



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 05:54 AM UTC

PDB ID : 7R3Y / pdb_00007r3y
Title : The crystal structure of the V426L variant of Pol2CORE in complex with DNA and an incoming nucleotide
Authors : Barbari, S.R.; Beach, A.K.; Markgren, J.G.; Parkash, V.; Johansson, E.; Shcherbakova, P.V.
Deposited on : 2022-02-08
Resolution : 2.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

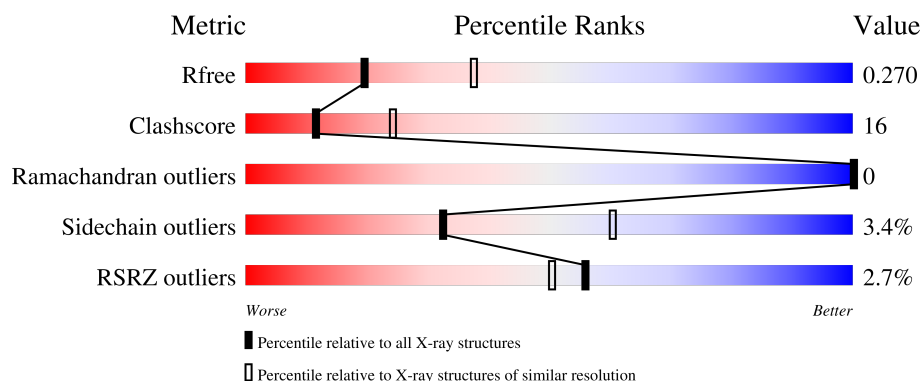
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	1186	3% 63% 28% 7%
1	B	1186	2% 62% 29% 7%
2	C	11	27% 73%
2	P	11	64% 27% 9%

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Mol	Chain	Length	Quality of chain
3	T	16	50% 44% 6%
4	D	16	62% 31% 6%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 18825 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 DNA polymerase epsilon catalytic subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1105	Total	C	N	O	S	0	0	0
			8917	5712	1481	1681	43			
1	B	1102	Total	C	N	O	S	0	0	0
			8772	5618	1452	1660	42			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	426	LEU	VAL	engineered mutation	UNP A0A7I9C3S1
B	426	LEU	VAL	engineered mutation	UNP A0A7I9C3S1

- Molecule 2 is a DNA chain called DNA Primer.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	11	Total	C	N	O	P	0	0	0
			221	106	38	66	11			
2	C	11	Total	C	N	O	P	0	0	0
			221	106	38	66	11			

- Molecule 3 is a DNA chain called DNA Template.

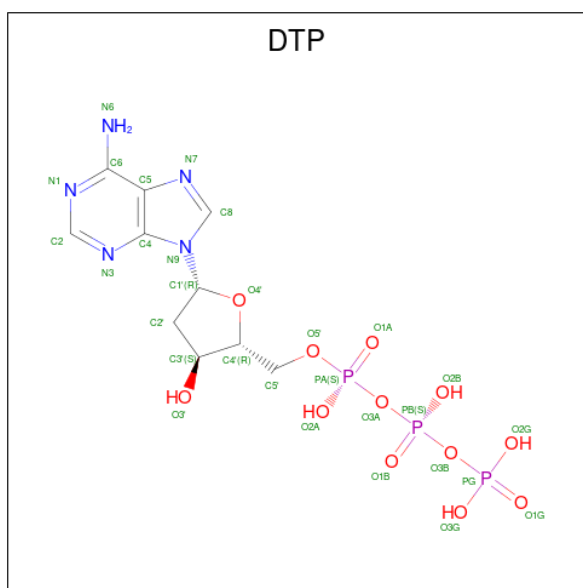
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	T	15	Total	C	N	O	P	0	0	0
			309	147	54	93	15			

- Molecule 4 is a DNA chain called DNA Template.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	15	Total	C	N	O	P	0	0	0
			308	147	54	92	15			

- Molecule 5 is 2'-DEOXYADENOSINE 5'-TRIPHOSPHATE (CCD ID: DTP) (formula: C₁₀H₁₆N₅O₁₂P₃)

(labeled as "Ligand of Interest" by depositor).



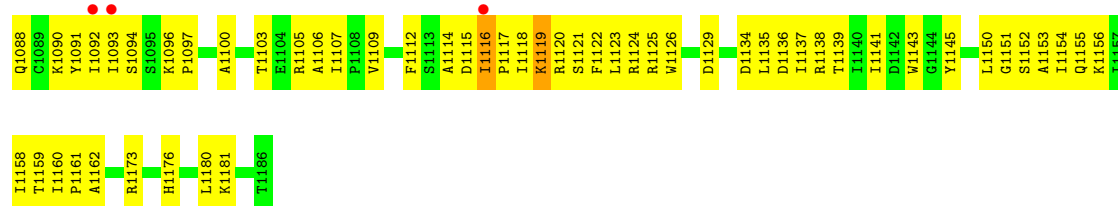
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			30	10	5	12	3		
5	B	1	Total	C	N	O	P	0	0
			30	10	5	12	3		

- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca).

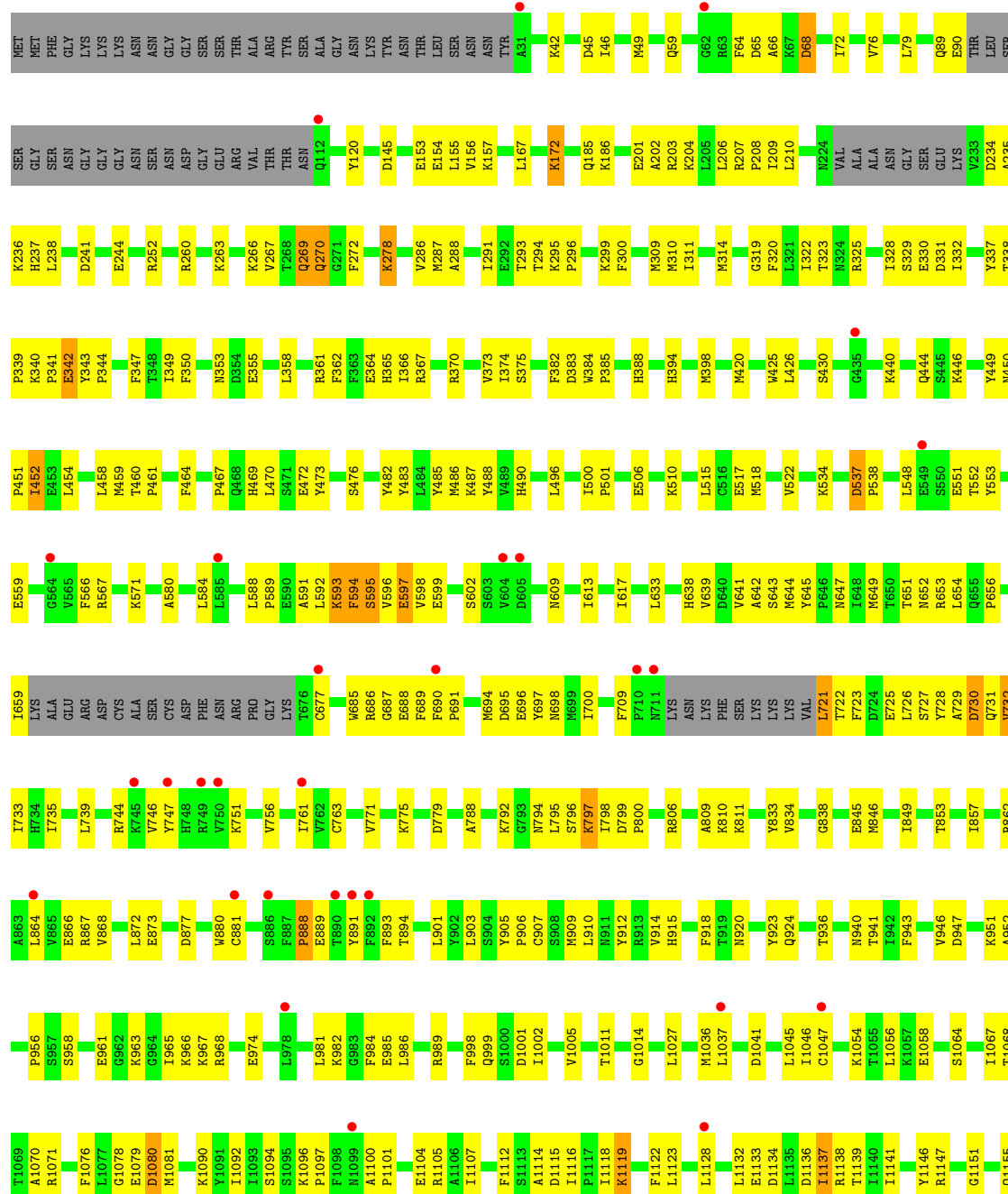
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	2	Total	Ca	0	0
			2	2		
6	B	2	Total	Ca	0	0
			2	2		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	2	Total	O	0	0
			2	2		
7	T	6	Total	O	0	0
			6	6		
7	B	5	Total	O	0	0
			5	5		



• Molecule 1: DNA polymerase epsilon catalytic subunit

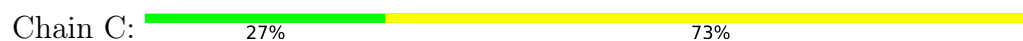




- Molecule 2: DNA Primer



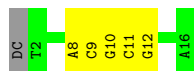
- Molecule 2: DNA Primer



- Molecule 3: DNA Template



- Molecule 4: DNA Template



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	154.40Å 70.10Å 159.50Å 90.00° 113.10° 90.00°	Depositor
Resolution (Å)	47.84 – 2.60 47.84 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.2 (47.84-2.60) 99.6 (47.84-2.60)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.13 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.220 , 0.270 0.225 , 0.270	Depositor DCC
R_{free} test set	4841 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	76.3	Xtriage
Anisotropy	0.309	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 59.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	18825	wwPDB-VP
Average B, all atoms (Å ²)	98.0	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 71.68 % 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 2.5186e-06. 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

5.1 Standard geometry

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

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	0.41	0/9122	0.75	4/12348 (0.0%)
1	B	0.40	0/8971	0.74	5/12157 (0.0%)
2	C	0.35	0/226	0.72	1/346 (0.3%)
2	P	0.34	0/226	0.69	1/346 (0.3%)
3	T	0.24	0/345	0.45	0/531
4	D	0.25	0/344	0.43	0/529
All	All	0.40	0/19234	0.73	11/26257 (0.0%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	9	DT	P-O3'-C3'	-7.45	109.03	120.20
1	B	888	PRO	CB-CA-C	6.90	120.06	111.23
2	P	9	DT	P-O3'-C3'	-6.80	109.99	120.20
1	B	730	ASP	N-CA-C	-6.13	104.60	111.28
1	A	1002	ILE	N-CA-C	5.25	116.02	110.72
1	B	873	GLU	CB-CG-CD	5.12	121.31	112.60
1	B	1119	LYS	N-CA-C	-5.06	105.77	111.28
1	B	66	ALA	N-CA-C	-5.04	106.23	112.38
1	A	1009	GLY	CA-C-N	-5.03	114.69	122.49
1	A	1009	GLY	C-N-CA	-5.03	114.69	122.49
1	A	283	ASP	CB-CA-C	5.02	115.14	110.17

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	8917	0	8704	281	0
1	B	8772	0	8490	296	0
2	C	221	0	125	7	0
2	P	221	0	125	5	0
3	T	309	0	171	5	0
4	D	308	0	171	5	0
5	A	30	0	12	2	0
5	B	30	0	12	1	0
6	A	2	0	0	0	0
6	B	2	0	0	0	0
7	A	2	0	0	0	0
7	B	5	0	0	0	0
7	T	6	0	0	0	0
All	All	18825	0	17810	585	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 16.

All (585) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:10:DT:H2''	2:C:11:DOC:H5'	1.55	0.88
1:A:299:LYS:HA	1:A:1081:MET:HE1	1.55	0.88
1:A:356:VAL:HG23	1:A:394:HIS:HB3	1.57	0.85
1:A:332:ILE:HG23	1:A:349:ILE:HG21	1.60	0.84
1:A:1115:ASP:HB2	1:A:1118:ILE:HD13	1.60	0.84
1:A:1117:PRO:HG2	1:A:1118:ILE:HD12	1.59	0.83
1:B:594:PHE:HE2	1:B:915:HIS:HD1	1.25	0.82
1:B:362:PHE:O	1:B:366:ILE:HD12	1.79	0.81
1:A:1092:ILE:HD12	1:A:1109:VAL:HG22	1.64	0.80
1:A:558:VAL:HG12	1:A:966:LYS:HD2	1.65	0.78
1:A:552:THR:HG22	1:A:553:TYR:H	1.49	0.77
1:B:338:THR:HG23	1:B:344:PRO:HA	1.65	0.77
1:A:594:PHE:CE1	1:A:915:HIS:HD2	2.04	0.75
1:B:593:LYS:O	1:B:597:GLU:HG3	1.87	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:10:DT:H2''	2:P:11:DOC:H5'	1.69	0.74
1:B:732:VAL:HA	1:B:735:ILE:HD12	1.70	0.74
1:A:711:ASN:HB2	1:A:721:LEU:HD13	1.71	0.73
1:A:860:MET:HE1	1:A:913:ARG:HB3	1.71	0.73
1:A:709:PHE:CD2	1:A:726:LEU:HD11	2.25	0.71
1:A:630:ARG:NE	1:A:632:GLU:OE2	2.23	0.71
1:B:506:GLU:O	1:B:510:LYS:HG2	1.91	0.71
1:A:350:PHE:HD1	1:A:361:ARG:HD2	1.55	0.71
1:B:744:ARG:HD2	1:B:746:VAL:H	1.55	0.71
1:B:965:ILE:HD11	4:D:10:DG:H3'	1.72	0.70
1:B:1151:GLY:O	1:B:1155:GLN:HG3	1.90	0.70
1:A:989:ARG:HH21	2:P:8:DG:P	2.14	0.70
1:A:314:MET:HE1	1:A:479:VAL:HA	1.73	0.70
1:A:1137:ILE:HD12	1:A:1137:ILE:H	1.55	0.70
1:B:500:ILE:HD13	1:B:515:LEU:HD22	1.73	0.70
1:B:580:ALA:HB2	1:B:867:ARG:HE	1.56	0.69
1:A:332:ILE:HG13	1:A:333:GLU:N	2.06	0.69
1:B:234:ASP:OD2	1:B:235:ALA:N	2.25	0.69
1:B:496:LEU:HG	1:B:500:ILE:HD12	1.74	0.69
1:A:1097:PRO:HD2	1:A:1105:ARG:HG2	1.73	0.68
1:A:1160:ILE:HG23	1:A:1180:LEU:HD22	1.74	0.68
1:B:342:GLU:HG2	1:B:811:LYS:HZ1	1.57	0.68
1:A:455:ASP:HB3	1:A:458:LEU:HD23	1.76	0.68
1:A:1005:VAL:HG21	1:A:1022:VAL:HG21	1.76	0.68
1:B:426:LEU:HA	1:B:430:SER:HB3	1.74	0.68
1:A:1138:ARG:HG2	1:A:1138:ARG:HH11	1.59	0.68
1:B:989:ARG:HH21	2:C:8:DG:P	2.17	0.68
1:B:452:ILE:HG23	1:B:476:SER:HB2	1.76	0.67
1:B:319:GLY:O	1:B:347:PHE:HA	1.95	0.67
1:B:452:ILE:HD11	1:B:473:TYR:HB2	1.75	0.67
1:B:325:ARG:NH1	1:B:328:ILE:O	2.27	0.67
1:A:798:ILE:HD12	1:A:805:ALA:HB1	1.76	0.67
1:A:234:ASP:OD1	1:A:235:ALA:N	2.29	0.66
1:A:355:GLU:O	1:A:358:LEU:N	2.28	0.66
1:B:235:ALA:HA	1:B:238:LEU:HD23	1.78	0.66
1:B:300:PHE:H	1:B:1081:MET:HE1	1.60	0.66
1:B:641:VAL:HG22	1:B:877:ASP:HB2	1.75	0.66
1:A:538:PRO:HD2	1:A:541:ARG:HH11	1.59	0.65
1:A:315:ILE:HG21	1:A:369:VAL:HG11	1.77	0.65
1:A:588:LEU:N	1:A:589:PRO:HD2	2.11	0.65
1:B:728:TYR:O	1:B:732:VAL:HG13	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:635:LEU:HD21	1:A:885:LYS:HD2	1.78	0.65
1:B:1011:THR:HG23	1:B:1014:GLY:H	1.61	0.65
1:A:679:ARG:HG2	1:A:681:LEU:HD13	1.79	0.64
1:B:342:GLU:HG2	1:B:811:LYS:NZ	2.12	0.64
1:A:1120:ARG:O	1:A:1124:ARG:HG2	1.96	0.64
1:B:647:ASN:O	1:B:651:THR:HG23	1.97	0.64
1:A:548:LEU:HD23	1:A:689:PHE:HB3	1.80	0.64
1:A:596:VAL:HG23	1:A:597:GLU:HG2	1.79	0.64
1:B:1092:ILE:HG21	1:B:1141:ILE:HD12	1.79	0.64
1:B:337:TYR:O	1:B:339:PRO:HD3	1.98	0.64
1:A:760:ALA:HB3	1:A:849:ILE:HD11	1.78	0.63
1:A:1116:ILE:N	1:A:1117:PRO:HD2	2.13	0.63
1:A:334:ASP:HA	1:A:349:ILE:CD1	2.29	0.63
1:B:452:ILE:HG12	1:B:473:TYR:HA	1.79	0.63
1:B:1137:ILE:O	1:B:1141:ILE:HG12	1.99	0.62
1:B:295:LYS:H	1:B:460:THR:HG21	1.65	0.62
1:B:64:PHE:CZ	1:B:270:GLN:HB3	2.35	0.62
1:B:89:GLN:OE1	1:B:89:GLN:N	2.33	0.62
1:B:1100:ALA:O	1:B:1105:ARG:NH1	2.31	0.62
1:B:1115:ASP:O	1:B:1119:LYS:HG3	1.99	0.62
1:A:594:PHE:HE1	1:A:915:HIS:CD2	2.17	0.62
1:B:593:LYS:O	1:B:596:VAL:HG22	1.98	0.62
1:B:652:ASN:HB2	1:B:654:LEU:CD2	2.30	0.62
1:B:440:LYS:HA	1:B:451:PRO:HG3	1.82	0.61
1:A:747:TYR:O	1:A:748:HIS:HB2	1.99	0.61
1:B:872:LEU:HD13	1:B:881:CYS:HA	1.82	0.61
1:A:594:PHE:CE1	1:A:915:HIS:CD2	2.87	0.61
1:B:729:ALA:O	1:B:732:VAL:HG22	2.00	0.61
1:A:1088:GLN:N	1:A:1088:GLN:OE1	2.34	0.61
1:B:343:TYR:HE1	1:B:487:LYS:HE3	1.65	0.61
1:B:1134:ASP:HB3	1:B:1139:THR:HG21	1.83	0.61
1:A:34:ALA:HA	1:A:37:LEU:HD12	1.83	0.61
1:B:727:SER:O	1:B:731:GLN:HG3	2.01	0.61
1:B:155:LEU:HD22	1:B:235:ALA:HB3	1.81	0.61
1:B:548:LEU:HD23	1:B:689:PHE:HB3	1.83	0.61
1:A:956:PRO:HB2	1:A:965:ILE:HD12	1.82	0.61
1:B:64:PHE:CE2	1:B:270:GLN:HB3	2.36	0.61
1:B:322:ILE:HG22	1:B:358:LEU:HD12	1.83	0.60
1:A:905:TYR:O	1:A:909:MET:HG2	2.02	0.60
1:B:617:ILE:HG12	1:B:891:TYR:CE1	2.36	0.60
1:A:966:LYS:HE3	3:T:9:DC:H5"	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1137:ILE:O	1:A:1141:ILE:HG13	2.00	0.60
1:A:510:LYS:HD2	1:A:514:THR:HG21	1.83	0.60
1:B:915:HIS:CD2	1:B:940:ASN:CG	2.79	0.60
1:B:286:VAL:HG13	1:B:373:VAL:HG13	1.83	0.60
1:A:627:ASN:HB2	1:A:630:ARG:NH1	2.16	0.59
1:A:723:PHE:HA	1:A:726:LEU:HD11	1.84	0.59
1:A:649:MET:HA	1:A:654:LEU:HD12	1.82	0.59
1:B:696:GLU:O	1:B:700:ILE:HG12	2.02	0.59
1:B:537:ASP:OD2	1:B:538:PRO:HD2	2.03	0.59
1:A:613:ILE:HD12	1:A:891:TYR:HB3	1.84	0.59
1:B:72:ILE:O	1:B:266:LYS:NZ	2.27	0.59
1:A:458:LEU:HB3	1:A:462:TYR:HD1	1.68	0.58
1:A:979:ALA:C	1:A:980:GLU:HG2	2.28	0.58
1:A:356:VAL:HG13	1:A:360:GLN:OE1	2.03	0.58
1:A:383:ASP:O	1:A:387:ILE:HG22	2.04	0.58
1:B:460:THR:OG1	1:B:461:PRO:HD3	2.03	0.58
1:B:730:ASP:HA	1:B:733:ILE:HD12	1.85	0.58
1:B:595:SER:HA	1:B:599:GLU:HB2	1.86	0.58
1:A:834:VAL:HG11	1:A:846:MET:CE	2.33	0.58
1:B:649:MET:HA	1:B:654:LEU:HD23	1.86	0.58
1:B:967:LYS:O	1:B:968:ARG:HG3	2.04	0.58
1:A:595:SER:O	1:A:599:GLU:HB2	2.03	0.58
1:B:651:THR:HG22	1:B:941:THR:H	1.69	0.58
1:B:591:ALA:HB2	1:B:912:TYR:HD2	1.69	0.57
1:A:64:PHE:CE1	1:A:270:GLN:HB2	2.38	0.57
1:A:1120:ARG:HB2	1:A:1135:LEU:HD11	1.86	0.57
1:B:567:ARG:HG3	1:B:952:ALA:HB2	1.86	0.57
1:B:797:LYS:HG3	1:B:798:ILE:N	2.20	0.57
1:A:1151:GLY:O	1:A:1155:GLN:HB2	2.05	0.57
1:B:744:ARG:NE	1:B:747:TYR:H	2.00	0.57
1:A:1116:ILE:HD12	1:A:1116:ILE:H	1.69	0.57
1:A:709:PHE:CE2	1:A:726:LEU:HD11	2.40	0.57
1:B:382:PHE:C	1:B:385:PRO:HD2	2.30	0.57
1:A:332:ILE:HG13	1:A:333:GLU:H	1.69	0.57
1:A:1160:ILE:N	1:A:1161:PRO:CD	2.68	0.56
1:B:642:ALA:O	1:B:643:SER:C	2.48	0.56
1:A:868:VAL:HG21	1:A:887:PHE:CE2	2.40	0.56
1:B:795:LEU:HD13	1:B:809:ALA:HB3	1.87	0.56
1:A:1115:ASP:HB2	1:A:1118:ILE:CD1	2.34	0.56
1:B:688:GLU:HB3	1:B:751:LYS:HE3	1.87	0.56
1:B:744:ARG:HE	1:B:747:TYR:H	1.54	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1081:MET:HE2	1:B:1081:MET:HA	1.87	0.56
1:A:872:LEU:HD11	1:A:882:ILE:HG23	1.87	0.56
1:B:209:ILE:HD12	1:B:209:ILE:H	1.70	0.56
1:A:876:THR:HB	2:P:11:DOC:H3'2	1.86	0.56
1:A:350:PHE:CD1	1:A:361:ARG:HD2	2.40	0.56
1:A:383:ASP:N	1:A:383:ASP:OD1	2.39	0.56
1:B:905:TYR:CE1	1:B:909:MET:HB3	2.41	0.56
1:B:320:PHE:CD2	1:B:365:HIS:HE1	2.24	0.55
1:A:744:ARG:O	1:A:748:HIS:HA	2.06	0.55
1:B:888:PRO:HB2	1:B:905:TYR:HD2	1.71	0.55
1:A:293:THR:O	1:A:309:MET:HE3	2.05	0.55
1:B:961:GLU:HB2	1:B:1179:TRP:CD2	2.40	0.55
3:T:11:DC:H2''	3:T:12:DG:C8	2.42	0.55
1:B:319:GLY:O	1:B:320:PHE:HD1	1.89	0.55
1:B:364:GLU:HA	1:B:367:ARG:NH1	2.21	0.55
1:A:365:HIS:O	1:A:369:VAL:HG23	2.07	0.55
1:A:1138:ARG:HG2	1:A:1138:ARG:NH1	2.22	0.55
4:D:11:DC:H2''	4:D:12:DG:C8	2.41	0.55
1:A:616:GLN:O	1:A:620:LYS:HD2	2.07	0.55
1:B:1101:PRO:HD2	1:B:1104:GLU:OE2	2.07	0.55
1:A:291:ILE:HG13	1:A:291:ILE:O	2.06	0.55
1:A:334:ASP:HA	1:A:349:ILE:HD13	1.88	0.55
1:A:1096:LYS:HE2	1:A:1129:ASP:HB2	1.89	0.55
1:B:951:LYS:HB2	1:B:974:GLU:HA	1.89	0.54
1:A:294:THR:HA	1:A:309:MET:HE2	1.89	0.54
1:B:924:GLN:HG2	1:B:936:THR:HG22	1.88	0.54
1:B:966:LYS:HD3	4:D:9:DC:H5''	1.88	0.54
1:A:207:ARG:HA	1:A:210:LEU:HB2	1.90	0.54
1:B:1047:CYS:SG	1:B:1090:LYS:HB3	2.48	0.54
1:A:723:PHE:HA	1:A:726:LEU:CD1	2.38	0.54
1:A:321:LEU:HB3	1:A:349:ILE:HG13	1.89	0.54
1:B:201:GLU:O	1:B:204:LYS:HG2	2.06	0.54
1:A:458:LEU:HB3	1:A:462:TYR:CD1	2.43	0.54
1:A:1155:GLN:HA	1:A:1159:THR:OG1	2.07	0.54
1:B:314:MET:HG2	1:B:319:GLY:HA2	1.90	0.54
1:B:320:PHE:CD2	1:B:365:HIS:CE1	2.96	0.54
1:B:686:ARG:NH2	4:D:8:DA:OP2	2.28	0.54
1:B:613:ILE:HD12	1:B:891:TYR:HB3	1.90	0.53
1:A:39:ASN:O	1:A:43:ILE:HD12	2.09	0.53
1:A:244:GLU:OE1	1:A:252:ARG:NH2	2.41	0.53
1:A:310:MET:HE1	1:A:321:LEU:HD21	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:382:PHE:C	1:A:385:PRO:HD2	2.33	0.53
1:B:469:HIS:O	1:B:472:GLU:HG2	2.07	0.53
1:A:645:TYR:CG	5:A:1301:DTP:H2'1	2.43	0.53
1:B:1096:LYS:HG3	1:B:1097:PRO:HA	1.90	0.53
1:A:322:ILE:HD13	1:A:350:PHE:HB2	1.89	0.53
1:A:628:ASN:OD1	1:A:628:ASN:N	2.38	0.53
1:B:651:THR:CG2	1:B:941:THR:H	2.21	0.53
1:B:337:TYR:CZ	1:B:339:PRO:HG3	2.43	0.53
1:B:1114:ALA:HB3	1:B:1119:LYS:HG2	1.91	0.53
1:A:865:VAL:O	1:A:869:GLY:N	2.35	0.53
1:B:454:LEU:HD22	1:B:459:MET:CG	2.39	0.53
1:A:287:MET:HE1	1:A:366:ILE:HG12	1.91	0.53
1:B:311:ILE:HG13	1:B:358:LEU:HD21	1.90	0.53
1:B:910:LEU:O	1:B:914:VAL:HG23	2.08	0.53
1:B:1138:ARG:HG3	1:B:1138:ARG:HH11	1.72	0.53
1:A:868:VAL:HG21	1:A:887:PHE:HE2	1.73	0.53
1:B:905:TYR:O	1:B:909:MET:HG2	2.09	0.53
1:A:728:TYR:O	1:A:732:VAL:HG23	2.09	0.53
1:A:1112:PHE:CD1	1:A:1137:ILE:HG13	2.44	0.53
1:B:723:PHE:CZ	1:B:731:GLN:HB3	2.44	0.53
1:B:723:PHE:CE1	1:B:731:GLN:HA	2.44	0.52
1:B:744:ARG:HD2	1:B:746:VAL:N	2.22	0.52
1:B:319:GLY:C	1:B:320:PHE:HD1	2.17	0.52
1:A:46:ILE:HD12	1:A:399:PHE:CE1	2.43	0.52
1:A:153:GLU:CD	1:A:169:ILE:HD11	2.34	0.52
1:B:244:GLU:OE1	1:B:252:ARG:NH2	2.42	0.52
1:B:332:ILE:HB	1:B:349:ILE:HG21	1.90	0.52
1:B:534:LYS:HG2	1:B:838:GLY:O	2.09	0.52
1:B:645:TYR:CG	5:B:1301:DTP:H2'1	2.44	0.52
1:B:958:SER:HB3	1:B:963:LYS:O	2.10	0.52
1:A:399:PHE:HD1	1:A:403:GLY:HA2	1.74	0.52
1:A:700:ILE:HD13	1:A:739:LEU:HD22	1.91	0.52
1:B:320:PHE:CE2	1:B:365:HIS:CE1	2.98	0.52
1:B:744:ARG:CD	1:B:746:VAL:H	2.21	0.52
1:B:685:TRP:HE3	1:B:756:VAL:HG12	1.74	0.52
1:B:985:GLU:OE1	1:B:999:GLN:NE2	2.39	0.52
1:B:203:ARG:HH21	1:B:207:ARG:HH12	1.58	0.51
1:B:355:GLU:HB3	1:B:394:HIS:HE1	1.75	0.51
1:A:426:LEU:HA	1:A:430:SER:HB3	1.92	0.51
1:B:343:TYR:CE1	1:B:487:LYS:HE3	2.45	0.51
1:B:722:THR:HG22	1:B:725:GLU:OE1	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:998:PHE:CZ	1:B:1002:ILE:HG13	2.45	0.51
1:B:1094:SER:HB3	1:B:1107:ILE:HD13	1.92	0.51
1:B:915:HIS:HD2	1:B:940:ASN:CG	2.18	0.51
1:A:1112:PHE:HA	1:A:1119:LYS:HD3	1.92	0.51
1:A:33:SER:O	1:A:34:ALA:C	2.53	0.51
1:A:594:PHE:CZ	1:A:915:HIS:HD2	2.29	0.51
1:A:1152:SER:O	1:A:1156:LYS:HG3	2.10	0.51
1:A:1124:ARG:HB2	1:A:1129:ASP:O	2.10	0.51
1:B:775:LYS:NZ	1:B:779:ASP:OD2	2.26	0.51
1:A:155:LEU:HD21	1:A:236:LYS:HG2	1.93	0.51
1:A:645:TYR:O	1:A:649:MET:HG3	2.11	0.51
1:B:330:GLU:HG2	1:B:467:PRO:HG2	1.92	0.51
1:B:981:LEU:HD21	1:B:986:LEU:HD23	1.92	0.51
1:B:1056:LEU:HD21	1:B:1071:ARG:HH21	1.75	0.51
1:A:1056:LEU:HB3	1:A:1082:VAL:CG1	2.41	0.50
1:A:577:ASP:HB3	1:A:867:ARG:HB3	1.92	0.50
1:B:794:ASN:O	1:B:798:ILE:HD12	2.11	0.50
1:A:547:LEU:HD22	1:A:690:PHE:HE1	1.77	0.50
1:A:1056:LEU:HD21	1:A:1071:ARG:HG2	1.94	0.50
1:B:1160:ILE:N	1:B:1161:PRO:CD	2.74	0.50
1:A:986:LEU:HA	1:A:996:LYS:HG2	1.94	0.50
1:A:340:LYS:HD2	1:A:448:GLY:O	2.11	0.50
1:B:559:GLU:OE1	1:B:862:ARG:NH1	2.44	0.50
1:B:1176:HIS:CG	1:B:1180:LEU:HD23	2.46	0.50
1:A:292:GLU:HB3	1:A:459:MET:HE1	1.93	0.50
1:A:355:GLU:O	1:A:356:VAL:C	2.54	0.50
1:A:1094:SER:OG	1:A:1096:LYS:O	2.21	0.50
1:B:420:MET:HA	1:B:420:MET:HE2	1.94	0.50
1:B:1078:GLY:O	1:B:1079:GLU:C	2.54	0.50
1:A:990:GLY:O	1:A:996:LYS:HE2	2.11	0.50
1:A:60:TYR:CZ	1:A:62:GLY:HA3	2.47	0.50
1:A:349:ILE:C	1:A:350:PHE:HD2	2.20	0.50
1:A:593:LYS:O	1:A:596:VAL:HG22	2.12	0.50
1:B:965:ILE:HD11	4:D:10:DG:C3'	2.38	0.50
1:B:1155:GLN:HA	1:B:1159:THR:OG1	2.11	0.50
2:C:5:DC:H2''	2:C:6:DG:C8	2.46	0.50
1:A:323:THR:HB	1:A:328:ILE:HG13	1.94	0.50
1:A:454:LEU:HD22	1:A:459:MET:SD	2.52	0.50
1:B:639:VAL:HG12	1:B:946:VAL:HG22	1.93	0.50
1:B:947:ASP:OD1	1:B:947:ASP:N	2.44	0.50
1:A:388:HIS:HB2	1:A:398:MET:HE1	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:208:PRO:HA	1:A:211:GLN:HG2	1.94	0.49
1:B:325:ARG:NE	1:B:331:ASP:OD1	2.44	0.49
1:B:652:ASN:HB2	1:B:654:LEU:HD21	1.94	0.49
1:B:656:PRO:HD3	1:B:846:MET:HE2	1.94	0.49
1:B:845:GLU:O	1:B:849:ILE:HD12	2.12	0.49
1:B:1118:ILE:HD12	1:B:1118:ILE:H	1.77	0.49
1:A:907:CYS:HB2	1:A:946:VAL:CG2	2.43	0.49
1:B:295:LYS:NZ	1:B:296:PRO:O	2.46	0.49
1:B:956:PRO:HG3	1:B:984:PHE:HZ	1.77	0.49
1:B:1159:THR:OG1	1:B:1160:ILE:N	2.45	0.49
1:B:287:MET:HA	1:B:314:MET:O	2.13	0.49
1:B:690:PHE:CD2	1:B:739:LEU:HB3	2.47	0.49
1:B:695:ASP:OD1	1:B:696:GLU:N	2.45	0.49
1:B:726:LEU:O	1:B:731:GLN:NE2	2.41	0.49
1:B:207:ARG:HA	1:B:210:LEU:HB2	1.95	0.49
1:B:1180:LEU:O	1:B:1184:ILE:HG12	2.13	0.49
1:A:180:HIS:NE2	1:A:766:GLU:OE2	2.38	0.49
1:A:1103:THR:HG23	3:T:13:DG:O3'	2.13	0.49
1:A:288:ALA:HA	1:A:375:SER:O	2.13	0.49
1:A:313:TYR:CE1	1:A:320:PHE:HB2	2.48	0.49
1:B:653:ARG:HD2	1:B:923:TYR:CD1	2.47	0.49
1:B:1137:ILE:HG23	1:B:1141:ILE:HD11	1.94	0.49
1:A:710:PRO:O	1:A:711:ASN:HB3	2.13	0.48
1:B:452:ILE:HG23	1:B:476:SER:CB	2.42	0.48
1:A:379:GLY:O	1:A:384:TRP:HB2	2.13	0.48
1:A:298:LEU:N	1:A:457:GLU:OE1	2.46	0.48
1:A:645:TYR:CD2	5:A:1301:DTP:H2'1	2.48	0.48
1:B:1157:ILE:HG22	1:B:1158:ILE:HG13	1.94	0.48
1:A:1092:ILE:CD1	1:A:1109:VAL:HG22	2.38	0.48
1:A:834:VAL:HG21	1:A:846:MET:HE3	1.96	0.48
1:B:291:ILE:HG22	1:B:311:ILE:HG12	1.94	0.48
1:A:588:LEU:CD1	1:A:617:ILE:HG21	2.44	0.48
1:A:1093:ILE:HD11	1:A:1145:TYR:CG	2.48	0.48
1:B:444:GLN:NE2	1:B:450:ASN:OD1	2.36	0.48
1:B:1112:PHE:CE2	1:B:1137:ILE:HG13	2.48	0.48
1:B:834:VAL:HG11	1:B:846:MET:CE	2.43	0.48
1:A:292:GLU:HB3	1:A:459:MET:CE	2.44	0.48
1:A:649:MET:HA	1:A:654:LEU:HB2	1.95	0.48
1:A:864:LEU:O	1:A:868:VAL:HG12	2.13	0.48
1:B:709:PHE:O	1:B:721:LEU:HB2	2.14	0.48
1:B:982:LYS:HB3	2:C:10:DT:H5''	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:627:ASN:O	1:A:630:ARG:HD2	2.14	0.48
1:A:968:ARG:HA	1:A:982:LYS:O	2.14	0.48
1:A:1118:ILE:HD12	1:A:1118:ILE:H	1.79	0.48
1:B:207:ARG:N	1:B:208:PRO:HD2	2.29	0.48
1:B:278:LYS:HB3	1:B:278:LYS:HE3	1.67	0.48
1:B:296:PRO:HB2	1:B:299:LYS:HD3	1.95	0.48
1:B:454:LEU:HD22	1:B:459:MET:HG3	1.95	0.48
1:B:659:ILE:HA	1:B:761:ILE:O	2.14	0.48
1:B:694:MET:HA	1:B:697:TYR:CB	2.44	0.47
1:B:1092:ILE:HG21	1:B:1141:ILE:CD1	2.43	0.47
1:A:55:TYR:CZ	1:A:57:PRO:HA	2.49	0.47
1:B:309:MET:HE1	1:B:470:LEU:CD1	2.44	0.47
1:B:446:LYS:O	1:B:488:TYR:OH	2.30	0.47
1:B:799:ASP:O	1:B:800:PRO:C	2.57	0.47
1:B:1046:ILE:HG22	1:B:1092:ILE:HD12	1.96	0.47
1:A:53:GLU:OE2	1:A:53:GLU:N	2.46	0.47
1:A:363:PHE:O	1:A:367:ARG:HG3	2.14	0.47
1:A:382:PHE:HD2	1:A:383:ASP:OD1	1.97	0.47
1:B:76:VAL:HA	1:B:266:LYS:HA	1.96	0.47
1:B:735:ILE:O	1:B:739:LEU:HD23	2.14	0.47
1:A:913:ARG:O	1:A:917:LYS:HD2	2.14	0.47
1:A:1116:ILE:H	1:A:1116:ILE:CD1	2.22	0.47
1:A:1049:ASN:O	1:A:1050:ARG:HG3	2.15	0.47
1:B:1078:GLY:C	1:B:1080:ASP:N	2.71	0.47
1:A:1134:ASP:O	1:A:1135:LEU:HD23	2.15	0.47
1:A:1034:GLY:C	1:A:1036:MET:H	2.23	0.47
1:B:309:MET:O	1:B:328:ILE:HD11	2.14	0.47
1:B:685:TRP:CE3	1:B:756:VAL:HG12	2.50	0.47
1:B:425:TRP:CZ3	1:B:426:LEU:HD23	2.49	0.47
1:B:458:LEU:C	1:B:461:PRO:HD2	2.39	0.47
1:B:690:PHE:HD2	1:B:739:LEU:HB3	1.80	0.47
1:B:788:ALA:O	1:B:792:LYS:HG3	2.14	0.47
1:B:864:LEU:O	1:B:868:VAL:HG12	2.15	0.47
1:B:909:MET:HG3	1:B:910:LEU:HD12	1.96	0.47
1:A:291:ILE:HG22	1:A:311:ILE:HG12	1.97	0.47
1:A:1034:GLY:HA3	1:A:1143:TRP:CH2	2.50	0.47
1:B:287:MET:O	1:B:374:ILE:HA	2.14	0.47
1:A:1052:MET:HB3	1:A:1052:MET:HE2	1.75	0.46
1:A:296:PRO:HD3	1:A:306:ASP:OD2	2.15	0.46
1:B:338:THR:HG22	1:B:340:LYS:O	2.15	0.46
1:B:1076:PHE:HA	1:B:1122:PHE:CE2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:501:PRO:HD2	1:B:518:MET:HB3	1.97	0.46
1:A:153:GLU:CG	1:A:167:LEU:HD21	2.45	0.46
1:B:291:ILE:HG13	1:B:291:ILE:O	2.15	0.46
1:B:1076:PHE:O	1:B:1076:PHE:CD1	2.68	0.46
1:A:354:ASP:OD1	1:A:356:VAL:HG12	2.16	0.46
1:A:438:GLY:O	1:A:442:VAL:HG23	2.16	0.46
1:A:627:ASN:HB2	1:A:630:ARG:HH11	1.79	0.46
1:A:998:PHE:CZ	1:A:1154:ILE:HG12	2.50	0.46
1:B:915:HIS:HD2	1:B:940:ASN:ND2	2.13	0.46
1:B:1046:ILE:HG23	1:B:1146:TYR:CE1	2.51	0.46
1:A:310:MET:CE	1:A:321:LEU:HD11	2.46	0.46
3:T:6:G:O2'	3:T:7:DA:H5'	2.15	0.46
1:B:552:THR:OG1	1:B:553:TYR:N	2.48	0.46
1:B:800:PRO:HA	1:B:806:ARG:HD2	1.98	0.46
1:B:965:ILE:HD12	1:B:965:ILE:HA	1.83	0.46
1:A:638:HIS:HB3	1:A:947:ASP:OD1	2.15	0.46
1:B:425:TRP:CE3	1:B:426:LEU:HD23	2.51	0.46
1:B:594:PHE:HA	1:B:597:GLU:CD	2.40	0.46
1:A:1031:ASP:OD2	1:A:1173:ARG:NH2	2.47	0.46
1:A:153:GLU:HG3	1:A:167:LEU:HD21	1.97	0.46
1:A:731:GLN:O	1:A:735:ILE:HG13	2.16	0.46
1:A:365:HIS:O	1:A:368:ASP:N	2.47	0.46
1:A:500:ILE:HD13	1:A:515:LEU:HD22	1.98	0.46
1:B:654:LEU:HB3	1:B:846:MET:SD	2.56	0.46
1:B:691:PRO:HB2	1:B:744:ARG:HG3	1.99	0.46
1:B:920:ASN:ND2	1:B:923:TYR:HB2	2.31	0.46
1:A:399:PHE:CD1	1:A:403:GLY:HA2	2.51	0.45
1:A:953:MET:HE2	1:A:955:LEU:HD11	1.97	0.45
1:A:1176:HIS:O	1:A:1181:LYS:HE3	2.15	0.45
1:B:384:TRP:N	1:B:385:PRO:CD	2.78	0.45
1:A:291:ILE:HG12	1:A:383:ASP:HB3	1.98	0.45
1:A:384:TRP:N	1:A:385:PRO:CD	2.79	0.45
1:B:260:ARG:HB2	1:B:263:LYS:HD2	1.98	0.45
1:B:337:TYR:CE2	1:B:476:SER:HA	2.52	0.45
1:B:485:TYR:CE2	1:B:490:HIS:HB2	2.51	0.45
1:B:597:GLU:HG3	1:B:597:GLU:H	1.48	0.45
1:B:744:ARG:HD2	1:B:744:ARG:C	2.41	0.45
1:A:588:LEU:N	1:A:589:PRO:CD	2.78	0.45
1:A:920:ASN:O	1:A:938:SER:HA	2.16	0.45
1:A:1159:THR:OG1	1:A:1160:ILE:N	2.49	0.45
1:B:260:ARG:NH2	1:B:522:VAL:HG21	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:328:ILE:HG23	1:B:467:PRO:HB3	1.97	0.45
1:B:638:HIS:HB2	1:B:880:TRP:CZ3	2.51	0.45
1:A:923:TYR:O	1:A:937:HIS:N	2.50	0.45
1:B:310:MET:HE2	1:B:323:THR:HG22	1.96	0.45
1:B:566:PHE:CD1	1:B:566:PHE:N	2.84	0.45
1:B:367:ARG:O	1:B:370:ARG:NH1	2.49	0.45
1:B:1076:PHE:CD1	1:B:1076:PHE:C	2.94	0.45
1:B:1160:ILE:N	1:B:1161:PRO:HD2	2.32	0.45
1:A:310:MET:HE2	1:A:321:LEU:HD11	1.98	0.45
1:A:722:THR:HG22	1:A:725:GLU:HB2	1.98	0.45
1:A:1072:ARG:NH1	1:A:1106:ALA:O	2.49	0.45
1:B:452:ILE:CG1	1:B:473:TYR:HA	2.47	0.45
1:A:1056:LEU:HB3	1:A:1082:VAL:HG11	1.97	0.45
1:B:210:LEU:HD11	1:B:241:ASP:HA	1.99	0.45
1:A:295:LYS:NZ	1:A:299:LYS:H	2.14	0.45
1:A:893:PHE:HB2	1:A:901:LEU:HB2	1.99	0.45
1:A:1012:LEU:HD21	1:A:1016:TYR:HE2	1.82	0.45
1:B:968:ARG:HA	1:B:982:LYS:O	2.17	0.45
1:A:337:TYR:CZ	1:A:339:PRO:HG3	2.51	0.45
1:A:1013:GLU:CD	1:A:1013:GLU:H	2.24	0.45
1:A:157:LYS:HD3	1:A:157:LYS:C	2.41	0.44
1:A:679:ARG:HG2	1:A:681:LEU:CD1	2.45	0.44
1:B:893:PHE:HB2	1:B:901:LEU:HB2	1.99	0.44
1:A:1076:PHE:C	1:A:1076:PHE:CD1	2.94	0.44
1:B:236:LYS:HD2	1:B:237:HIS:N	2.32	0.44
1:A:433:PRO:HB3	2:P:9:DT:H5'	1.98	0.44
1:A:1160:ILE:N	1:A:1161:PRO:HD2	2.33	0.44
1:B:295:LYS:H	1:B:460:THR:CG2	2.30	0.44
1:B:454:LEU:HD22	1:B:459:MET:HG2	1.99	0.44
1:A:656:PRO:HD3	1:A:846:MET:HE2	2.00	0.44
1:A:1100:ALA:HB3	1:A:1105:ARG:HD3	1.99	0.44
1:A:293:THR:OG1	1:A:294:THR:N	2.50	0.44
1:A:308:ILE:N	1:A:355:GLU:OE2	2.45	0.44
1:A:680:LYS:O	1:A:681:LEU:HD12	2.18	0.44
1:B:90:GLU:OE1	1:B:90:GLU:N	2.50	0.44
1:B:329:SER:HB3	1:B:464:PHE:HA	1.99	0.44
1:B:337:TYR:HE2	1:B:476:SER:HA	1.81	0.44
1:B:918:PHE:O	1:B:940:ASN:ND2	2.51	0.44
1:A:145:ASP:OD1	1:A:147:SER:OG	2.35	0.44
1:A:907:CYS:HB2	1:A:946:VAL:HG21	2.00	0.44
1:A:1077:LEU:HB3	1:A:1081:MET:HE3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1134:ASP:C	1:A:1135:LEU:HD23	2.43	0.44
1:A:787:LEU:HD23	1:A:787:LEU:HA	1.74	0.44
1:A:1094:SER:HB3	1:A:1107:ILE:HD11	1.99	0.44
1:B:153:GLU:O	1:B:156:VAL:HG22	2.17	0.44
1:B:482:TYR:OH	1:B:486:MET:HE3	2.17	0.44
1:B:551:GLU:HA	1:B:687:GLY:HA2	2.00	0.44
1:B:1079:GLU:C	1:B:1081:MET:N	2.74	0.44
1:A:891:TYR:C	1:A:892:PHE:HD1	2.26	0.44
1:B:340:LYS:HB3	1:B:341:PRO:HD2	2.00	0.44
1:B:1041:ASP:O	1:B:1045:LEU:HD23	2.17	0.44
1:A:54:ARG:HA	1:A:130:LYS:HG3	1.99	0.44
1:A:982:LYS:HG2	2:P:10:DT:H5"	1.99	0.44
1:B:319:GLY:C	1:B:320:PHE:CD1	2.96	0.44
1:B:382:PHE:HD2	1:B:383:ASP:OD1	2.00	0.44
1:B:956:PRO:HB2	1:B:965:ILE:HG21	2.00	0.44
1:A:404:PHE:CE2	1:A:414:SER:HB3	2.53	0.43
1:A:563:ALA:HA	1:A:955:LEU:HB2	2.00	0.43
1:B:1112:PHE:CZ	1:B:1123:LEU:HD21	2.53	0.43
1:A:203:ARG:NH2	1:A:207:ARG:HH22	2.16	0.43
1:A:76:VAL:HG13	1:A:124:GLU:HG3	2.00	0.43
1:B:915:HIS:HE1	1:B:943:PHE:CZ	2.36	0.43
1:A:546:HIS:HB3	1:A:690:PHE:O	2.19	0.43
1:A:582:ASP:OD1	1:A:625:LYS:NZ	2.48	0.43
1:A:953:MET:HE3	1:A:969:TYR:CD2	2.54	0.43
1:B:343:TYR:HB3	1:B:483:TYR:CD2	2.52	0.43
1:B:584:LEU:O	1:B:588:LEU:N	2.51	0.43
1:B:613:ILE:O	1:B:617:ILE:HG13	2.19	0.43
1:B:677:CYS:O	1:B:763:CYS:HA	2.18	0.43
1:B:723:PHE:CE2	1:B:731:GLN:HB3	2.54	0.43
1:A:547:LEU:HD23	1:A:548:LEU:N	2.33	0.43
1:A:620:LYS:O	1:A:624:LEU:HD13	2.18	0.43
1:B:643:SER:O	1:B:647:ASN:HB2	2.19	0.43
1:B:654:LEU:O	1:B:771:VAL:HG22	2.19	0.43
1:B:862:ARG:HD2	1:B:866:GLU:CD	2.44	0.43
1:A:722:THR:HG22	1:A:725:GLU:OE2	2.18	0.43
1:A:1136:ASP:O	1:A:1139:THR:OG1	2.36	0.43
1:B:907:CYS:HB2	1:B:946:VAL:CG2	2.49	0.43
1:B:1027:LEU:HD12	1:B:1147:ARG:CZ	2.48	0.43
1:A:79:LEU:HD12	1:A:120:TYR:O	2.19	0.43
1:A:1046:ILE:HG22	1:A:1092:ILE:HG12	2.01	0.43
1:A:1097:PRO:HB2	1:A:1100:ALA:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:65:ASP:HB3	1:B:68:ASP:OD2	2.18	0.43
1:B:963:LYS:HD3	1:B:963:LYS:HA	1.79	0.43
1:A:792:LYS:HA	1:A:813:ILE:HD11	2.00	0.43
1:B:641:VAL:HG23	1:B:644:MET:HB2	2.00	0.43
1:B:889:GLU:O	1:B:906:PRO:HD2	2.19	0.43
1:B:891:TYR:O	1:B:903:LEU:HB3	2.19	0.43
1:B:1064:SER:OG	1:B:1067:ILE:HG12	2.19	0.43
1:A:234:ASP:O	1:A:238:LEU:HD22	2.19	0.42
1:B:517:GLU:HB2	1:B:833:TYR:CE1	2.54	0.42
1:A:64:PHE:CD1	1:A:270:GLN:HB2	2.54	0.42
1:A:290:ASP:OD1	1:A:291:ILE:N	2.52	0.42
1:A:315:ILE:HD13	1:A:369:VAL:HG21	2.00	0.42
1:A:1024:ASN:OD1	1:A:1173:ARG:HD3	2.19	0.42
1:B:45:ASP:O	1:B:46:ILE:C	2.61	0.42
1:B:294:THR:HA	1:B:460:THR:HG22	2.01	0.42
1:B:362:PHE:C	1:B:366:ILE:HD12	2.44	0.42
1:B:296:PRO:HB2	1:B:299:LYS:HB2	2.01	0.42
1:B:989:ARG:NH2	2:C:8:DG:OP2	2.51	0.42
1:A:54:ARG:HG2	1:A:130:LYS:HD2	2.00	0.42
1:A:314:MET:HE3	1:A:314:MET:HB2	1.76	0.42
1:A:596:VAL:HG23	1:A:597:GLU:N	2.34	0.42
1:A:1090:LYS:C	1:A:1109:VAL:HG23	2.43	0.42
1:B:145:ASP:HB3	1:B:238:LEU:HD12	2.01	0.42
1:B:320:PHE:CE2	1:B:365:HIS:HE1	2.37	0.42
1:B:609:ASN:ND2	1:B:894:THR:HB	2.34	0.42
1:B:1056:LEU:HD12	1:B:1070:ALA:CB	2.48	0.42
1:A:287:MET:HE2	1:A:315:ILE:HD11	2.02	0.42
1:A:356:VAL:CG2	1:A:394:HIS:HB3	2.40	0.42
1:A:700:ILE:O	1:A:703:ALA:HB3	2.20	0.42
1:A:951:LYS:HB2	1:A:974:GLU:HA	2.01	0.42
1:A:1114:ALA:O	1:A:1119:LYS:NZ	2.53	0.42
1:A:267:VAL:HG22	1:A:272:PHE:CE2	2.54	0.42
1:A:296:PRO:HB2	1:A:299:LYS:CB	2.49	0.42
1:A:485:TYR:CZ	1:A:490:HIS:HB2	2.55	0.42
1:A:702:ARG:O	1:A:703:ALA:C	2.62	0.42
1:A:261:VAL:HB	1:A:497:CYS:HB3	2.00	0.42
1:A:745:LYS:HA	1:A:745:LYS:HD3	1.74	0.42
1:B:1068:THR:HA	1:B:1071:ARG:HG2	2.00	0.42
1:A:123:ASP:OD1	1:A:127:GLY:N	2.46	0.42
1:A:1072:ARG:HB3	1:A:1126:TRP:CZ2	2.55	0.42
1:B:46:ILE:O	1:B:49:MET:HB3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:172:LYS:O	1:B:185:GLN:HB2	2.20	0.42
1:B:694:MET:O	1:B:698:ASN:N	2.51	0.42
1:B:744:ARG:HH21	1:B:747:TYR:CB	2.32	0.42
1:A:517:GLU:HB2	1:A:833:TYR:CE1	2.55	0.42
1:A:619:GLN:O	1:A:623:GLU:HG2	2.20	0.42
1:A:696:GLU:H	1:A:696:GLU:CD	2.27	0.42
1:A:1118:ILE:HG23	1:A:1122:PHE:HE1	1.85	0.42
1:B:340:LYS:HD2	1:B:449:TYR:HB3	2.02	0.42
1:B:1094:SER:HB3	1:B:1107:ILE:CD1	2.50	0.42
1:A:310:MET:HE3	1:A:310:MET:HB2	1.69	0.42
1:B:293:THR:OG1	1:B:294:THR:N	2.53	0.42
1:A:207:ARG:O	1:A:211:GLN:N	2.53	0.41
1:A:373:VAL:HG11	1:A:485:TYR:CZ	2.55	0.41
1:A:548:LEU:HD23	1:A:548:LEU:HA	1.91	0.41
1:B:761:ILE:O	1:B:761:ILE:HG13	2.20	0.41
1:A:466:LYS:O	1:A:467:PRO:C	2.63	0.41
1:B:1001:ASP:O	1:B:1005:VAL:HG23	2.20	0.41
1:B:153:GLU:HG3	1:B:167:LEU:HD11	2.01	0.41
1:B:267:VAL:HG13	1:B:272:PHE:CE1	2.55	0.41
1:B:350:PHE:HD2	1:B:361:ARG:HG2	1.85	0.41
1:B:473:TYR:CD2	1:B:473:TYR:C	2.98	0.41
1:B:588:LEU:N	1:B:589:PRO:HD2	2.35	0.41
1:B:592:LEU:HD23	1:B:592:LEU:HA	1.88	0.41
1:B:594:PHE:CE1	1:B:599:GLU:HG3	2.56	0.41
1:B:597:GLU:HA	1:B:602:SER:O	2.19	0.41
1:B:744:ARG:CZ	1:B:746:VAL:HB	2.50	0.41
1:B:806:ARG:O	1:B:810:LYS:HG2	2.21	0.41
1:A:169:ILE:HD12	1:A:169:ILE:HG23	1.84	0.41
1:A:382:PHE:O	1:A:385:PRO:HD2	2.20	0.41
1:A:1137:ILE:HG22	1:A:1141:ILE:HD11	2.03	0.41
1:A:330:GLU:HG2	1:A:331:ASP:O	2.21	0.41
1:A:1050:ARG:HD3	1:A:1091:TYR:HE2	1.85	0.41
1:B:288:ALA:HA	1:B:375:SER:O	2.20	0.41
1:A:353:ASN:OD1	1:A:353:ASN:N	2.40	0.41
1:A:981:LEU:HD21	1:A:986:LEU:HD23	2.02	0.41
1:A:1072:ARG:HD3	1:A:1126:TRP:CE2	2.55	0.41
1:B:79:LEU:HD12	1:B:120:TYR:O	2.20	0.41
1:B:1116:ILE:HD13	1:B:1116:ILE:HA	1.91	0.41
2:C:1:DT:H2"	2:C:2:DA:C8	2.55	0.41
1:A:691:PRO:HG3	1:A:749:ARG:O	2.20	0.41
1:A:754:GLU:HG2	1:A:755:ILE:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:314:MET:HG2	1:B:319:GLY:CA	2.51	0.41
1:A:260:ARG:HB2	1:A:263:LYS:HD2	2.03	0.41
1:B:202:ALA:O	1:B:206:LEU:HG	2.21	0.41
1:B:907:CYS:HB2	1:B:946:VAL:HG23	2.02	0.41
1:A:50:MET:HG3	1:A:416:TYR:CZ	2.56	0.41
1:A:209:ILE:HD12	1:A:209:ILE:H	1.85	0.41
1:A:710:PRO:O	1:A:711:ASN:CB	2.68	0.41
1:A:723:PHE:O	1:A:726:LEU:HG	2.21	0.41
1:A:967:LYS:HE3	3:T:8:DA:N3	2.36	0.41
1:A:1155:GLN:HG2	1:A:1160:ILE:HD11	2.03	0.41
1:B:172:LYS:O	1:B:186:LYS:N	2.53	0.41
1:B:325:ARG:HB2	1:B:353:ASN:HA	2.02	0.41
1:A:335:PHE:CZ	1:A:475:VAL:HG21	2.55	0.41
1:A:1150:LEU:O	1:A:1153:ALA:HB3	2.21	0.41
1:B:594:PHE:O	1:B:595:SER:C	2.62	0.41
1:B:598:VAL:O	1:B:599:GLU:C	2.64	0.41
1:A:315:ILE:HG21	1:A:369:VAL:CG1	2.47	0.40
1:A:332:ILE:HG23	1:A:349:ILE:CG2	2.41	0.40
1:A:727:SER:O	1:A:728:TYR:C	2.63	0.40
1:A:1016:TYR:CZ	1:A:1162:ALA:HA	2.57	0.40
1:A:1154:ILE:HG23	1:A:1158:ILE:HD13	2.04	0.40
1:B:1097:PRO:HG3	1:B:1128:LEU:HB2	2.02	0.40
2:C:10:DT:C2'	2:C:11:DOC:H5'	2.39	0.40
1:A:549:GLU:N	1:A:688:GLU:O	2.53	0.40
1:A:858:ILE:HD12	1:A:858:ILE:HA	1.89	0.40
1:B:853:THR:O	1:B:857:ILE:HG13	2.21	0.40
1:A:356:VAL:HG23	1:A:394:HIS:CB	2.41	0.40
1:B:59:GLN:OE1	1:B:269:GLN:NE2	2.47	0.40
1:B:388:HIS:ND1	1:B:398:MET:HE2	2.36	0.40
1:B:1096:LYS:HA	1:B:1097:PRO:C	2.46	0.40
1:A:486:MET:HE3	1:A:486:MET:HB3	1.77	0.40
1:B:300:PHE:N	1:B:1081:MET:HE1	2.30	0.40
1:B:440:LYS:O	1:B:444:GLN:HG3	2.22	0.40
1:B:1054:LYS:HB3	1:B:1058:GLU:CD	2.47	0.40
1:A:534:LYS:HG2	1:A:838:GLY:O	2.21	0.40
1:B:633:LEU:HA	1:B:633:LEU:HD23	1.84	0.40
1:B:723:PHE:CZ	1:B:731:GLN:HA	2.57	0.40
1:B:732:VAL:CA	1:B:735:ILE:HD12	2.47	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	1095/1186 (92%)	1050 (96%)	45 (4%)	0	100	100
1	B	1092/1186 (92%)	1035 (95%)	57 (5%)	0	100	100
All	All	2187/2372 (92%)	2085 (95%)	102 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	973/1064 (91%)	935 (96%)	38 (4%)	28	55
1	B	945/1064 (89%)	918 (97%)	27 (3%)	37	65
All	All	1918/2128 (90%)	1853 (97%)	65 (3%)	32	60

All (65) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	LEU
1	A	38	LEU
1	A	41	SER
1	A	46	ILE
1	A	178	ASP
1	A	220	ARG
1	A	238	LEU
1	A	332	ILE

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Mol	Chain	Res	Type
1	A	333	GLU
1	A	353	ASN
1	A	354	ASP
1	A	356	VAL
1	A	369	VAL
1	A	372	THR
1	A	383	ASP
1	A	465	GLU
1	A	695	ASP
1	A	699	MET
1	A	711	ASN
1	A	725	GLU
1	A	726	LEU
1	A	741	GLU
1	A	744	ARG
1	A	745	LYS
1	A	746	VAL
1	A	749	ARG
1	A	751	LYS
1	A	890	THR
1	A	980	GLU
1	A	982	LYS
1	A	1002	ILE
1	A	1013	GLU
1	A	1076	PHE
1	A	1116	ILE
1	A	1119	LYS
1	A	1121	SER
1	A	1123	LEU
1	A	1125	ARG
1	B	42	LYS
1	B	68	ASP
1	B	154	GLU
1	B	157	LYS
1	B	172	LYS
1	B	269	GLN
1	B	270	GLN
1	B	278	LYS
1	B	342	GLU
1	B	452	ILE
1	B	537	ASP
1	B	571	LYS

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Mol	Chain	Res	Type
1	B	593	LYS
1	B	594	PHE
1	B	595	SER
1	B	597	GLU
1	B	721	LEU
1	B	732	VAL
1	B	796	SER
1	B	797	LYS
1	B	1036	MET
1	B	1037	LEU
1	B	1080	ASP
1	B	1132	LEU
1	B	1133	GLU
1	B	1136	ASP
1	B	1137	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	GLN
1	A	168	GLN
1	A	224	ASN
1	A	631	ASN
1	A	859	GLN
1	A	916	GLN
1	A	973	ASN
1	A	993	GLN
1	A	997	ASN
1	B	360	GLN
1	B	600	ASN
1	B	616	GLN
1	B	859	GLN
1	B	915	HIS
1	B	937	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	DOC	C	11	4,2	16,19,20	0.38	0	20,26,29	0.33	0
2	DOC	P	11	3,2	16,19,20	0.39	0	20,26,29	0.39	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	DOC	C	11	4,2	-	3/7/18/19	0/2/2/2
2	DOC	P	11	3,2	-	2/7/18/19	0/2/2/2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	P	11	DOC	C3'-C4'-C5'-O5'
2	P	11	DOC	O4'-C4'-C5'-O5'
2	C	11	DOC	C3'-C4'-C5'-O5'
2	C	11	DOC	O4'-C4'-C5'-O5'
2	C	11	DOC	C4'-C5'-O5'-P

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	11	DOC	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	P	11	DOC	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 4 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	$\# Z > 2$
5	DTP	B	1301	6	31,32,32	0.54	0	46,50,50	0.60	0
5	DTP	A	1301	6	31,32,32	0.54	0	46,50,50	0.58	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	DTP	B	1301	6	-	5/22/34/34	0/3/3/3
5	DTP	A	1301	6	-	4/22/34/34	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1301	DTP	PB-O3B-PG-O2G

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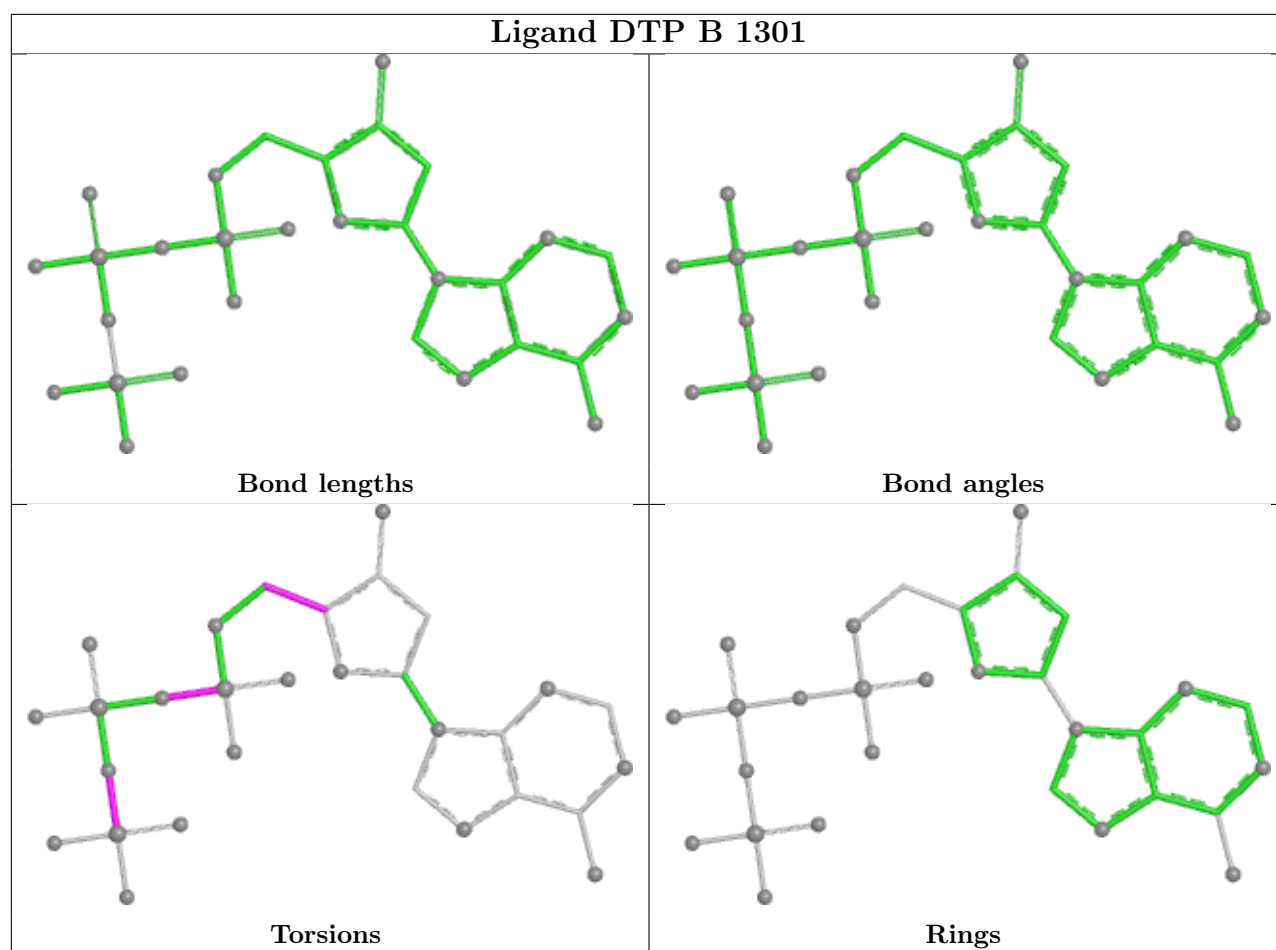
Mol	Chain	Res	Type	Atoms
5	A	1301	DTP	PB-O3B-PG-O3G
5	B	1301	DTP	PB-O3B-PG-O2G
5	B	1301	DTP	PB-O3B-PG-O3G
5	A	1301	DTP	O4'-C4'-C5'-O5'
5	B	1301	DTP	O4'-C4'-C5'-O5'
5	B	1301	DTP	PB-O3B-PG-O1G
5	A	1301	DTP	C3'-C4'-C5'-O5'
5	B	1301	DTP	PB-O3A-PA-O2A

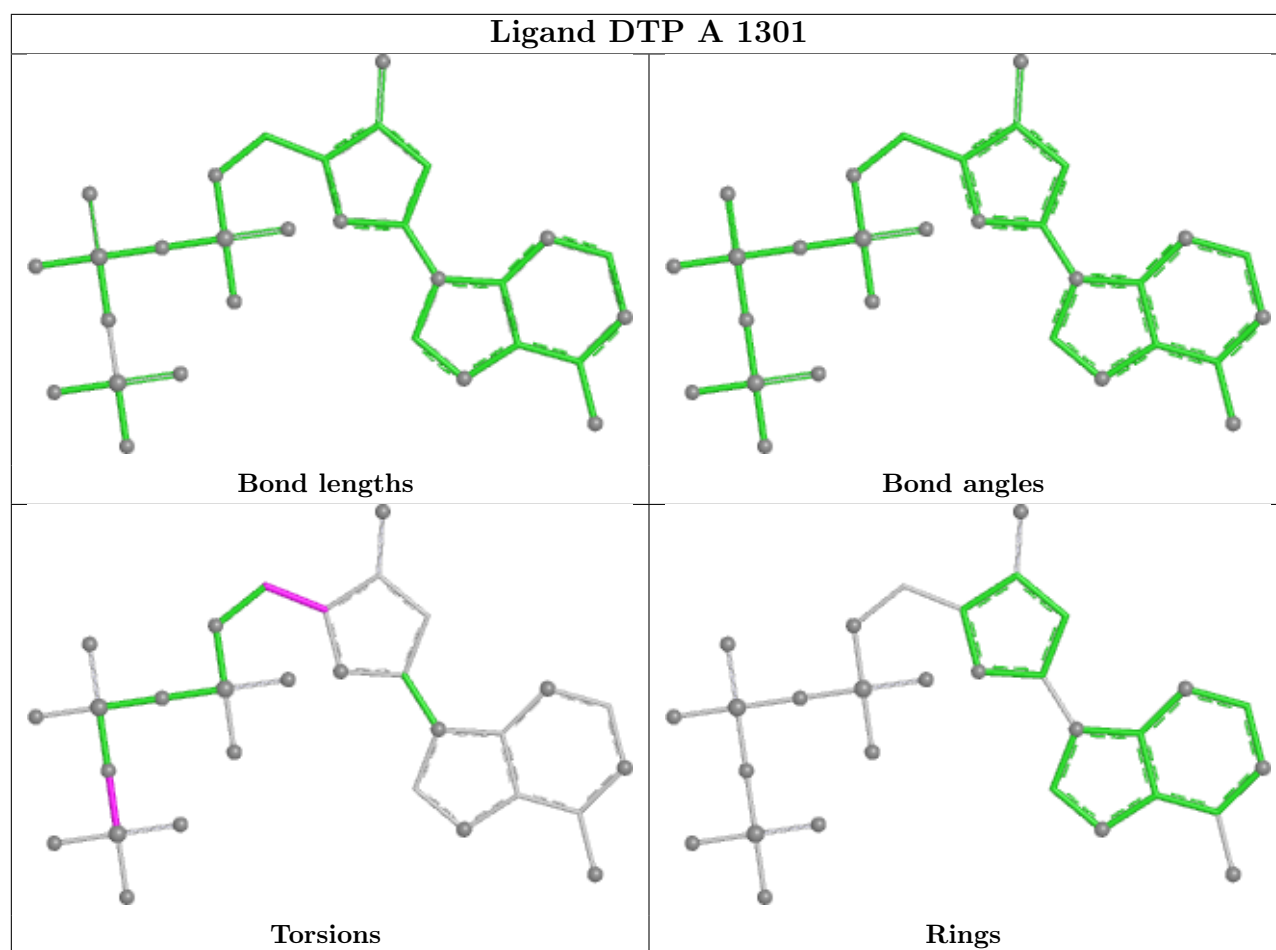
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	1301	DTP	1	0
5	A	1301	DTP	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

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	1105/1186 (93%)	0.22	33 (2%)	52	47	51, 94, 142, 194	0
1	B	1102/1186 (92%)	0.29	29 (2%)	57	51	54, 98, 155, 222	0
2	C	10/11 (90%)	0.04	0	100	100	77, 93, 128, 144	0
2	P	10/11 (90%)	-0.25	0	100	100	71, 85, 123, 141	0
3	T	15/16 (93%)	-0.29	0	100	100	62, 81, 127, 133	0
4	D	15/16 (93%)	-0.22	0	100	100	66, 82, 127, 130	0
All	All	2257/2426 (93%)	0.24	62 (2%)	56	50	51, 95, 149, 222	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	31	ALA	4.2
1	B	677	CYS	4.1
1	A	750	VAL	4.0
1	A	661	ALA	3.5
1	A	677	CYS	3.4
1	A	216	ASN	3.4
1	B	711	ASN	3.4
1	B	750	VAL	3.4
1	A	359	LEU	3.4
1	B	890	THR	3.2
1	A	610	PHE	3.1
1	A	742	TYR	3.1
1	B	1099	ASN	3.1
1	B	761	ILE	3.0
1	A	31	ALA	3.0
1	A	639	VAL	2.9
1	A	434	GLN	2.8
1	A	637	TYR	2.8
1	A	1046	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	62	GLY	2.8
1	A	381	PHE	2.8
1	A	64	PHE	2.8
1	B	978	LEU	2.8
1	A	1093	ILE	2.7
1	A	746	VAL	2.7
1	A	881	CYS	2.7
1	B	690	PHE	2.7
1	B	1047	CYS	2.6
1	A	218	VAL	2.6
1	A	298	LEU	2.6
1	A	225	VAL	2.6
1	B	886	SER	2.5
1	B	864	LEU	2.5
1	A	873	GLU	2.5
1	A	874	LEU	2.5
1	B	745	LYS	2.4
1	A	706	ASN	2.4
1	B	585	LEU	2.4
1	A	802	ASP	2.3
1	A	1042	LEU	2.3
1	B	881	CYS	2.3
1	A	879	ILE	2.3
1	B	749	ARG	2.3
1	B	1037	LEU	2.3
1	B	605	ASP	2.3
1	A	541	ARG	2.2
1	A	219	GLN	2.2
1	B	710	PRO	2.2
1	B	435	GLY	2.2
1	B	604	VAL	2.2
1	B	112	GLN	2.1
1	B	564	GLY	2.1
1	B	891	TYR	2.1
1	A	1116	ILE	2.1
1	B	549	GLU	2.1
1	A	635	LEU	2.1
1	B	747	TYR	2.1
1	A	272	PHE	2.1
1	B	892	PHE	2.1
1	A	1092	ILE	2.0
1	B	1128	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	279	ILE	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	DOC	P	11	18/19	0.94	0.10	45,55,71,72	0
2	DOC	C	11	18/19	0.96	0.08	45,62,80,80	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

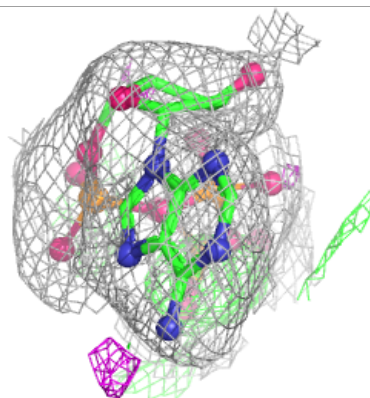
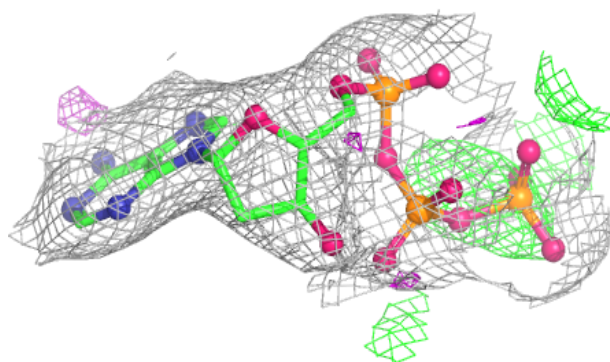
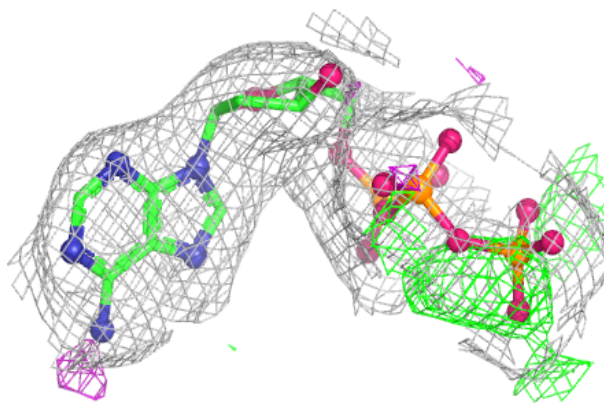
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	CA	A	1303	1/1	0.63	0.15	134,134,134,134	0
6	CA	B	1303	1/1	0.91	0.10	111,111,111,111	0
5	DTP	A	1301	30/30	0.94	0.09	45,60,69,85	0
5	DTP	B	1301	30/30	0.95	0.09	47,64,76,79	0
6	CA	A	1302	1/1	0.98	0.06	74,74,74,74	0
6	CA	B	1302	1/1	0.99	0.06	64,64,64,64	0

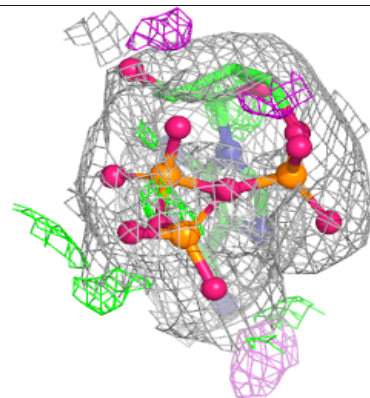
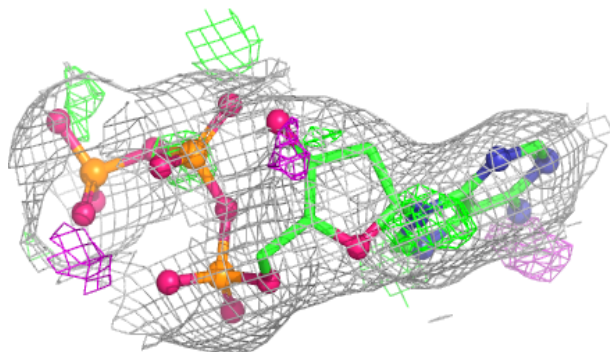
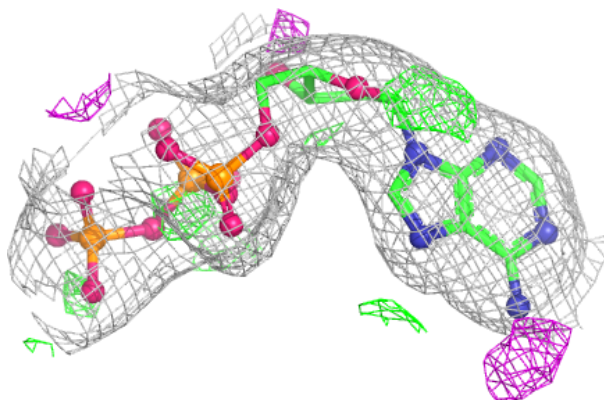
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around DTP A 1301:

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

**Electron density around DTP B 1301:**

$2mF_o-DF_c$ (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.