP	O4'-C4'-C5'-O5'
2	A	901	DTP	PG-O3B-PB-O3A
2	A	901	DTP	PB-O3A-PA-O5'
2	A	902	DTP	O4'-C1'-N9-C4
2	A	902	DTP	O4'-C1'-N9-C8

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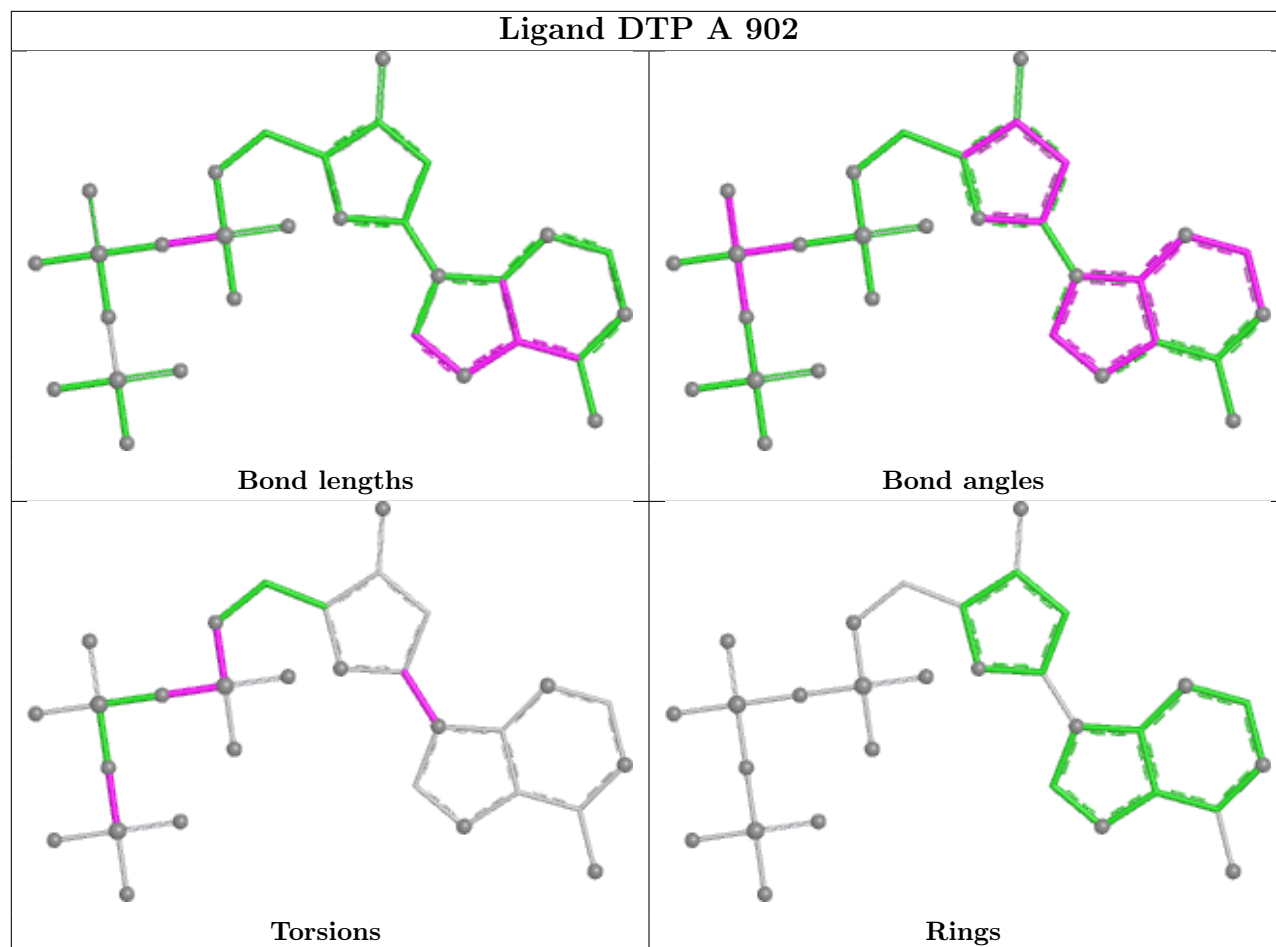
Mol	Chain	Res	Type	Atoms
2	A	902	DTP	PB-O3B-PG-O2G
2	A	901	DTP	PG-O3B-PB-O1B
2	A	901	DTP	PG-O3B-PB-O2B

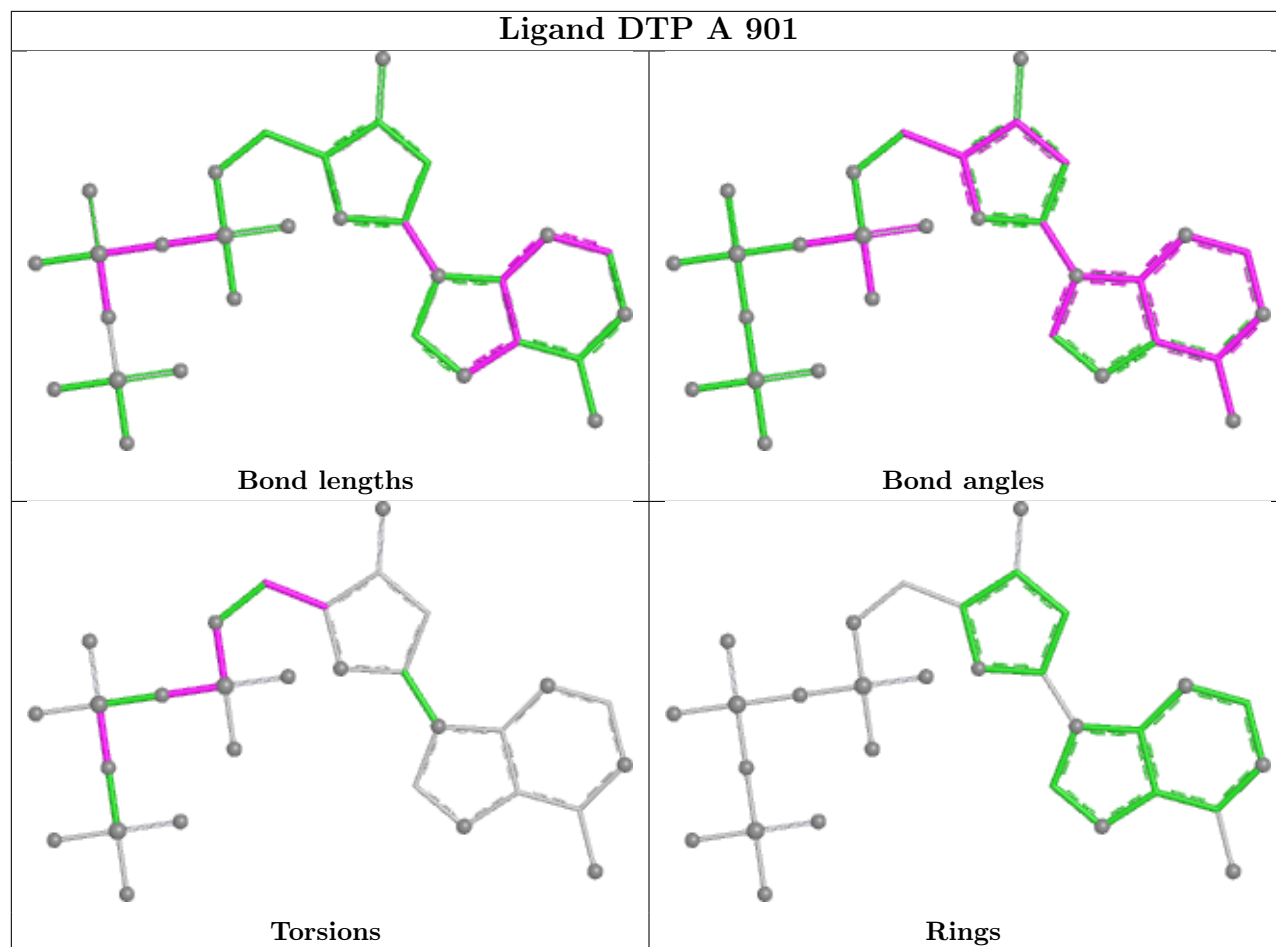
There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	902	DTP	1	0
2	A	901	DTP	4	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(Å ²)	Q<0.9
1	A	616/784 (78%)	0.15	26 (4%) 40 22	49, 66, 88, 104	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	95	TRP	5.6
1	A	696	ALA	5.2
1	A	697	LEU	5.0
1	A	140	LEU	4.5
1	A	59	PHE	4.3
1	A	698	PHE	4.2
1	A	37	PHE	3.7
1	A	129	TYR	3.3
1	A	268	LEU	3.1
1	A	662	GLY	3.0
1	A	121	SER	2.8
1	A	661	ALA	2.7
1	A	415	THR	2.6
1	A	736	ILE	2.5
1	A	162	TRP	2.5
1	A	444	VAL	2.5
1	A	416	CYS	2.4
1	A	270	GLY	2.4
1	A	577	THR	2.3
1	A	663	ILE	2.3
1	A	71	MET	2.3
1	A	703	THR	2.3
1	A	116	SER	2.2
1	A	148	SER	2.2
1	A	706	TRP	2.2
1	A	202	MET	2.1

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](#)

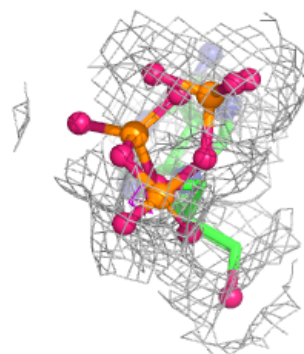
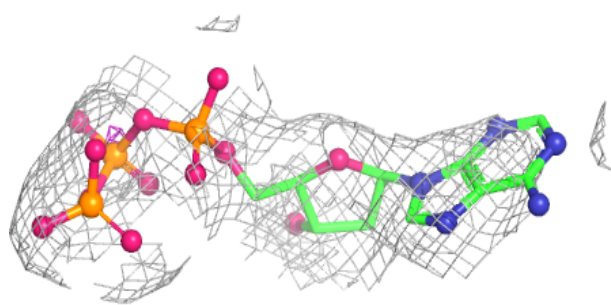
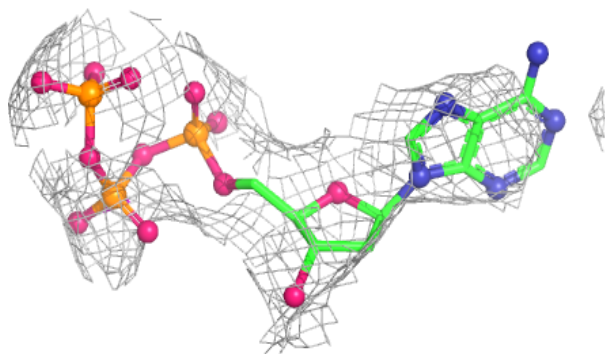
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	DTP	A	901	30/30	0.80	0.11	68,83,114,127	0
2	DTP	A	902	30/30	0.90	0.10	51,63,77,101	0
3	MG	A	904	1/1	0.95	0.12	21,21,21,21	0
3	MG	A	903	1/1	0.98	0.23	14,14,14,14	0

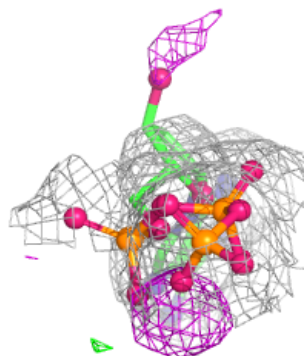
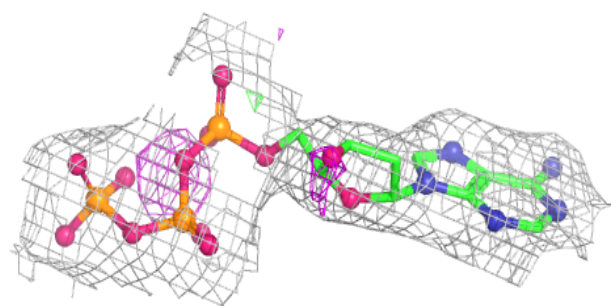
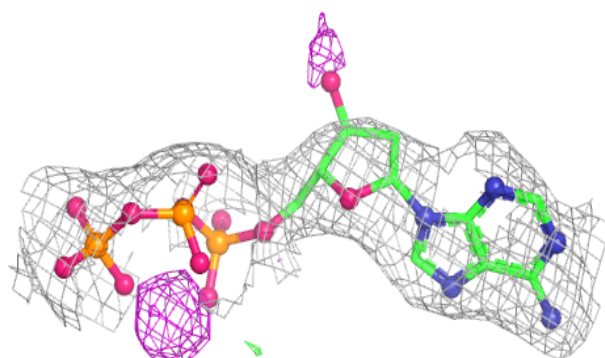
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around DTP 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)

**Electron density around DTP A 902:**

$2mF_o-DF_c$ (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.