



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 27, 2020 – 02:06 PM BST

PDB ID : 6UUA
Title : E. coli sigma-S transcription initiation complex with a mismatching CTP
("Fresh" crystal soaked with CTP for 2 hours)
Authors : Zuo, Y.; De, S.; Steitz, T.A.
Deposited on : 2019-10-30
Resolution : 4.00 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13

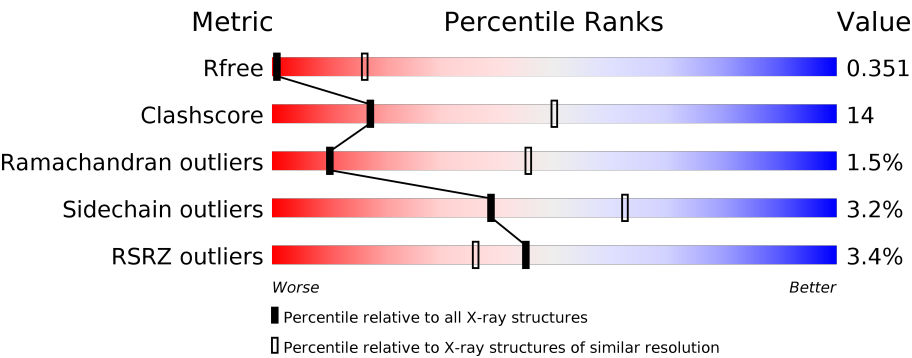
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.00 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.



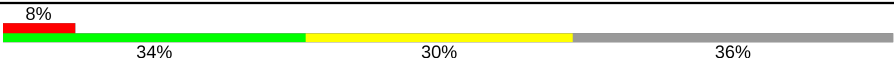

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1087 (4.30-3.70)
Clashscore	141614	1148 (4.30-3.70)
Ramachandran outliers	138981	1108 (4.30-3.70)
Sidechain outliers	138945	1099 (4.30-3.70)
RSRZ outliers	127900	1028 (4.34-3.66)

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 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	AAA	242	<div><div>4%</div><div><div></div><div>70%</div><div>23%</div><div>5%</div></div></div>
1	BBB	242	<div><div>3%</div><div><div></div><div>70%</div><div>22%</div><div>6%</div></div></div>
2	CCC	1342	<div><div>2%</div><div><div></div><div>77%</div><div>21%</div><div></div></div></div>
3	DDD	1407	<div><div>3%</div><div><div></div><div>70%</div><div>26%</div><div></div></div></div>
4	EEE	90	<div><div>2%</div><div><div></div><div>71%</div><div>17%</div><div>12%</div></div></div>
5	FFF	336	<div><div>6%</div><div><div></div><div>58%</div><div>23%</div><div>18%</div></div></div>

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Mol	Chain	Length	Quality of chain
6	111	50	
7	222	50	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
8	ZN	DDD	1502	-	-	X	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 28961 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-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	230	Total	C	N	O	S	0	0	0
			1787	1112	317	352	6			
1	BBB	228	Total	C	N	O	S	0	0	0
			1767	1100	312	349	6			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	-6	ALA	-	expression tag	UNP A0A377D9Q8
AAA	-5	HIS	-	expression tag	UNP A0A377D9Q8
AAA	-4	HIS	-	expression tag	UNP A0A377D9Q8
AAA	-3	HIS	-	expression tag	UNP A0A377D9Q8
AAA	-2	HIS	-	expression tag	UNP A0A377D9Q8
AAA	-1	HIS	-	expression tag	UNP A0A377D9Q8
AAA	0	HIS	-	expression tag	UNP A0A377D9Q8
BBB	-6	ALA	-	expression tag	UNP A0A377D9Q8
BBB	-5	HIS	-	expression tag	UNP A0A377D9Q8
BBB	-4	HIS	-	expression tag	UNP A0A377D9Q8
BBB	-3	HIS	-	expression tag	UNP A0A377D9Q8
BBB	-2	HIS	-	expression tag	UNP A0A377D9Q8
BBB	-1	HIS	-	expression tag	UNP A0A377D9Q8
BBB	0	HIS	-	expression tag	UNP A0A377D9Q8

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	CCC	1340	Total	C	N	O	S	0	0	0
			10570	6631	1841	2055	43			

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	DDD	1362	Total	C	N	O	S	0	0	0
			10568	6633	1887	1998	50			

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	EEE	79	Total	C	N	O	S	0	0	0
			627	382	118	126	1			

- Molecule 5 is a protein called RNA polymerase sigma factor RpoS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	FFF	277	Total	C	N	O	S	0	0	0
			2253	1411	415	423	4			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
FFF	2	GLY	SER	conflict	UNP P13445
FFF	33	GLU	GLN	conflict	UNP P13445
FFF	329	LEU	-	expression tag	UNP P13445
FFF	330	GLU	-	expression tag	UNP P13445
FFF	331	HIS	-	expression tag	UNP P13445
FFF	332	HIS	-	expression tag	UNP P13445
FFF	333	HIS	-	expression tag	UNP P13445
FFF	334	HIS	-	expression tag	UNP P13445
FFF	335	HIS	-	expression tag	UNP P13445
FFF	336	HIS	-	expression tag	UNP P13445

- Molecule 6 is a DNA chain called Synthetic DNA 50-MER (promoter non-template strand).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	111	32	Total	C	N	O	P	0	0	0
			661	314	121	194	32			

- Molecule 7 is a DNA chain called Synthetic DNA 50-MER (promoter template strand).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	222	34	Total	C	N	O	P	0	0	0
			695	332	127	203	33			

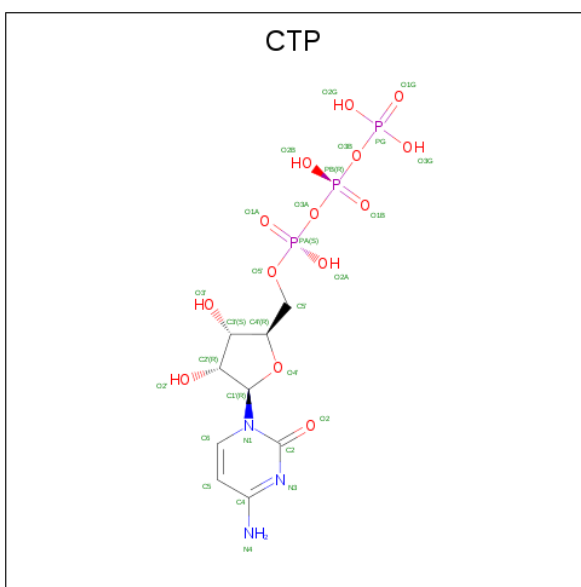
- Molecule 8 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	DDD	2	Total	Zn	0	0
			2	2		

- Molecule 9 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	DDD	2	Total	Mg	0	0
			2	2		

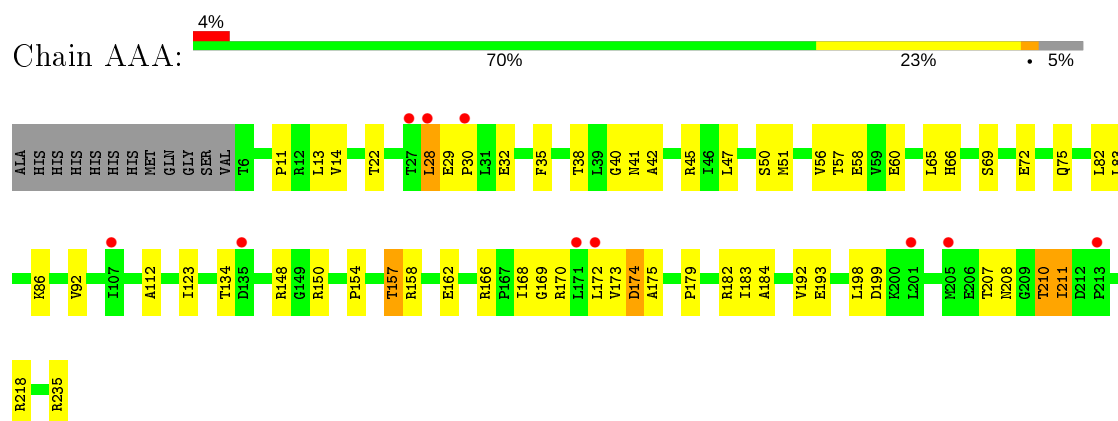
- Molecule 10 is CYTIDINE-5'-TRIPHOSPHATE (three-letter code: CTP) (formula: $C_9H_{16}N_3O_{14}P_3$).



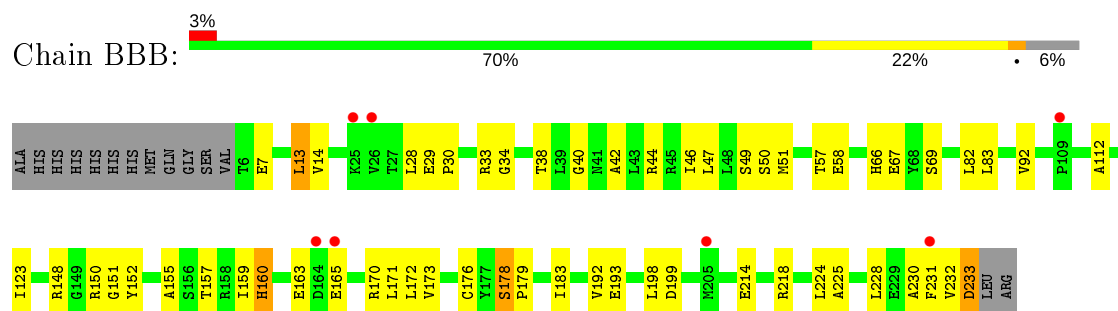
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

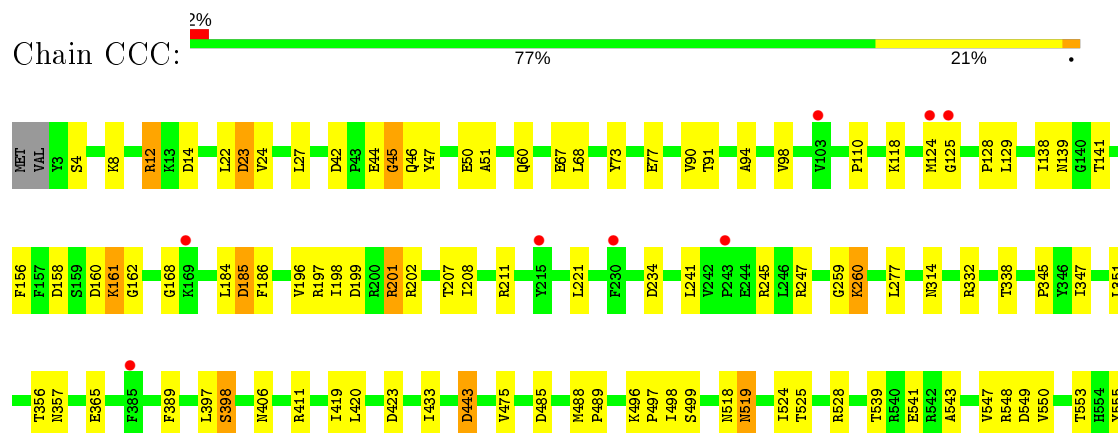
- Molecule 1: DNA-directed RNA polymerase subunit alpha

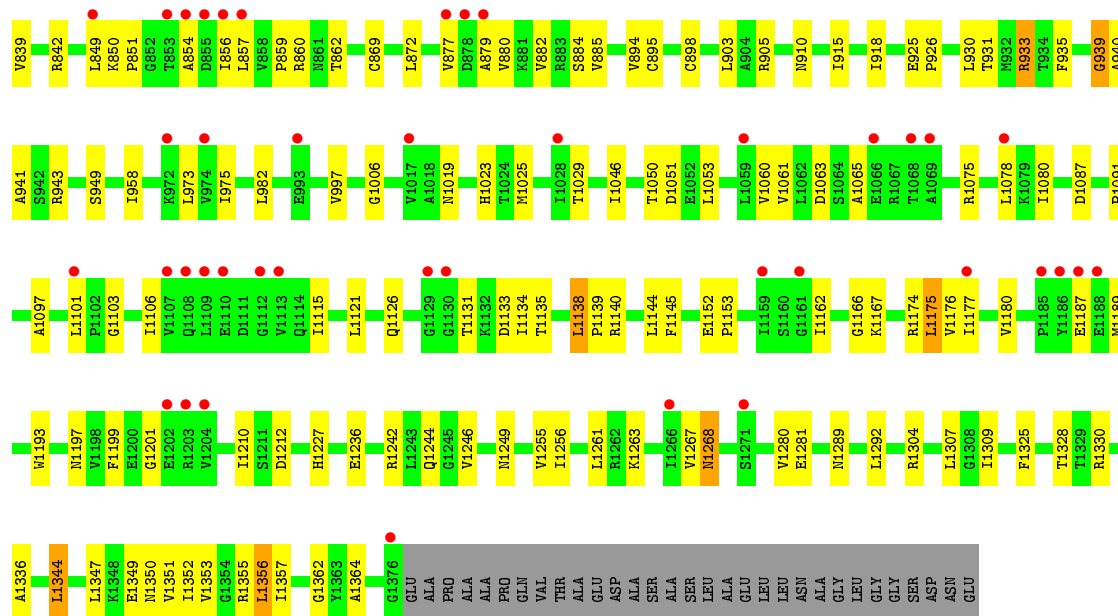


- Molecule 1: DNA-directed RNA polymerase subunit alpha

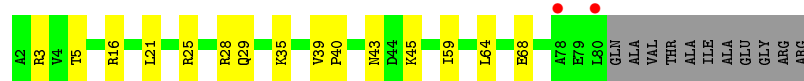
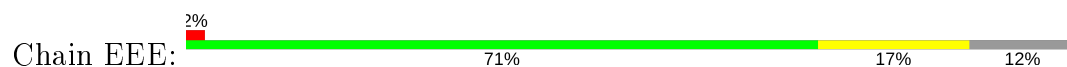


- Molecule 2: DNA-directed RNA polymerase subunit beta

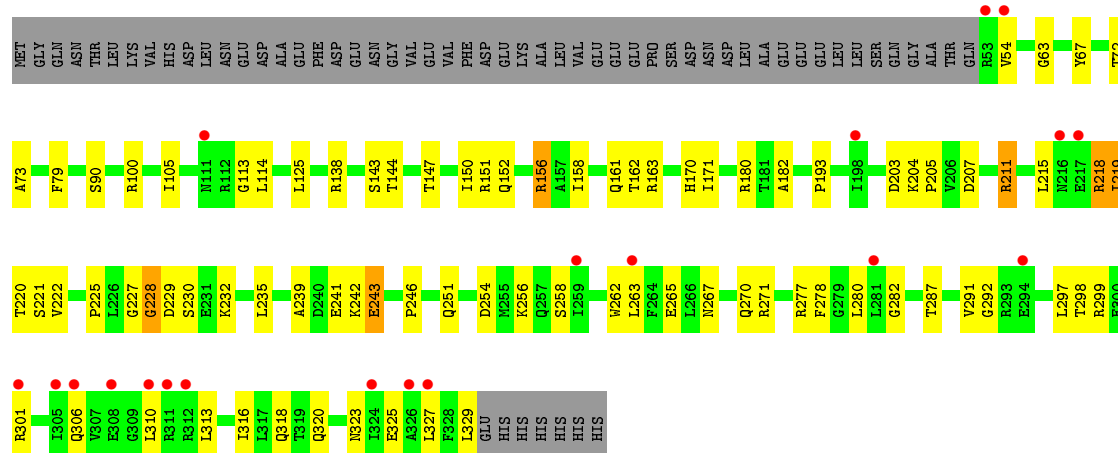




- Molecule 4: DNA-directed RNA polymerase subunit omega



- Molecule 5: RNA polymerase sigma factor RpoS



- Molecule 6: Synthetic DNA 50-MER (promoter non-template strand)





- Molecule 7: Synthetic DNA 50-MER (promoter template strand)



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	132.96Å 153.83Å 231.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.89 – 4.00 47.85 – 4.00	Depositor EDS
% Data completeness (in resolution range)	91.6 (47.89-4.00) 91.7 (47.85-4.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.05 (at 4.00Å)	Xtriage
Refinement program	REFMAC 5.8.0257	Depositor
R, R_{free}	0.302 , 0.365 0.297 , 0.351	Depositor DCC
R_{free} test set	1811 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å ²)	184.9	Xtriage
Anisotropy	0.914	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 243.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.34$, $\langle L^2 \rangle = 0.17$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	28961	wwPDB-VP
Average B, all atoms (Å ²)	321.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.85% 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: ZN, CTP, MG

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	AAA	0.65	0/1809	0.70	0/2450
1	BBB	0.65	0/1789	0.71	1/2425 (0.0%)
2	CCC	0.64	0/10739	0.73	1/14489 (0.0%)
3	DDD	0.64	0/10729	0.72	0/14487
4	EEE	0.63	0/629	0.71	0/847
5	FFF	0.65	0/2282	0.63	0/3076
6	111	0.28	0/741	0.65	0/1143
7	222	0.31	0/779	0.63	0/1201
All	All	0.63	0/29497	0.71	2/40118 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	CCC	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	CCC	891	GLY	C-N-CA	-5.59	107.73	121.70
1	BBB	178	SER	N-CA-CB	5.56	118.84	110.50

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	CCC	891	GLY	Peptide

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	AAA	1787	0	1813	70	0
1	BBB	1767	0	1789	68	0
2	CCC	10570	0	10582	264	0
3	DDD	10568	0	10782	433	0
4	EEE	627	0	634	9	0
5	FFF	2253	0	2298	82	1
6	111	661	0	362	21	0
7	222	695	0	385	16	0
8	DDD	2	0	0	2	0
9	DDD	2	0	0	0	0
10	DDD	29	0	12	6	0
All	All	28961	0	28657	795	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 14.

All (795) 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)
3:DDD:750:PRO:HA	3:DDD:781:LYS:CG	1.45	1.46
3:DDD:898:CYS:SG	8:DDD:1502:ZN:ZN	1.17	1.30
3:DDD:750:PRO:CA	3:DDD:781:LYS:HD2	1.61	1.30
3:DDD:750:PRO:HA	3:DDD:781:LYS:CD	1.65	1.27
3:DDD:750:PRO:O	3:DDD:781:LYS:HE3	1.25	1.25
3:DDD:750:PRO:HA	3:DDD:781:LYS:CB	1.69	1.21
3:DDD:690:ASN:ND2	3:DDD:738:ARG:NH1	1.91	1.19
3:DDD:525:MET:N	3:DDD:548:VAL:HG22	1.56	1.19
3:DDD:690:ASN:CG	3:DDD:738:ARG:HH12	1.45	1.18
3:DDD:751:ASP:C	3:DDD:781:LYS:HZ1	1.47	1.18
3:DDD:680:ASN:ND2	3:DDD:1023:HIS:ND1	1.94	1.15
2:CCC:891:GLY:O	2:CCC:893:THR:N	1.80	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AAA:82:LEU:HD22	1:AAA:173:VAL:HG21	1.30	1.14
3:DDD:821:MET:HA	3:DDD:880:VAL:O	1.44	1.14
3:DDD:821:MET:HE3	3:DDD:879:ALA:HB1	1.25	1.14
3:DDD:739:GLN:HG3	3:DDD:744:ARG:HA	1.16	1.13
3:DDD:680:ASN:ND2	3:DDD:1023:HIS:CG	2.15	1.13
3:DDD:690:ASN:ND2	3:DDD:738:ARG:HH12	1.47	1.11
3:DDD:748:ALA:O	3:DDD:778:GLY:HA2	1.48	1.11
2:CCC:549:ASP:CG	3:DDD:750:PRO:HB2	1.69	1.11
3:DDD:752:GLY:N	3:DDD:781:LYS:HZ2	1.50	1.10
3:DDD:751:ASP:C	3:DDD:781:LYS:NZ	2.03	1.10
3:DDD:752:GLY:N	3:DDD:781:LYS:NZ	2.00	1.07
3:DDD:750:PRO:O	3:DDD:781:LYS:CE	2.03	1.06
3:DDD:750:PRO:CA	3:DDD:781:LYS:HB2	1.86	1.05
2:CCC:563:THR:OG1	2:CCC:569:ILE:O	1.73	1.04
2:CCC:1106:ARG:CZ	10:DDD:1505:CTP:O2G	2.05	1.04
2:CCC:549:ASP:OD1	3:DDD:750:PRO:HB2	1.57	1.03
3:DDD:821:MET:CE	3:DDD:879:ALA:HB1	1.89	1.03
3:DDD:750:PRO:CA	3:DDD:781:LYS:CD	2.29	1.03
3:DDD:680:ASN:HD22	3:DDD:1023:HIS:HB3	1.20	1.02
2:CCC:549:ASP:CG	3:DDD:750:PRO:CB	2.27	1.01
3:DDD:749:LYS:O	3:DDD:781:LYS:HD2	1.60	1.01
1:BBB:50:SER:O	1:BBB:150:ARG:HD2	1.60	0.99
3:DDD:749:LYS:O	3:DDD:781:LYS:CD	2.10	0.99
2:CCC:1106:ARG:NH1	10:DDD:1505:CTP:O2G	1.96	0.98
3:DDD:750:PRO:C	3:DDD:781:LYS:HD2	1.82	0.98
3:DDD:750:PRO:CA	3:DDD:781:LYS:CG	2.40	0.98
1:BBB:176:CYS:SG	3:DDD:535:ARG:NH2	2.37	0.97
3:DDD:525:MET:H	3:DDD:548:VAL:HG22	1.19	0.97
2:CCC:549:ASP:CG	3:DDD:750:PRO:CG	2.32	0.96
1:AAA:235:ARG:HB2	1:BBB:13:LEU:HD23	1.46	0.96
3:DDD:849:LEU:HD12	3:DDD:850:LYS:O	1.67	0.95
3:DDD:525:MET:H	3:DDD:548:VAL:CG2	1.80	0.95
2:CCC:1242:LYS:HD2	3:DDD:465:GLN:HE22	1.32	0.94
3:DDD:739:GLN:HG3	3:DDD:744:ARG:CA	1.97	0.94
3:DDD:752:GLY:CA	3:DDD:781:LYS:NZ	2.31	0.94
2:CCC:1287:LEU:HD23	3:DDD:1357:ILE:HD11	1.49	0.94
3:DDD:750:PRO:HA	3:DDD:781:LYS:HB2	1.45	0.93
3:DDD:690:ASN:HD21	3:DDD:738:ARG:NH1	1.61	0.92
2:CCC:911:SER:O	2:CCC:913:VAL:N	2.03	0.91
5:FFF:220:THR:HG21	7:222:22:DA:N1	1.86	0.91
2:CCC:901:LEU:HD13	5:FFF:278:PHE:CE2	2.05	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:DDD:898:CYS:HG	8:DDD:1502:ZN:ZN	0.68	0.90
2:CCC:888:THR:O	2:CCC:914:LYS:N	2.04	0.90
3:DDD:750:PRO:C	3:DDD:781:LYS:CD	2.39	0.90
2:CCC:560:PRO:O	3:DDD:780:ARG:NH2	2.05	0.90
3:DDD:680:ASN:HD22	3:DDD:1023:HIS:CB	1.85	0.89
2:CCC:549:ASP:OD2	3:DDD:750:PRO:HG2	1.71	0.89
2:CCC:890:LYS:HE3	2:CCC:893:THR:HG21	1.55	0.89
3:DDD:750:PRO:CA	3:DDD:781:LYS:CB	2.46	0.88
3:DDD:481:ARG:NH1	4:EEE:3:ARG:O	2.06	0.88
3:DDD:786:THR:OG1	3:DDD:935:PHE:HB3	1.71	0.88
3:DDD:739:GLN:HG2	3:DDD:744:ARG:HH11	1.39	0.87
1:AAA:45:ARG:NE	1:BBB:38:THR:OG1	2.07	0.87
3:DDD:750:PRO:CB	3:DDD:781:LYS:HB2	2.04	0.86
3:DDD:555:TYR:CD1	3:DDD:585:LYS:HD2	2.10	0.86
1:AAA:56:VAL:O	1:AAA:175:ALA:HB2	1.74	0.86
3:DDD:690:ASN:CG	3:DDD:738:ARG:NH1	2.25	0.86
3:DDD:822:MET:HE1	3:DDD:882:VAL:HG21	1.58	0.86
2:CCC:549:ASP:HB3	3:DDD:750:PRO:HG3	1.58	0.86
3:DDD:260:PHE:O	5:FFF:219:ILE:HG22	1.77	0.85
3:DDD:752:GLY:HA2	3:DDD:781:LYS:HZ3	1.39	0.84
3:DDD:615:LYS:HB2	3:DDD:616:PRO:HD3	1.60	0.84
3:DDD:260:PHE:C	5:FFF:219:ILE:HG22	1.98	0.84
1:BBB:82:LEU:HD22	1:BBB:173:VAL:CG2	2.07	0.83
3:DDD:820:ILE:N	3:DDD:882:VAL:O	2.10	0.83
3:DDD:739:GLN:NE2	3:DDD:744:ARG:O	2.11	0.83
1:AAA:82:LEU:HB3	1:AAA:173:VAL:HG11	1.59	0.83
2:CCC:891:GLY:O	2:CCC:892:GLU:C	2.17	0.83
1:AAA:182:ARG:NH1	2:CCC:1090:ASN:O	2.13	0.82
3:DDD:750:PRO:HA	3:DDD:781:LYS:HG3	1.60	0.82
3:DDD:750:PRO:C	3:DDD:781:LYS:CE	2.48	0.82
1:AAA:82:LEU:HD22	1:AAA:173:VAL:CG2	2.09	0.81
2:CCC:549:ASP:OD2	3:DDD:750:PRO:CG	2.29	0.81
3:DDD:832:LYS:HG3	3:DDD:1242:ARG:HD3	1.60	0.81
1:AAA:11:PRO:HG2	1:BBB:230:ALA:HB3	1.63	0.81
2:CCC:560:PRO:HB2	3:DDD:776:THR:HG21	1.63	0.81
3:DDD:739:GLN:CG	3:DDD:744:ARG:HA	2.08	0.81
2:CCC:549:ASP:OD2	3:DDD:750:PRO:HB2	1.81	0.81
2:CCC:1342:GLU:HA	3:DDD:18:ASP:HB2	1.63	0.80
3:DDD:690:ASN:HD21	3:DDD:738:ARG:HH11	1.26	0.80
3:DDD:750:PRO:HB3	3:DDD:781:LYS:HB2	1.62	0.80
2:CCC:901:LEU:HD11	5:FFF:310:LEU:HD21	1.64	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AAA:11:PRO:HG2	1:BBB:230:ALA:CB	2.13	0.78
3:DDD:555:TYR:CE1	3:DDD:585:LYS:HD2	2.19	0.78
3:DDD:749:LYS:O	3:DDD:781:LYS:HD3	1.83	0.78
3:DDD:849:LEU:CD1	3:DDD:850:LYS:O	2.30	0.78
2:CCC:1242:LYS:HD2	3:DDD:465:GLN:NE2	1.99	0.78
5:FFF:220:THR:CG2	7:222:22:DA:N1	2.48	0.76
1:AAA:92:VAL:O	1:AAA:148:ARG:NH2	2.18	0.76
2:CCC:550:VAL:HG21	3:DDD:776:THR:HG22	1.67	0.76
3:DDD:822:MET:CE	3:DDD:882:VAL:HG11	2.15	0.76
1:BBB:92:VAL:O	1:BBB:148:ARG:NH2	2.18	0.76
3:DDD:752:GLY:HA2	3:DDD:781:LYS:NZ	1.98	0.76
2:CCC:1284:ALA:HA	3:DDD:1357:ILE:HD12	1.67	0.76
3:DDD:749:LYS:C	3:DDD:781:LYS:HD2	2.06	0.76
3:DDD:680:ASN:ND2	3:DDD:1023:HIS:HB3	2.01	0.75
3:DDD:525:MET:CA	3:DDD:548:VAL:HG22	2.17	0.75
5:FFF:242:LYS:HG3	5:FFF:243:GLU:H	1.50	0.75
2:CCC:678:ARG:NH1	10:DDD:1505:CTP:O3G	2.19	0.75
2:CCC:898:GLU:HG2	5:FFF:256:LYS:HG2	1.69	0.74
2:CCC:1103:VAL:HB	2:CCC:1104:PRO:HD3	1.70	0.74
3:DDD:680:ASN:ND2	3:DDD:1023:HIS:CB	2.47	0.74
2:CCC:549:ASP:OD2	3:DDD:750:PRO:CB	2.35	0.74
3:DDD:925:GLU:HB3	3:DDD:926:PRO:HD3	1.70	0.74
1:AAA:38:THR:HG21	1:BBB:46:ILE:HD11	1.69	0.74
3:DDD:378:LYS:H	3:DDD:379:PRO:HD2	1.54	0.73
2:CCC:1308:ILE:HG23	3:DDD:380:PHE:CE1	2.23	0.73
3:DDD:1075:ARG:NH2	3:DDD:1193:TRP:CE3	2.57	0.73
2:CCC:550:VAL:HG22	3:DDD:780:ARG:CZ	2.19	0.72
2:CCC:549:ASP:OD1	3:DDD:750:PRO:CB	2.31	0.72
3:DDD:260:PHE:C	5:FFF:219:ILE:CG2	2.57	0.72
2:CCC:560:PRO:CB	3:DDD:776:THR:HG21	2.18	0.72
2:CCC:549:ASP:CB	3:DDD:750:PRO:HG3	2.18	0.72
1:AAA:218:ARG:HG3	1:BBB:233:ASP:HB2	1.71	0.71
1:BBB:82:LEU:HD22	1:BBB:173:VAL:HG21	1.72	0.71
4:EEE:25:ARG:NH2	4:EEE:68:GLU:OE1	2.23	0.71
3:DDD:821:MET:CE	3:DDD:879:ALA:CB	2.69	0.71
2:CCC:221:LEU:HD11	2:CCC:314:ASN:HB2	1.73	0.71
3:DDD:750:PRO:N	3:DDD:781:LYS:HD2	2.06	0.71
2:CCC:1287:LEU:HD23	3:DDD:1357:ILE:CD1	2.21	0.70
1:AAA:174:ASP:OD2	2:CCC:826:ASP:OD2	2.08	0.70
3:DDD:378:LYS:N	3:DDD:379:PRO:HD2	2.06	0.70
2:CCC:675:ASP:OD1	3:DDD:744:ARG:NH2	2.23	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:DDD:752:GLY:CA	3:DDD:781:LYS:HZ3	1.97	0.69
1:AAA:57:THR:HG23	1:AAA:158:ARG:CZ	2.22	0.69
5:FFF:262:TRP:HE1	5:FFF:320:GLN:HE22	1.39	0.69
3:DDD:822:MET:CE	3:DDD:882:VAL:HG21	2.22	0.69
1:AAA:158:ARG:HB3	1:AAA:172:LEU:HD21	1.75	0.69
3:DDD:747:MET:HE3	3:DDD:939:GLY:O	1.92	0.69
3:DDD:747:MET:SD	3:DDD:940:ALA:HB2	2.32	0.69
3:DDD:822:MET:HE2	3:DDD:882:VAL:HG11	1.75	0.69
2:CCC:549:ASP:CB	3:DDD:750:PRO:CG	2.71	0.68
2:CCC:118:LYS:NZ	2:CCC:485:ASP:O	2.27	0.68
2:CCC:528:ARG:NH2	2:CCC:576:SER:O	2.26	0.68
2:CCC:1314:GLN:HA	4:EEE:28:ARG:NH2	2.09	0.68
5:FFF:242:LYS:HG3	5:FFF:243:GLU:N	2.08	0.68
3:DDD:697:MET:SD	3:DDD:737:ILE:HG22	2.34	0.68
3:DDD:748:ALA:O	3:DDD:778:GLY:CA	2.37	0.68
3:DDD:849:LEU:HD12	3:DDD:850:LYS:N	2.09	0.68
2:CCC:1234:LYS:HE2	2:CCC:1238:LEU:HD21	1.76	0.68
3:DDD:555:TYR:CD1	3:DDD:585:LYS:CD	2.77	0.68
5:FFF:235:LEU:O	5:FFF:235:LEU:HD12	1.94	0.67
2:CCC:549:ASP:HB3	3:DDD:750:PRO:CG	2.23	0.67
5:FFF:138:ARG:NH1	6:111:37:DA:N7	2.42	0.67
1:BBB:66:HIS:C	1:BBB:171:LEU:HD21	2.14	0.67
1:AAA:218:ARG:CG	1:BBB:233:ASP:HB2	2.24	0.67
3:DDD:905:ARG:NH1	3:DDD:910:ASN:OD1	2.27	0.67
2:CCC:548:ARG:HB3	2:CCC:570:GLY:HA3	1.76	0.67
3:DDD:134:ASP:HB3	3:DDD:159:ILE:HD11	1.77	0.66
3:DDD:694:SER:HB2	3:DDD:738:ARG:NE	2.10	0.66
3:DDD:140:TYR:OH	3:DDD:312:ARG:HD2	1.94	0.66
5:FFF:218:ARG:HA	5:FFF:218:ARG:HE	1.61	0.66
3:DDD:508:LEU:HD12	3:DDD:508:LEU:O	1.95	0.66
3:DDD:836:ARG:HG3	3:DDD:869:CYS:HB3	1.78	0.66
1:BBB:82:LEU:HD22	1:BBB:173:VAL:HG22	1.79	0.65
2:CCC:821:ARG:HH11	2:CCC:1082:ILE:HD13	1.61	0.65
3:DDD:504:GLN:HE22	3:DDD:731:ARG:NH2	1.94	0.65
3:DDD:1140:ARG:NH1	3:DDD:1144:LEU:HD11	2.11	0.65
2:CCC:700:VAL:HG21	2:CCC:1114:GLU:HG3	1.78	0.65
2:CCC:1029:LEU:HG	2:CCC:1033:ARG:HD3	1.79	0.65
1:BBB:58:GLU:OE1	1:BBB:170:ARG:NE	2.30	0.65
5:FFF:241:GLU:HG3	5:FFF:242:LYS:N	2.11	0.65
3:DDD:555:TYR:CE1	3:DDD:585:LYS:CD	2.80	0.65
2:CCC:550:VAL:HG21	3:DDD:776:THR:CG2	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:DDD:738:ARG:O	3:DDD:743:MET:N	2.31	0.64
1:AAA:11:PRO:O	1:BBB:230:ALA:HB2	1.97	0.64
2:CCC:672:GLU:HG3	2:CCC:673:HIS:CD2	2.32	0.64
1:AAA:65:LEU:HB3	2:CCC:874:GLY:HA3	1.77	0.64
2:CCC:890:LYS:HE3	2:CCC:893:THR:CG2	2.28	0.64
3:DDD:739:GLN:HG2	3:DDD:744:ARG:NH1	2.11	0.64
2:CCC:576:SER:OG	2:CCC:659:GLN:O	2.15	0.64
3:DDD:518:VAL:HG23	3:DDD:716:GLN:NE2	2.12	0.64
1:AAA:45:ARG:NH2	1:BBB:34:GLY:O	2.24	0.63
2:CCC:887:VAL:HB	2:CCC:913:VAL:HG12	1.81	0.63
5:FFF:72:THR:HG22	5:FFF:73:ALA:H	1.63	0.63
3:DDD:820:ILE:O	3:DDD:882:VAL:HG22	1.99	0.63
3:DDD:839:VAL:HG13	3:DDD:882:VAL:HG11	1.80	0.63
3:DDD:1075:ARG:HD2	3:DDD:1193:TRP:HB3	1.81	0.63
2:CCC:547:VAL:HG22	6:111:49:DG:C6	2.33	0.62
5:FFF:156:ARG:NH2	6:111:34:DG:O6	2.32	0.62
3:DDD:746:LEU:O	3:DDD:940:ALA:HB1	1.99	0.62
3:DDD:809:VAL:CG2	3:DDD:915:ILE:HD11	2.30	0.62
3:DDD:832:LYS:CG	3:DDD:1242:ARG:HD3	2.26	0.62
2:CCC:397:LEU:O	2:CCC:398:SER:OG	2.10	0.62
2:CCC:1269:ARG:NH2	3:DDD:340:GLN:O	2.32	0.62
3:DDD:821:MET:CA	3:DDD:880:VAL:O	2.35	0.62
2:CCC:1269:ARG:HH22	3:DDD:340:GLN:HA	1.63	0.62
3:DDD:395:LYS:HD3	5:FFF:329:LEU:HD13	1.80	0.62
3:DDD:910:ASN:HD21	4:EEE:16:ARG:HD2	1.65	0.62
3:DDD:747:MET:CE	3:DDD:939:GLY:O	2.48	0.62
2:CCC:1269:ARG:HA	3:DDD:346:ARG:HA	1.82	0.61
1:AAA:29:GLU:HB2	1:AAA:30:PRO:HA	1.82	0.61
2:CCC:186:PHE:CD1	2:CCC:196:VAL:HG22	2.35	0.61
5:FFF:262:TRP:HE1	5:FFF:320:GLN:NE2	1.99	0.61
2:CCC:547:VAL:HG22	6:111:49:DG:N1	2.15	0.61
2:CCC:12:ARG:HG3	2:CCC:1181:PRO:HB2	1.82	0.61
3:DDD:935:PHE:CZ	3:DDD:1135:THR:OG1	2.53	0.61
2:CCC:46:GLN:HB2	2:CCC:51:ALA:HA	1.82	0.61
3:DDD:926:PRO:HB3	3:DDD:1246:VAL:HG13	1.82	0.61
2:CCC:1252:SER:HG	2:CCC:1257:GLN:N	1.98	0.61
2:CCC:259:GLY:O	2:CCC:260:LYS:HB2	2.01	0.61
1:BBB:29:GLU:HB2	1:BBB:30:PRO:HA	1.82	0.61
3:DDD:935:PHE:CE1	3:DDD:1135:THR:OG1	2.54	0.60
3:DDD:334:LYS:NZ	7:222:15:DT:OP2	2.31	0.60
1:AAA:72:GLU:OE2	2:CCC:726:TYR:OH	2.18	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:DDD:378:LYS:N	3:DDD:379:PRO:CD	2.65	0.60
5:FFF:114:LEU:HD21	5:FFF:161:GLN:HB2	1.82	0.60
1:BBB:44:ARG:HH12	3:DDD:538:ARG:HG2	1.67	0.60
3:DDD:614:LEU:O	3:DDD:617:THR:OG1	2.17	0.60
3:DDD:623:GLN:HA	3:DDD:623:GLN:HE21	1.67	0.60
2:CCC:804:PHE:O	2:CCC:1225:VAL:HG13	2.02	0.60
2:CCC:1123:GLY:HA3	2:CCC:1204:LEU:HD11	1.84	0.60
3:DDD:527:LEU:HB2	3:DDD:550:VAL:HG13	1.84	0.60
1:AAA:66:HIS:HB3	2:CCC:927:THR:HG21	1.84	0.60
2:CCC:992:LEU:HB3	2:CCC:993:PRO:HD2	1.84	0.60
3:DDD:1140:ARG:HH12	3:DDD:1144:LEU:HD11	1.66	0.60
2:CCC:812:PHE:HB3	3:DDD:357:VAL:HG11	1.84	0.60
3:DDD:22:ILE:HG22	3:DDD:1336:ALA:HA	1.84	0.59
3:DDD:1140:ARG:HH12	3:DDD:1236:GLU:HG3	1.66	0.59
2:CCC:901:LEU:HD13	5:FFF:278:PHE:CZ	2.37	0.59
1:BBB:225:ALA:HA	1:BBB:228:LEU:HD12	1.84	0.59
2:CCC:207:THR:HG21	2:CCC:351:LEU:HG	1.85	0.59
3:DDD:1267:VAL:O	3:DDD:1268:ASN:CB	2.51	0.59
3:DDD:702:GLN:O	3:DDD:718:SER:N	2.35	0.59
3:DDD:822:MET:HE2	3:DDD:882:VAL:CG1	2.32	0.59
2:CCC:1318:GLY:O	2:CCC:1319:MET:HB2	2.02	0.59
2:CCC:560:PRO:HB2	3:DDD:776:THR:CG2	2.33	0.59
3:DDD:694:SER:HB2	3:DDD:738:ARG:CZ	2.33	0.59
3:DDD:739:GLN:O	3:DDD:762:ASN:HB2	2.03	0.59
2:CCC:638:SER:O	2:CCC:641:GLU:N	2.36	0.58
3:DDD:332:LYS:HA	3:DDD:1328:THR:HG21	1.83	0.58
1:AAA:41:ASN:ND2	2:CCC:1217:THR:O	2.36	0.58
2:CCC:525:THR:HG21	2:CCC:687:ARG:CD	2.32	0.58
2:CCC:873:ILE:HG13	2:CCC:944:ARG:NH2	2.19	0.58
3:DDD:1263:LYS:HB2	3:DDD:1307:LEU:HD11	1.85	0.58
3:DDD:425:ARG:HH22	10:DDD:1505:CTP:H4'	1.69	0.58
2:CCC:1313:HIS:CE1	3:DDD:380:PHE:HE1	2.22	0.58
2:CCC:1145:ILE:HG22	2:CCC:1161:LEU:HD11	1.86	0.58
2:CCC:868:SER:HB3	2:CCC:942:ASP:HB3	1.85	0.58
5:FFF:218:ARG:HA	5:FFF:218:ARG:NE	2.18	0.58
2:CCC:1107:MET:HB3	3:DDD:763:PHE:CE2	2.39	0.58
2:CCC:1077:SER:HA	3:DDD:356:THR:OG1	2.04	0.58
3:DDD:680:ASN:CG	3:DDD:1023:HIS:CG	2.76	0.57
3:DDD:690:ASN:OD1	3:DDD:738:ARG:NH1	2.36	0.57
2:CCC:1120:ALA:HA	2:CCC:1204:LEU:HD12	1.86	0.57
2:CCC:564:PRO:HG2	2:CCC:568:ASN:O	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:DDD:751:ASP:C	3:DDD:781:LYS:HZ2	1.90	0.57
3:DDD:949:SER:HB3	3:DDD:1019:ASN:HD22	1.69	0.57
1:AAA:154:PRO:HG2	1:AAA:157:THR:HB	1.86	0.57
1:AAA:57:THR:HG23	1:AAA:158:ARG:NH2	2.20	0.57
1:AAA:75:GLN:HG2	2:CCC:727:VAL:HG11	1.86	0.57
3:DDD:1063:ASP:HB3	3:DDD:1103:GLY:HA3	1.86	0.57
3:DDD:122:SER:O	3:DDD:123:ARG:HB2	2.04	0.57
3:DDD:173:GLY:O	3:DDD:175:GLU:N	2.35	0.57
3:DDD:517:CYS:HB3	3:DDD:545:HIS:HB2	1.86	0.57
2:CCC:1296:ASP:O	2:CCC:1297:ASP:C	2.43	0.57
1:AAA:184:ALA:HB2	2:CCC:1091:GLY:HA3	1.87	0.57
2:CCC:1212:LEU:HD21	2:CCC:1227:VAL:HG21	1.87	0.57
2:CCC:882:ILE:HG12	2:CCC:919:ARG:HB3	1.87	0.57
3:DDD:702:GLN:HG3	3:DDD:723:TYR:OH	2.04	0.57
3:DDD:930:LEU:HB3	3:DDD:1134:ILE:HG13	1.87	0.57
1:BBB:67:GLU:HB3	1:BBB:171:LEU:HD22	1.86	0.56
3:DDD:331:ILE:O	3:DDD:331:ILE:HG22	2.06	0.56
3:DDD:301:GLU:HG3	3:DDD:312:ARG:NH2	2.19	0.56
5:FFF:227:GLY:O	5:FFF:229:ASP:N	2.38	0.56
3:DDD:1080:ILE:HB	3:DDD:1097:ALA:HB3	1.86	0.56
2:CCC:27:LEU:O	2:CCC:528:ARG:NH1	2.38	0.56
3:DDD:747:MET:CE	3:DDD:940:ALA:HB2	2.35	0.56
3:DDD:1261:LEU:HB3	3:DDD:1304:ARG:HD3	1.87	0.56
1:BBB:49:SER:O	1:BBB:151:GLY:HA3	2.06	0.56
2:CCC:911:SER:C	2:CCC:913:VAL:N	2.58	0.55
3:DDD:691:ASP:HA	3:DDD:738:ARG:NH2	2.20	0.55
3:DDD:736:GLN:HA	3:DDD:736:GLN:HE21	1.71	0.55
1:AAA:199:ASP:OD1	1:AAA:199:ASP:N	2.40	0.55
2:CCC:635:THR:HG22	2:CCC:644:LEU:HD23	1.87	0.55
2:CCC:660:VAL:HG11	3:DDD:769:VAL:HG13	1.89	0.55
1:BBB:49:SER:O	1:BBB:151:GLY:CA	2.54	0.55
3:DDD:1167:LYS:HB2	3:DDD:1174:ARG:HD2	1.88	0.55
3:DDD:351:GLY:O	3:DDD:468:VAL:N	2.23	0.55
3:DDD:895:CYS:SG	3:DDD:898:CYS:SG	3.03	0.55
2:CCC:1301:ARG:HG3	2:CCC:1302:THR:N	2.22	0.55
3:DDD:683:ILE:HG21	3:DDD:943:ARG:NH2	2.22	0.55
1:BBB:199:ASP:N	1:BBB:199:ASP:OD1	2.40	0.55
2:CCC:660:VAL:HG11	3:DDD:769:VAL:CG1	2.37	0.55
3:DDD:1347:LEU:HD22	3:DDD:1357:ILE:HG23	1.87	0.55
3:DDD:747:MET:HE1	3:DDD:940:ALA:HB2	1.88	0.55
5:FFF:232:LYS:HE2	7:222:19:DA:H62	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:FFF:218:ARG:HB2	7:222:23:DT:H73	1.88	0.55
3:DDD:321:LYS:O	3:DDD:321:LYS:HD2	2.06	0.55
5:FFF:72:THR:HG22	5:FFF:73:ALA:N	2.22	0.54
1:AAA:11:PRO:C	1:BBB:230:ALA:CB	2.75	0.54
3:DDD:518:VAL:O	3:DDD:519:ASN:C	2.44	0.54
2:CCC:821:ARG:NH1	2:CCC:1082:ILE:HD13	2.23	0.54
3:DDD:807:LEU:HD11	3:DDD:894:VAL:HG13	1.90	0.54
2:CCC:1313:HIS:CE1	3:DDD:380:PHE:CE1	2.95	0.54
5:FFF:143:SER:CB	6:111:41:DT:H72	2.38	0.54
3:DDD:301:GLU:HG3	3:DDD:312:ARG:HH22	1.71	0.54
2:CCC:68:LEU:HD12	2:CCC:475:VAL:HG13	1.89	0.54
3:DDD:235:GLU:OE2	3:DDD:235:GLU:N	2.36	0.54
2:CCC:211:ARG:NH1	2:CCC:357:ASN:O	2.41	0.54
3:DDD:820:ILE:O	3:DDD:882:VAL:N	2.32	0.54
2:CCC:198:ILE:O	2:CCC:201:ARG:HG3	2.08	0.54
3:DDD:93:THR:HG22	3:DDD:94:GLN:H	1.72	0.54
3:DDD:931:THR:O	3:DDD:931:THR:HG22	2.08	0.54
5:FFF:100:ARG:HB3	6:111:42:DG:H5"	1.90	0.54
2:CCC:1101:LEU:HD12	3:DDD:504:GLN:HG3	1.90	0.54
3:DDD:24:LEU:HD21	3:DDD:116:PHE:CZ	2.43	0.53
6:111:55:DC:H2"	6:111:56:DG:C8	2.43	0.53
2:CCC:68:LEU:HD12	2:CCC:475:VAL:CG1	2.39	0.53
2:CCC:797:GLY:HA3	2:CCC:1233:LEU:HD23	1.88	0.53
2:CCC:539:THR:O	2:CCC:543:ALA:N	2.41	0.53
1:BBB:152:TYR:CE2	3:DDD:536:LEU:HD21	2.44	0.53
2:CCC:549:ASP:CG	3:DDD:750:PRO:HG2	2.15	0.53
3:DDD:825:VAL:HG12	3:DDD:832:LYS:HB3	1.90	0.53
3:DDD:260:PHE:O	5:FFF:219:ILE:CG2	2.52	0.53
1:BBB:163:GLU:O	1:BBB:163:GLU:HG3	2.07	0.53
2:CCC:4:SER:O	2:CCC:8:LYS:HG3	2.09	0.53
2:CCC:1042:LEU:HD13	2:CCC:1046:VAL:HG12	1.91	0.53
2:CCC:168:GLY:O	3:DDD:1065:ALA:HB1	2.09	0.53
1:AAA:45:ARG:HE	1:BBB:38:THR:HG1	1.51	0.53
1:BBB:157:THR:O	1:BBB:157:THR:HG22	2.09	0.52
2:CCC:709:ALA:HB3	2:CCC:792:GLY:O	2.09	0.52
3:DDD:800:LEU:HD22	3:DDD:1256:ILE:HG12	1.90	0.52
2:CCC:1269:ARG:NH2	3:DDD:340:GLN:HA	2.24	0.52
3:DDD:646:ILE:HG12	3:DDD:741:ALA:O	2.09	0.52
5:FFF:152:GLN:HE21	5:FFF:156:ARG:HH11	1.57	0.52
3:DDD:119:SER:HA	3:DDD:311:ARG:HH21	1.73	0.52
3:DDD:807:LEU:HD22	3:DDD:1255:VAL:HG13	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:DDD:347:VAL:O	3:DDD:350:SER:OG	2.13	0.52
2:CCC:873:ILE:CG1	2:CCC:944:ARG:NH2	2.73	0.52
3:DDD:368:LEU:HD23	3:DDD:439:PRO:HB3	1.91	0.52
6:111:56:DG:O6	7:222:6:DG:O6	2.27	0.52
1:AAA:82:LEU:HB3	1:AAA:173:VAL:CG1	2.35	0.52
2:CCC:1184:THR:HG23	2:CCC:1189:GLY:HA3	1.92	0.52
3:DDD:525:MET:HB2	3:DDD:548:VAL:HG21	1.90	0.52
1:AAA:11:PRO:O	1:BBB:230:ALA:CB	2.57	0.52
3:DDD:368:LEU:HD12	3:DDD:369:PRO:HD2	1.92	0.52
1:AAA:150:ARG:HH12	1:BBB:7:GLU:HB2	1.73	0.52
2:CCC:548:ARG:CB	2:CCC:570:GLY:HA3	2.40	0.52
2:CCC:668:ILE:HD11	2:CCC:683:ALA:HB2	1.92	0.52
3:DDD:926:PRO:HB3	3:DDD:1246:VAL:CG1	2.39	0.52
3:DDD:746:LEU:H	3:DDD:746:LEU:HD12	1.75	0.52
3:DDD:134:ASP:CB	3:DDD:159:ILE:HD11	2.39	0.52
3:DDD:1267:VAL:O	3:DDD:1268:ASN:HB2	2.09	0.52
3:DDD:736:GLN:CA	3:DDD:736:GLN:HE21	2.23	0.52
5:FFF:263:LEU:HD11	5:FFF:280:LEU:HD23	1.91	0.52
5:FFF:292:GLY:HA2	5:FFF:297:LEU:H	1.74	0.52
2:CCC:1057:LYS:O	2:CCC:1057:LYS:HG2	2.08	0.52
2:CCC:519:ASN:HD21	2:CCC:796:LEU:HD22	1.75	0.52
3:DDD:799:ARG:HB3	3:DDD:1309:ILE:HG21	1.90	0.52
1:BBB:165:GLU:HG3	1:BBB:165:GLU:O	2.10	0.51
3:DDD:1140:ARG:NH2	3:DDD:1236:GLU:OE2	2.43	0.51
3:DDD:582:ILE:HG23	3:DDD:623:GLN:CB	2.40	0.51
3:DDD:821:MET:HE1	3:DDD:879:ALA:CB	2.38	0.51
3:DDD:504:GLN:HE22	3:DDD:731:ARG:HH21	1.58	0.51
3:DDD:518:VAL:O	3:DDD:520:ALA:N	2.43	0.51
3:DDD:62:PHE:CD1	3:DDD:247:PRO:HD3	2.45	0.51
1:AAA:60:GLU:HG3	1:AAA:169:GLY:O	2.11	0.51
1:BBB:46:ILE:HD11	1:BBB:224:LEU:HD13	1.92	0.51
2:CCC:389:PHE:O	2:CCC:419:ILE:HG23	2.11	0.51
2:CCC:576:SER:HB3	2:CCC:579:ALA:HB2	1.92	0.51
3:DDD:839:VAL:HG13	3:DDD:882:VAL:CG1	2.41	0.51
3:DDD:355:ILE:HG21	3:DDD:466:MET:HG3	1.93	0.51
3:DDD:915:ILE:O	3:DDD:918:ILE:N	2.44	0.51
4:EEE:29:GLN:HB3	4:EEE:35:LYS:HG3	1.93	0.51
2:CCC:1257:GLN:HB2	2:CCC:1258:PRO:HD2	1.92	0.51
2:CCC:1342:GLU:HA	3:DDD:18:ASP:CB	2.39	0.51
2:CCC:967:LEU:HD21	2:CCC:1021:LEU:HD22	1.93	0.51
2:CCC:94:ALA:HB2	2:CCC:129:LEU:HD11	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:DDD:941:ALA:HA	3:DDD:1131:THR:HG21	1.93	0.51
1:AAA:210:THR:HG22	1:AAA:211:ILE:N	2.26	0.51
1:BBB:47:LEU:HD13	1:BBB:183:ILE:HD12	1.92	0.51
2:CCC:160:ASP:O	2:CCC:162:GLY:N	2.39	0.51
3:DDD:120:LEU:HA	3:DDD:121:PRO:C	2.32	0.51
3:DDD:460:ASP:OD2	10:DDD:1505:CTP:O2A	2.28	0.51
1:AAA:11:PRO:C	1:BBB:230:ALA:HB2	2.31	0.50
2:CCC:73:TYR:HB2	2:CCC:98:VAL:HG22	1.93	0.50
3:DDD:739:GLN:HA	3:DDD:744:ARG:HA	1.93	0.50
2:CCC:676:ALA:HA	3:DDD:772:TYR:OH	2.12	0.50
5:FFF:287:THR:O	5:FFF:291:VAL:HG23	2.11	0.50
1:AAA:134:THR:HA	2:CCC:773:LEU:HD22	1.94	0.50
3:DDD:1347:LEU:HD22	3:DDD:1357:ILE:CG2	2.41	0.50
3:DDD:680:ASN:CG	3:DDD:1023:HIS:ND1	2.61	0.50
3:DDD:134:ASP:O	3:DDD:138:VAL:HG23	2.11	0.50
1:AAA:66:HIS:CE1	2:CCC:929:ILE:HG22	2.46	0.50
1:BBB:67:GLU:N	1:BBB:171:LEU:CD2	2.74	0.50
1:AAA:11:PRO:CG	1:BBB:230:ALA:CB	2.89	0.50
2:CCC:1210:ILE:HD12	2:CCC:1227:VAL:HB	1.93	0.50
3:DDD:789:LYS:HG3	3:DDD:1135:THR:HG23	1.93	0.50
3:DDD:157:GLN:HG2	3:DDD:188:LEU:HD21	1.93	0.50
3:DDD:1330:ARG:HH22	7:222:10:DC:H4'	1.77	0.49
2:CCC:241:LEU:HD23	2:CCC:277:LEU:HD21	1.93	0.49
2:CCC:338:THR:HG23	2:CCC:345:PRO:HG3	1.93	0.49
3:DDD:1166:GLY:HA3	3:DDD:1176:VAL:HG23	1.92	0.49
3:DDD:1140:ARG:NH1	3:DDD:1236:GLU:HG3	2.27	0.49
3:DDD:1197:ASN:N	3:DDD:1210:ILE:O	2.45	0.49
3:DDD:490:ILE:HD11	3:DDD:614:LEU:HD13	1.93	0.49
3:DDD:282:LEU:HD21	5:FFF:125:LEU:HD21	1.94	0.49
2:CCC:525:THR:HG21	2:CCC:687:ARG:HD3	1.94	0.49
3:DDD:156:ARG:HH22	3:DDD:191:SER:HB2	1.78	0.49
2:CCC:1257:GLN:OE1	3:DDD:345:LYS:HG2	2.12	0.49
3:DDD:615:LYS:HB2	3:DDD:616:PRO:CD	2.39	0.49
3:DDD:770:LEU:O	3:DDD:773:PHE:N	2.44	0.49
1:AAA:47:LEU:HD13	1:AAA:183:ILE:HD12	1.94	0.49
2:CCC:758:ARG:HD3	2:CCC:835:GLU:HB2	1.95	0.49
2:CCC:620:ASN:HD21	3:DDD:768:ASN:HB2	1.78	0.49
3:DDD:926:PRO:CB	3:DDD:1246:VAL:CG1	2.90	0.49
2:CCC:1290:MET:HG2	2:CCC:1294:LYS:HD2	1.95	0.49
3:DDD:1212:ASP:OD1	3:DDD:1212:ASP:N	2.44	0.49
2:CCC:1294:LYS:HD3	3:DDD:347:VAL:HG13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CCC:347:ILE:HD11	2:CCC:433:ILE:HD11	1.94	0.49
3:DDD:935:PHE:HZ	3:DDD:1135:THR:HG1	1.58	0.49
3:DDD:793:SER:HB2	3:DDD:1138:LEU:HD12	1.95	0.49
3:DDD:525:MET:N	3:DDD:548:VAL:CG2	2.42	0.49
5:FFF:262:TRP:HB3	5:FFF:313:LEU:HD11	1.93	0.49
2:CCC:1261:GLY:HA2	7:222:18:DT:OP1	2.12	0.49
2:CCC:547:VAL:CG2	6:111:49:DG:C6	2.96	0.49
2:CCC:1247:SER:HB3	3:DDD:375:GLU:O	2.12	0.49
3:DDD:510:LEU:CD2	3:DDD:579:LEU:HD21	2.43	0.49
5:FFF:265:GLU:OE2	5:FFF:316:ILE:HG12	2.13	0.49
2:CCC:91:THR:HG21	2:CCC:128:PRO:HG3	1.95	0.49
2:CCC:557:ARG:NH1	2:CCC:611:GLU:OE1	2.46	0.49
1:BBB:50:SER:O	1:BBB:150:ARG:HB2	2.12	0.48
2:CCC:24:VAL:HG11	2:CCC:704:MET:SD	2.53	0.48
3:DDD:1080:ILE:HD12	3:DDD:1115:ILE:HD11	1.95	0.48
1:AAA:47:LEU:HD13	1:AAA:183:ILE:CD1	2.43	0.48
3:DDD:519:ASN:O	3:DDD:520:ALA:HB3	2.13	0.48
3:DDD:750:PRO:O	3:DDD:781:LYS:CD	2.52	0.48
2:CCC:906:PHE:CD1	5:FFF:327:LEU:HD12	2.48	0.48
1:AAA:38:THR:HG23	1:BBB:42:ALA:O	2.12	0.48
2:CCC:1308:ILE:HG23	3:DDD:380:PHE:CD1	2.47	0.48
2:CCC:1219:GLU:OE2	3:DDD:634:ARG:NH1	2.45	0.48
2:CCC:728:ASP:OD1	2:CCC:729:ALA:N	2.46	0.48
2:CCC:984:VAL:O	2:CCC:984:VAL:HG13	2.13	0.48
3:DDD:1256:ILE:N	3:DDD:1256:ILE:HD12	2.29	0.48
3:DDD:378:LYS:H	3:DDD:379:PRO:CD	2.21	0.48
3:DDD:525:MET:O	3:DDD:548:VAL:HG13	2.13	0.48
3:DDD:582:ILE:HG23	3:DDD:623:GLN:HB3	1.94	0.48
2:CCC:842:ASP:N	2:CCC:1045:GLY:O	2.46	0.48
2:CCC:1257:GLN:HB3	2:CCC:1296:ASP:OD1	2.13	0.48
2:CCC:1269:ARG:HH22	3:DDD:340:GLN:CA	2.26	0.48
2:CCC:1291:LEU:HD11	3:DDD:1351:VAL:HG13	1.96	0.48
2:CCC:878:THR:HG22	2:CCC:879:GLY:N	2.29	0.48
3:DDD:357:VAL:HG12	3:DDD:461:PHE:CE2	2.49	0.48
2:CCC:928:VAL:HG22	2:CCC:1054:LEU:HD23	1.96	0.48
3:DDD:701:LEU:O	3:DDD:718:SER:CB	2.62	0.48
3:DDD:260:PHE:HB2	5:FFF:219:ILE:CG2	2.44	0.48
2:CCC:1242:LYS:CD	3:DDD:465:GLN:HE22	2.17	0.48
3:DDD:683:ILE:HD13	3:DDD:943:ARG:HH21	1.80	0.47
3:DDD:701:LEU:O	3:DDD:718:SER:HB3	2.14	0.47
2:CCC:156:PHE:CE2	2:CCC:158:ASP:HB2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CCC:566:GLY:O	2:CCC:568:ASN:N	2.47	0.47
5:FFF:105:ILE:HG21	5:FFF:150:ILE:HG22	1.95	0.47
1:AAA:35:PHE:CE1	1:BBB:46:ILE:HG12	2.50	0.47
2:CCC:615:VAL:HA	2:CCC:638:SER:HB3	1.96	0.47
3:DDD:760:THR:OG1	3:DDD:771:GLN:NE2	2.47	0.47
3:DDD:872:LEU:HD22	3:DDD:877:VAL:HG21	1.96	0.47
2:CCC:185:ASP:HB2	2:CCC:197:ARG:HG3	1.97	0.47
3:DDD:380:PHE:HB3	3:DDD:415:VAL:HG11	1.96	0.47
3:DDD:738:ARG:O	3:DDD:742:GLY:C	2.52	0.47
5:FFF:211:ARG:HD3	5:FFF:211:ARG:HA	1.78	0.47
3:DDD:761:ALA:HB3	3:DDD:767:LEU:CD2	2.44	0.47
6:111:32:DA:C2	7:222:32:DA:C6	3.02	0.47
2:CCC:550:VAL:CG2	3:DDD:780:ARG:CZ	2.91	0.47
5:FFF:171:ILE:HG21	5:FFF:215:LEU:HD13	1.97	0.47
1:BBB:214:GLU:OE2	1:BBB:218:ARG:NH2	2.47	0.47
3:DDD:1075:ARG:CD	3:DDD:1193:TRP:HB3	2.43	0.47
3:DDD:713:GLU:HG2	3:DDD:714:GLU:N	2.29	0.47
2:CCC:1119:MET:HB2	2:CCC:1228:GLY:HA2	1.97	0.47
3:DDD:930:LEU:HD12	3:DDD:1134:ILE:HD11	1.95	0.47
3:DDD:709:ARG:O	3:DDD:710:ASP:CB	2.62	0.47
3:DDD:850:LYS:HB2	3:DDD:851:PRO:HD2	1.97	0.47
5:FFF:204:LYS:HB3	5:FFF:205:PRO:HD2	1.96	0.47
1:AAA:38:THR:HG21	1:BBB:46:ILE:CD1	2.43	0.47
3:DDD:823:THR:HB	3:DDD:824:PRO:HD2	1.95	0.47
1:AAA:192:VAL:CG2	1:AAA:198:LEU:HD12	2.44	0.47
3:DDD:1075:ARG:CZ	3:DDD:1193:TRP:HB3	2.45	0.47
3:DDD:451:PRO:HA	3:DDD:454:CYS:SG	2.55	0.47
3:DDD:747:MET:HA	3:DDD:940:ALA:HA	1.96	0.47
3:DDD:926:PRO:CB	3:DDD:1246:VAL:HG13	2.45	0.47
3:DDD:322:ARG:NH2	5:FFF:221:SER:HB3	2.29	0.47
3:DDD:645:VAL:HG23	3:DDD:645:VAL:O	2.15	0.47
2:CCC:488:MET:HB3	2:CCC:489:PRO:HD2	1.96	0.46
3:DDD:45:ASN:HB3	3:DDD:48:THR:OG1	2.15	0.46
3:DDD:495:ASN:O	3:DDD:497:GLU:N	2.37	0.46
1:AAA:112:ALA:HB1	1:AAA:123:ILE:HG21	1.96	0.46
2:CCC:1004:ASP:OD1	2:CCC:1004:ASP:N	2.48	0.46
3:DDD:708:ASN:HD22	3:DDD:714:GLU:HB3	1.80	0.46
3:DDD:1060:VAL:HG22	3:DDD:1106:ILE:HG12	1.96	0.46
3:DDD:430:HIS:CD2	3:DDD:432:LEU:HB2	2.50	0.46
2:CCC:208:ILE:HD11	2:CCC:365:GLU:HB2	1.97	0.46
3:DDD:1356:LEU:HD22	3:DDD:1362:GLY:HA3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BBB:83:LEU:HD21	3:DDD:526:VAL:CG2	2.45	0.46
3:DDD:747:MET:HA	3:DDD:940:ALA:CB	2.45	0.46
1:BBB:160:HIS:C	1:BBB:160:HIS:CD2	2.88	0.46
2:CCC:397:LEU:O	2:CCC:398:SER:CB	2.63	0.46
1:AAA:11:PRO:C	1:BBB:230:ALA:HB1	2.35	0.46
3:DDD:1350:ASN:HA	3:DDD:1353:VAL:HG22	1.98	0.46
3:DDD:320:ASN:O	3:DDD:322:ARG:N	2.49	0.46
3:DDD:435:GLN:HB2	3:DDD:457:TYR:OH	2.16	0.46
3:DDD:820:ILE:HG13	3:DDD:884:SER:HB3	1.98	0.46
1:BBB:47:LEU:HD13	1:BBB:183:ILE:CD1	2.46	0.46
2:CCC:1318:GLY:O	2:CCC:1319:MET:CB	2.64	0.46
2:CCC:635:THR:CG2	2:CCC:644:LEU:HD23	2.46	0.46
2:CCC:906:PHE:HZ	5:FFF:323:ASN:OD1	1.98	0.46
1:BBB:83:LEU:HD11	3:DDD:526:VAL:O	2.15	0.46
3:DDD:516:ASP:HB3	3:DDD:573:THR:HG21	1.97	0.46
2:CCC:808:ASN:HA	3:DDD:629:PHE:HB3	1.97	0.46
1:AAA:22:THR:OG1	1:AAA:207:THR:O	2.28	0.46
2:CCC:23:ASP:N	2:CCC:23:ASP:OD1	2.48	0.46
2:CCC:823:VAL:HG12	2:CCC:1059:ARG:NH2	2.31	0.46
2:CCC:1101:LEU:CD1	3:DDD:504:GLN:HG3	2.46	0.46
2:CCC:1307:ASN:HB3	2:CCC:1312:ASN:O	2.15	0.46
3:DDD:1152:GLU:N	3:DDD:1153:PRO:HD3	2.30	0.46
3:DDD:223:LEU:O	3:DDD:227:PHE:HB2	2.16	0.46
2:CCC:1101:LEU:O	3:DDD:731:ARG:HG2	2.16	0.46
2:CCC:800:MET:O	2:CCC:1229:TYR:HA	2.16	0.46
3:DDD:1029:THR:HG22	3:DDD:1121:LEU:HD11	1.98	0.46
5:FFF:225:PRO:HB3	5:FFF:230:SER:HA	1.98	0.46
1:AAA:35:PHE:HE1	1:BBB:46:ILE:HG12	1.81	0.45
1:AAA:83:LEU:HD12	2:CCC:694:ARG:NH2	2.30	0.45
1:AAA:56:VAL:O	1:AAA:175:ALA:CB	2.58	0.45
2:CCC:1085:MET:HE1	2:CCC:1097:VAL:HG23	1.98	0.45
2:CCC:890:LYS:HG2	2:CCC:893:THR:OG1	2.16	0.45
3:DDD:930:LEU:CB	3:DDD:1134:ILE:HG13	2.46	0.45
3:DDD:369:PRO:HB3	3:DDD:444:GLY:O	2.17	0.45
3:DDD:958:ILE:HG23	3:DDD:982:LEU:HD11	1.98	0.45
5:FFF:162:THR:HG23	5:FFF:163:ARG:HG3	1.98	0.45
1:AAA:158:ARG:HD2	1:AAA:172:LEU:HD21	1.98	0.45
3:DDD:535:ARG:O	3:DDD:539:SER:OG	2.25	0.45
5:FFF:227:GLY:O	5:FFF:228:GLY:C	2.53	0.45
1:BBB:82:LEU:HB3	1:BBB:173:VAL:CG1	2.46	0.45
3:DDD:809:VAL:HG22	3:DDD:915:ILE:HD11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:DDD:342:LEU:HD21	3:DDD:1352:ILE:HG23	1.99	0.45
3:DDD:849:LEU:C	3:DDD:849:LEU:HD12	2.36	0.45
1:BBB:33:ARG:NH2	2:CCC:1083:GLU:OE1	2.50	0.45
2:CCC:138:ILE:O	2:CCC:141:THR:OG1	2.32	0.45
5:FFF:144:THR:O	5:FFF:147:THR:OG1	2.34	0.45
5:FFF:207:ASP:O	5:FFF:211:ARG:HB2	2.17	0.45
5:FFF:292:GLY:HA2	5:FFF:297:LEU:N	2.32	0.45
3:DDD:394:ILE:N	5:FFF:254:ASP:OD2	2.49	0.45
3:DDD:519:ASN:HA	3:DDD:523:GLU:CG	2.47	0.45
3:DDD:644:MET:HG2	3:DDD:722:ILE:CD1	2.47	0.45
2:CCC:1210:ILE:HG22	2:CCC:1211:ARG:N	2.32	0.45
5:FFF:318:GLN:HA	5:FFF:323:ASN:HB2	1.99	0.45
5:FFF:79:PHE:O	5:FFF:90:SER:OG	2.29	0.45
1:AAA:58:GLU:OE1	1:AAA:170:ARG:HD3	2.17	0.45
2:CCC:555:TYR:OH	2:CCC:654:ASP:OD1	2.26	0.45
2:CCC:1286:THR:OG1	3:DDD:479:GLU:OE2	2.33	0.45
3:DDD:515:ARG:HH22	3:DDD:718:SER:C	2.20	0.45
3:DDD:516:ASP:CB	3:DDD:573:THR:HG21	2.47	0.45
3:DDD:517:CYS:SG	3:DDD:518:VAL:N	2.90	0.45
3:DDD:1364:ALA:HB3	4:EEE:21:LEU:HD11	1.99	0.45
5:FFF:267:ASN:HB2	5:FFF:270:GLN:HB2	1.99	0.45
3:DDD:57:PHE:O	3:DDD:98:ARG:NH2	2.50	0.44
1:BBB:44:ARG:HH12	3:DDD:538:ARG:CG	2.29	0.44
2:CCC:208:ILE:HG13	2:CCC:356:THR:HG21	1.98	0.44
2:CCC:44:GLU:O	2:CCC:46:GLN:N	2.50	0.44
2:CCC:686:GLN:HG2	2:CCC:796:LEU:HD13	1.99	0.44
3:DDD:1050:THR:HG22	3:DDD:1051:ASP:N	2.33	0.44
3:DDD:1289:ASN:HA	3:DDD:1292:LEU:HD12	1.99	0.44
1:AAA:42:ALA:HA	1:BBB:38:THR:HG23	2.00	0.44
2:CCC:1112:ILE:HG22	2:CCC:1116:HIS:CD2	2.52	0.44
2:CCC:811:ASN:HA	2:CCC:815:SER:O	2.17	0.44
3:DDD:1133:ASP:O	3:DDD:1244:GLN:NE2	2.51	0.44
3:DDD:320:ASN:O	3:DDD:321:LYS:HG3	2.17	0.44
3:DDD:355:ILE:HG21	3:DDD:466:MET:CG	2.47	0.44
3:DDD:48:THR:OG1	3:DDD:48:THR:O	2.35	0.44
3:DDD:508:LEU:HD12	3:DDD:508:LEU:C	2.38	0.44
3:DDD:644:MET:HG2	3:DDD:722:ILE:HD11	1.99	0.44
3:DDD:393:THR:HG22	5:FFF:258:SER:OG	2.18	0.44
6:111:47:DC:H1'	6:111:48:DA:C8	2.52	0.44
1:AAA:57:THR:HG22	1:AAA:58:GLU:HG3	1.99	0.44
1:BBB:178:SER:HA	1:BBB:179:PRO:HD2	1.77	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CCC:42:ASP:O	2:CCC:50:GLU:HG2	2.18	0.44
3:DDD:903:LEU:HD21	3:DDD:1249:ASN:HD22	1.81	0.44
5:FFF:204:LYS:HB3	5:FFF:205:PRO:CD	2.47	0.44
2:CCC:1252:SER:OG	2:CCC:1257:GLN:N	2.51	0.44
1:BBB:112:ALA:HB1	1:BBB:123:ILE:HG21	2.00	0.44
1:BBB:66:HIS:CA	1:BBB:171:LEU:HD21	2.48	0.44
2:CCC:443:ASP:N	2:CCC:443:ASP:OD1	2.51	0.44
2:CCC:556:GLY:HA3	2:CCC:589:THR:HG21	1.98	0.44
3:DDD:644:MET:CE	3:DDD:740:LEU:HB3	2.48	0.44
3:DDD:1364:ALA:HB3	4:EEE:21:LEU:CD1	2.48	0.44
4:EEE:59:ILE:HG23	4:EEE:64:LEU:HD11	2.00	0.44
1:AAA:158:ARG:HD2	1:AAA:172:LEU:HD11	1.99	0.44
2:CCC:1259:LEU:HD11	5:FFF:239:ALA:HB2	1.99	0.44
2:CCC:1268:GLN:OE1	3:DDD:352:ARG:HD2	2.18	0.44
2:CCC:245:ARG:C	2:CCC:247:ARG:H	2.22	0.43
3:DDD:1140:ARG:HG3	3:DDD:1140:ARG:HH11	1.83	0.43
3:DDD:314:ARG:HH11	3:DDD:314:ARG:HB2	1.83	0.43
3:DDD:832:LYS:CG	3:DDD:1242:ARG:CD	2.95	0.43
1:AAA:75:GLN:NE2	2:CCC:772:SER:HA	2.33	0.43
1:AAA:83:LEU:HD12	2:CCC:694:ARG:HH21	1.81	0.43
5:FFF:207:ASP:O	5:FFF:211:ARG:N	2.41	0.43
2:CCC:1293:VAL:HG11	2:CCC:1304:MET:HE3	1.99	0.43
2:CCC:139:ASN:ND2	7:222:22:DA:OP2	2.52	0.43
3:DDD:197:GLU:O	3:DDD:201:LEU:HG	2.18	0.43
3:DDD:592:VAL:O	3:DDD:592:VAL:HG22	2.17	0.43
3:DDD:786:THR:HG1	3:DDD:935:PHE:HB3	1.75	0.43
5:FFF:100:ARG:HB3	6:111:42:DG:C5'	2.49	0.43
1:AAA:179:PRO:HG3	1:AAA:211:ILE:HG13	2.01	0.43
2:CCC:557:ARG:HH12	2:CCC:611:GLU:CD	2.21	0.43
5:FFF:147:THR:O	5:FFF:151:ARG:HG2	2.18	0.43
5:FFF:158:ILE:O	5:FFF:162:THR:HB	2.19	0.43
5:FFF:182:ALA:HA	5:FFF:193:PRO:HG3	1.99	0.43
5:FFF:263:LEU:HD11	5:FFF:280:LEU:CD2	2.48	0.43
2:CCC:1294:LYS:O	3:DDD:348:ASP:OD2	2.37	0.43
2:CCC:905:ILE:HG12	5:FFF:310:LEU:HD22	1.99	0.43
3:DDD:1330:ARG:N	3:DDD:1330:ARG:HD2	2.33	0.43
3:DDD:27:PRO:HB3	3:DDD:240:THR:OG1	2.18	0.43
3:DDD:518:VAL:HG23	3:DDD:716:GLN:HE22	1.83	0.43
5:FFF:222:VAL:HG12	5:FFF:235:LEU:HB2	2.00	0.43
1:AAA:192:VAL:HG23	1:AAA:198:LEU:HD12	1.99	0.43
1:BBB:82:LEU:HB3	1:BBB:173:VAL:HG13	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:DDD:973:LEU:CD2	3:DDD:1006:GLY:HA2	2.49	0.43
3:DDD:849:LEU:CD1	3:DDD:850:LYS:N	2.77	0.43
5:FFF:170:HIS:CE1	6:111:31:DT:H72	2.53	0.43
1:BBB:192:VAL:HG23	1:BBB:198:LEU:HD12	1.99	0.43
3:DDD:500:ILE:HG22	3:DDD:500:ILE:O	2.18	0.43
2:CCC:1064:ASP:OD1	2:CCC:1239:VAL:HG12	2.18	0.43
2:CCC:60:GLN:HA	2:CCC:67:GLU:HA	2.00	0.43
3:DDD:282:LEU:HD21	5:FFF:125:LEU:CD2	2.49	0.43
2:CCC:1294:LYS:HB3	3:DDD:347:VAL:HG13	2.00	0.43
3:DDD:388:ARG:HB3	3:DDD:390:LEU:HD13	2.01	0.43
3:DDD:816:THR:HG22	3:DDD:818:GLU:H	1.83	0.43
4:EEE:39:VAL:HG13	4:EEE:40:PRO:HD2	2.01	0.43
2:CCC:1245:ALA:HB2	3:DDD:372:MET:HG3	2.00	0.43
2:CCC:518:ASN:O	2:CCC:519:ASN:HB2	2.19	0.43
3:DDD:1075:ARG:CZ	3:DDD:1193:TRP:CE3	3.01	0.43
3:DDD:1078:LEU:HG	3:DDD:1101:LEU:HD11	2.01	0.43
5:FFF:277:ARG:CD	5:FFF:306:GLN:HE21	2.31	0.43
5:FFF:313:LEU:HA	5:FFF:316:ILE:HD12	2.01	0.43
1:BBB:192:VAL:CG2	1:BBB:198:LEU:HD12	2.49	0.42
1:BBB:67:GLU:N	1:BBB:171:LEU:HD21	2.33	0.42
2:CCC:168:GLY:O	3:DDD:1065:ALA:CB	2.67	0.42
3:DDD:1280:VAL:HG12	3:DDD:1281:GLU:N	2.34	0.42
2:CCC:905:ILE:CG1	5:FFF:310:LEU:HD22	2.49	0.42
1:AAA:50:SER:O	1:AAA:150:ARG:HD2	2.19	0.42
1:AAA:32:GLU:CD	1:BBB:150:ARG:NH2	2.73	0.42
5:FFF:144:THR:HA	6:111:40:DA:N7	2.34	0.42
5:FFF:162:THR:HG23	5:FFF:163:ARG:N	2.34	0.42
2:CCC:1034:ARG:O	2:CCC:1038:GLN:N	2.45	0.42
2:CCC:389:PHE:HB3	2:CCC:420:LEU:HD12	2.01	0.42
3:DDD:935:PHE:HE1	3:DDD:1135:THR:OG1	2.02	0.42
3:DDD:1138:LEU:N	3:DDD:1139:PRO:CD	2.82	0.42
3:DDD:150:GLY:N	3:DDD:175:GLU:O	2.52	0.42
3:DDD:612:LEU:HB3	3:DDD:616:PRO:HG2	2.01	0.42
2:CCC:1146:GLN:HB2	2:CCC:1161:LEU:HD12	2.01	0.42
2:CCC:1066:MET:HG2	2:CCC:1234:LYS:HA	2.01	0.42
3:DDD:555:TYR:CE1	3:DDD:585:LYS:HD3	2.54	0.42
1:BBB:155:ALA:HB1	1:BBB:172:LEU:HD23	2.00	0.42
1:BBB:67:GLU:N	1:BBB:171:LEU:HD22	2.35	0.42
2:CCC:1105:SER:HB2	3:DDD:731:ARG:HD2	2.01	0.42
2:CCC:562:GLU:HG2	2:CCC:574:SER:HB2	2.02	0.42
2:CCC:757:THR:O	2:CCC:833:ILE:HD12	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:DDD:116:PHE:HB3	3:DDD:237:MET:SD	2.59	0.42
2:CCC:1308:ILE:CG2	3:DDD:380:PHE:CE1	3.00	0.42
3:DDD:821:MET:HA	3:DDD:880:VAL:C	2.31	0.42
3:DDD:822:MET:N	3:DDD:880:VAL:O	2.52	0.42
3:DDD:395:LYS:HG3	5:FFF:251:GLN:NE2	2.33	0.42
1:BBB:57:THR:HG22	1:BBB:58:GLU:HG3	2.01	0.42
2:CCC:882:ILE:HA	2:CCC:919:ARG:HA	2.00	0.42
3:DDD:322:ARG:HH21	5:FFF:221:SER:HB3	1.83	0.42
3:DDD:755:ILE:H	3:DDD:755:ILE:HD12	1.85	0.42
2:CCC:27:LEU:HB2	2:CCC:524:ILE:HD11	2.01	0.42
2:CCC:635:THR:CG2	2:CCC:644:LEU:CD2	2.98	0.42
2:CCC:802:VAL:HG12	2:CCC:803:ALA:N	2.35	0.42
3:DDD:450:HIS:HA	3:DDD:451:PRO:HD3	1.86	0.42
5:FFF:180:ARG:NH2	7:222:28:DG:OP2	2.53	0.42
6:111:32:DA:N3	7:222:32:DA:C2	2.87	0.42
1:AAA:86:LYS:HG2	1:AAA:174:ASP:O	2.20	0.42
2:CCC:1129:ASN:OD1	2:CCC:1177:ARG:NH2	2.52	0.42
2:CCC:1269:ARG:HH22	3:DDD:340:GLN:C	2.23	0.42
3:DDD:349:TYR:CE1	3:DDD:472:LEU:HD11	2.53	0.42
3:DDD:350:SER:HA	3:DDD:468:VAL:O	2.20	0.42
3:DDD:749:LYS:HB3	3:DDD:750:PRO:HD2	2.02	0.42
3:DDD:68:TYR:CZ	3:DDD:78:LEU:HD21	2.54	0.42
3:DDD:817:HIS:HB3	3:DDD:860:ARG:NH2	2.35	0.42
1:AAA:66:HIS:CE1	1:AAA:69:SER:HB3	2.55	0.42
2:CCC:800:MET:HE2	2:CCC:800:MET:HB3	1.96	0.42
1:BBB:47:LEU:HA	1:BBB:51:MET:HG2	2.01	0.42
2:CCC:1274:GLU:OE1	2:CCC:1274:GLU:N	2.51	0.42
2:CCC:887:VAL:HB	2:CCC:913:VAL:CG1	2.48	0.42
3:DDD:425:ARG:HH22	10:DDD:1505:CTP:C4'	2.31	0.42
6:111:47:DC:H4'	6:111:48:DA:OP1	2.20	0.41
1:AAA:134:THR:CA	2:CCC:773:LEU:HD22	2.50	0.41
3:DDD:571:ASP:N	3:DDD:571:ASP:OD1	2.50	0.41
3:DDD:530:PRO:HD3	3:DDD:552:ILE:CD1	2.50	0.41
3:DDD:51:PRO:HB3	3:DDD:57:PHE:O	2.20	0.41
3:DDD:732:GLY:HA2	3:DDD:736:GLN:HG3	2.02	0.41
3:DDD:733:SER:O	3:DDD:737:ILE:HG13	2.19	0.41
3:DDD:75:TYR:HB2	3:DDD:92:VAL:HG21	2.03	0.41
3:DDD:975:ILE:CD1	3:DDD:997:VAL:HG11	2.50	0.41
6:111:43:DT:H1'	6:111:44:DG:H5'	2.02	0.41
2:CCC:199:ASP:HB2	2:CCC:201:ARG:HG3	2.01	0.41
2:CCC:807:TRP:CD1	2:CCC:817:LEU:HD22	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:DDD:1175:LEU:HD12	3:DDD:1177:ILE:CG1	2.51	0.41
5:FFF:298:THR:HG21	5:FFF:301:ARG:HD3	2.01	0.41
3:DDD:259:ARG:NH2	7:222:22:DA:C8	2.88	0.41
1:AAA:174:ASP:OD1	1:AAA:174:ASP:N	2.53	0.41
1:BBB:192:VAL:O	1:BBB:193:GLU:C	2.58	0.41
2:CCC:625:GLU:O	2:CCC:626:GLU:HB3	2.20	0.41
2:CCC:805:MET:O	2:CCC:811:ASN:ND2	2.51	0.41
3:DDD:112:ALA:O	3:DDD:300:GLN:NE2	2.51	0.41
3:DDD:1344:LEU:HA	3:DDD:1349:GLU:OE1	2.20	0.41
3:DDD:168:ALA:O	3:DDD:173:GLY:N	2.53	0.41
3:DDD:859:PRO:HG2	3:DDD:862:THR:HG21	2.02	0.41
3:DDD:925:GLU:CB	3:DDD:926:PRO:HD3	2.46	0.41
1:AAA:192:VAL:O	1:AAA:193:GLU:C	2.59	0.41
1:BBB:66:HIS:CE1	1:BBB:69:SER:HB3	2.55	0.41
2:CCC:1337:ILE:HG23	2:CCC:1337:ILE:O	2.21	0.41
3:DDD:1256:ILE:H	3:DDD:1256:ILE:HD12	1.86	0.41
1:BBB:29:GLU:CB	1:BBB:30:PRO:HA	2.44	0.41
3:DDD:519:ASN:HA	3:DDD:523:GLU:HB2	2.02	0.41
6:111:55:DC:C2	7:222:8:DG:N2	2.89	0.41
2:CCC:1285:TYR:O	2:CCC:1289:GLU:N	2.46	0.41
2:CCC:22:LEU:HB3	2:CCC:655:VAL:HG11	2.01	0.41
2:CCC:706:ARG:HA	2:CCC:793:GLU:HA	2.02	0.41
3:DDD:1162:ILE:HG13	3:DDD:1180:VAL:HG13	2.03	0.41
3:DDD:93:THR:HG22	3:DDD:94:GLN:N	2.36	0.41
2:CCC:124:MET:HB2	2:CCC:498:ILE:HD12	2.02	0.41
3:DDD:1025:MET:HB2	3:DDD:1126:GLN:HE21	1.85	0.41
3:DDD:358:GLY:HA3	3:DDD:361:LEU:HD12	2.01	0.41
3:DDD:797:THR:O	3:DDD:801:VAL:HG23	2.21	0.41
2:CCC:259:GLY:O	2:CCC:260:LYS:CB	2.68	0.41
2:CCC:46:GLN:HB2	2:CCC:51:ALA:CA	2.49	0.41
2:CCC:125:GLY:HA2	2:CCC:499:SER:HB2	2.01	0.41
3:DDD:1087:ASP:OD1	3:DDD:1087:ASP:N	2.53	0.41
3:DDD:525:MET:HB2	3:DDD:548:VAL:CG2	2.50	0.41
3:DDD:644:MET:HE1	3:DDD:740:LEU:HB3	2.03	0.41
6:111:49:DG:H3'	6:111:50:DT:H5''	2.03	0.41
1:AAA:28:LEU:HG	1:BBB:231:PHE:CE1	2.56	0.41
2:CCC:989:LEU:HD13	2:CCC:1000:LEU:CD2	2.51	0.41
3:DDD:557:LYS:HA	3:DDD:563:LEU:HD23	2.02	0.41
3:DDD:694:SER:CB	3:DDD:738:ARG:NE	2.81	0.41
6:111:34:DG:C2	7:222:30:DA:C2	3.09	0.41
1:AAA:184:ALA:HB2	2:CCC:1091:GLY:CA	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CCC:161:LYS:H	2:CCC:161:LYS:HG2	1.72	0.41
2:CCC:496:LYS:N	2:CCC:497:PRO:CD	2.84	0.41
2:CCC:635:THR:HG22	2:CCC:644:LEU:CD2	2.51	0.41
3:DDD:1046:ILE:HG22	3:DDD:1061:VAL:HA	2.03	0.41
3:DDD:17:PHE:H	3:DDD:1355:ARG:NH1	2.19	0.41
3:DDD:807:LEU:CD2	3:DDD:1255:VAL:HG13	2.50	0.41
2:CCC:14:ASP:O	2:CCC:1155:VAL:HG13	2.22	0.40
2:CCC:160:ASP:N	2:CCC:160:ASP:OD1	2.54	0.40
2:CCC:598:VAL:HA	2:CCC:627:GLY:O	2.20	0.40
3:DDD:1075:ARG:NH1	3:DDD:1193:TRP:CG	2.89	0.40
3:DDD:933:ARG:HD3	3:DDD:933:ARG:O	2.21	0.40
3:DDD:260:PHE:CB	5:FFF:219:ILE:CG2	2.98	0.40
5:FFF:267:ASN:HB2	5:FFF:270:GLN:CG	2.51	0.40
1:AAA:47:LEU:HA	1:AAA:51:MET:HG2	2.03	0.40
2:CCC:1223:ARG:HH12	3:DDD:724:MET:HE1	1.86	0.40
2:CCC:1234:LYS:CE	2:CCC:1238:LEU:HD21	2.48	0.40
2:CCC:185:ASP:N	2:CCC:185:ASP:OD1	2.54	0.40
2:CCC:347:ILE:HD11	2:CCC:433:ILE:CD1	2.51	0.40
2:CCC:406:ASN:HB3	2:CCC:411:ARG:HB2	2.02	0.40
3:DDD:1145:PHE:HB3	3:DDD:1309:ILE:CD1	2.51	0.40
3:DDD:381:ILE:HD11	3:DDD:412:LEU:HD13	2.02	0.40
3:DDD:582:ILE:HG23	3:DDD:623:GLN:HB2	2.03	0.40
3:DDD:709:ARG:HB3	3:DDD:710:ASP:H	1.64	0.40
3:DDD:884:SER:OG	3:DDD:885:VAL:N	2.54	0.40
5:FFF:63:GLY:HA2	6:111:42:DG:N2	2.37	0.40
2:CCC:967:LEU:CD2	2:CCC:1021:LEU:HD22	2.51	0.40
2:CCC:1272:GLU:HG3	2:CCC:1272:GLU:H	1.71	0.40
3:DDD:1175:LEU:O	3:DDD:1187:GLU:HA	2.21	0.40
3:DDD:1075:ARG:NE	3:DDD:1193:TRP:HB3	2.36	0.40
5:FFF:151:ARG:HG3	5:FFF:152:GLN:N	2.37	0.40
2:CCC:1296:ASP:HB2	2:CCC:1320:PRO:HB3	2.04	0.40
2:CCC:44:GLU:CG	2:CCC:45:GLY:N	2.85	0.40
3:DDD:1078:LEU:HD12	3:DDD:1121:LEU:HB3	2.04	0.40
3:DDD:246:PRO:HA	3:DDD:247:PRO:HD3	1.93	0.40
3:DDD:518:VAL:N	3:DDD:716:GLN:HE22	2.20	0.40
3:DDD:903:LEU:H	3:DDD:903:LEU:HD12	1.85	0.40
5:FFF:265:GLU:CD	5:FFF:316:ILE:HD13	2.41	0.40
5:FFF:72:THR:CG2	5:FFF:73:ALA:H	2.33	0.40
7:222:20:DG:O5'	7:222:20:DG:H8	2.04	0.40
2:CCC:184:LEU:HB2	2:CCC:389:PHE:CE1	2.57	0.40
2:CCC:564:PRO:O	2:CCC:569:ILE:HA	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CCC:812:PHE:CB	3:DDD:357:VAL:HG11	2.51	0.40
3:DDD:417:ARG:C	3:DDD:418:GLU:HG2	2.42	0.40
2:CCC:620:ASN:HD21	3:DDD:768:ASN:CB	2.35	0.40
3:DDD:822:MET:HE1	3:DDD:842:ARG:HD3	2.04	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:FFF:67:TYR:O	5:FFF:299:ARG:NH2[3_644]	2.10	0.10

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	AAA	228/242 (94%)	205 (90%)	16 (7%)	7 (3%)	4	31
1	BBB	226/242 (93%)	204 (90%)	19 (8%)	3 (1%)	12	48
2	CCC	1338/1342 (100%)	1193 (89%)	123 (9%)	22 (2%)	9	44
3	DDD	1360/1407 (97%)	1218 (90%)	126 (9%)	16 (1%)	13	49
4	EEE	77/90 (86%)	70 (91%)	7 (9%)	0	100	100
5	FFF	275/336 (82%)	246 (90%)	25 (9%)	4 (2%)	10	45
All	All	3504/3659 (96%)	3136 (90%)	316 (9%)	52 (2%)	10	45

All (52) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	CCC	161	LYS
2	CCC	892	GLU
2	CCC	912	ASP
2	CCC	1319	MET

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Mol	Chain	Res	Type
3	DDD	519	ASN
3	DDD	710	ASP
3	DDD	1053	LEU
3	DDD	1268	ASN
1	AAA	168	ILE
1	BBB	232	VAL
2	CCC	45	GLY
2	CCC	398	SER
2	CCC	1004	ASP
2	CCC	1224	PRO
2	CCC	1297	ASP
3	DDD	207	GLU
5	FFF	113	GLY
5	FFF	228	GLY
2	CCC	201	ARG
2	CCC	234	ASP
2	CCC	260	LYS
2	CCC	812	PHE
2	CCC	909	LYS
2	CCC	1103	VAL
2	CCC	1318	GLY
3	DDD	321	LYS
3	DDD	342	LEU
3	DDD	1201	GLY
1	AAA	208	ASN
1	AAA	210	THR
2	CCC	567	PRO
3	DDD	81	ARG
2	CCC	110	PRO
2	CCC	519	ASN
2	CCC	937	ASP
3	DDD	854	ALA
3	DDD	939	GLY
3	DDD	1325	PHE
3	DDD	1344	LEU
1	AAA	162	GLU
3	DDD	117	LEU
1	AAA	211	ILE
3	DDD	829	GLY
1	BBB	14	VAL
1	BBB	40	GLY
5	FFF	246	PRO

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Mol	Chain	Res	Type
5	FFF	282	GLY
1	AAA	14	VAL
1	AAA	40	GLY
2	CCC	627	GLY
3	DDD	1091	PRO
2	CCC	1185	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	AAA	198/208 (95%)	193 (98%)	5 (2%)	47	68
1	BBB	196/208 (94%)	191 (97%)	5 (3%)	46	67
2	CCC	1155/1157 (100%)	1127 (98%)	28 (2%)	49	69
3	DDD	1135/1168 (97%)	1090 (96%)	45 (4%)	31	57
4	EEE	67/74 (90%)	64 (96%)	3 (4%)	27	55
5	FFF	240/292 (82%)	231 (96%)	9 (4%)	33	59
All	All	2991/3107 (96%)	2896 (97%)	95 (3%)	39	62

All (95) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	13	LEU
1	AAA	28	LEU
1	AAA	157	THR
1	AAA	166	ARG
1	AAA	174	ASP
1	BBB	13	LEU
1	BBB	28	LEU
1	BBB	159	ILE
1	BBB	160	HIS
1	BBB	233	ASP
2	CCC	12	ARG
2	CCC	23	ASP

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Mol	Chain	Res	Type
2	CCC	47	TYR
2	CCC	77	GLU
2	CCC	90	VAL
2	CCC	185	ASP
2	CCC	202	ARG
2	CCC	332	ARG
2	CCC	423	ASP
2	CCC	443	ASP
2	CCC	541	GLU
2	CCC	553	THR
2	CCC	561	ILE
2	CCC	628	HIS
2	CCC	635	THR
2	CCC	694	ARG
2	CCC	700	VAL
2	CCC	757	THR
2	CCC	788	SER
2	CCC	849	GLU
2	CCC	888	THR
2	CCC	914	LYS
2	CCC	940	GLU
2	CCC	994	ARG
2	CCC	1089	GLU
2	CCC	1224	PRO
2	CCC	1240	ASP
2	CCC	1272	GLU
3	DDD	28	ASP
3	DDD	52	GLU
3	DDD	199	GLU
3	DDD	216	LYS
3	DDD	281	ARG
3	DDD	298	MET
3	DDD	314	ARG
3	DDD	321	LYS
3	DDD	346	ARG
3	DDD	347	VAL
3	DDD	384	LYS
3	DDD	398	LYS
3	DDD	399	LYS
3	DDD	505	ASP
3	DDD	508	LEU
3	DDD	526	VAL

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Mol	Chain	Res	Type
3	DDD	538	ARG
3	DDD	548	VAL
3	DDD	549	LYS
3	DDD	571	ASP
3	DDD	572	THR
3	DDD	579	LEU
3	DDD	599	LYS
3	DDD	610	ARG
3	DDD	623	GLN
3	DDD	649	LYS
3	DDD	695	LYS
3	DDD	736	GLN
3	DDD	746	LEU
3	DDD	770	LEU
3	DDD	790	THR
3	DDD	798	ARG
3	DDD	830	ASP
3	DDD	831	VAL
3	DDD	835	LEU
3	DDD	838	ARG
3	DDD	856	ILE
3	DDD	857	LEU
3	DDD	933	ARG
3	DDD	1138	LEU
3	DDD	1175	LEU
3	DDD	1189	MET
3	DDD	1199	PHE
3	DDD	1227	HIS
3	DDD	1356	LEU
4	EEE	5	THR
4	EEE	43	ASN
4	EEE	45	LYS
5	FFF	54	VAL
5	FFF	156	ARG
5	FFF	203	ASP
5	FFF	211	ARG
5	FFF	218	ARG
5	FFF	219	ILE
5	FFF	243	GLU
5	FFF	271	ARG
5	FFF	325	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no

such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 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	$\# Z > 2$
10	CTP	DDD	1505	9	23,30,30	0.72	0	30,47,47	1.02	1 (3%)

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
10	CTP	DDD	1505	9	-	6/20/38/38	0/2/2/2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	DDD	1505	CTP	C2-N3-C4	3.81	120.20	116.34

There are no chirality outliers.

All (6) torsion outliers are listed below:

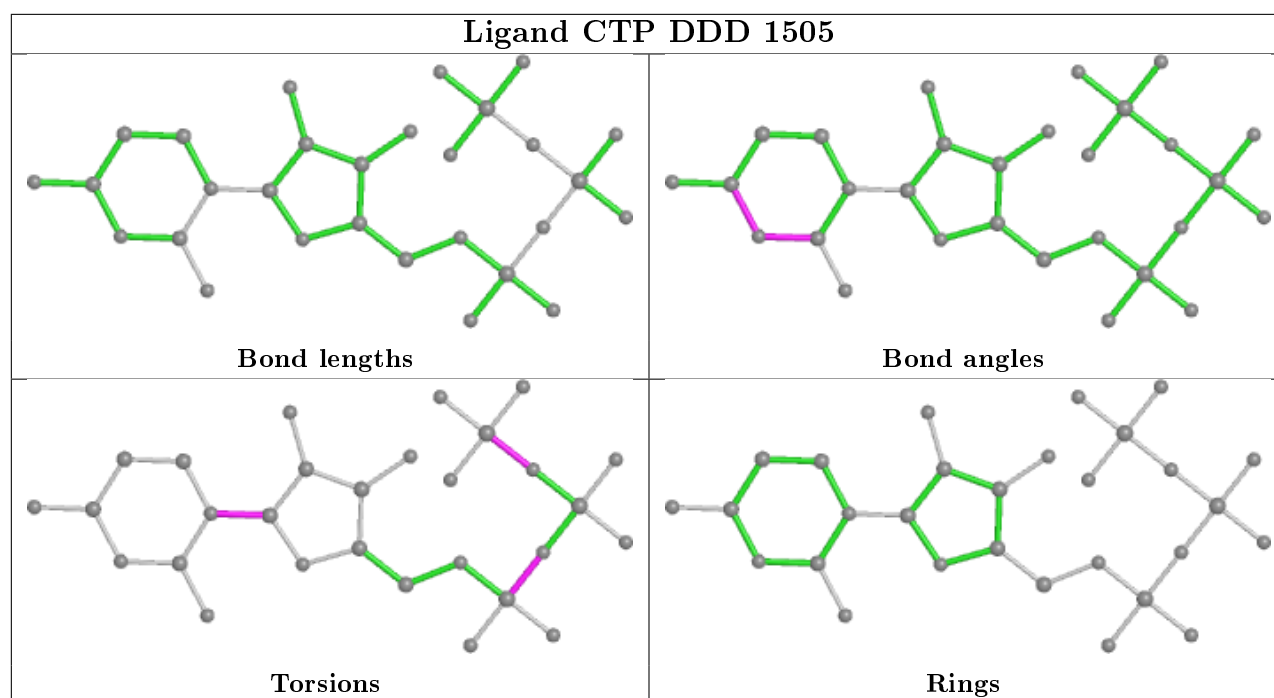
Mol	Chain	Res	Type	Atoms
10	DDD	1505	CTP	C2'-C1'-N1-C6
10	DDD	1505	CTP	PB-O3A-PA-O2A
10	DDD	1505	CTP	PB-O3B-PG-O1G
10	DDD	1505	CTP	PB-O3B-PG-O2G
10	DDD	1505	CTP	PB-O3B-PG-O3G
10	DDD	1505	CTP	PB-O3A-PA-O1A

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	DDD	1505	CTP	6	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	AAA	230/242 (95%)	-0.05	10 (4%) 35 29	232, 333, 427, 494	0
1	BBB	228/242 (94%)	-0.14	7 (3%) 49 38	238, 357, 440, 482	0
2	CCC	1340/1342 (99%)	-0.13	27 (2%) 65 56	146, 287, 429, 526	0
3	DDD	1362/1407 (96%)	-0.04	49 (3%) 42 34	168, 305, 433, 503	0
4	EEE	79/90 (87%)	-0.22	2 (2%) 57 47	258, 368, 476, 513	0
5	FFF	277/336 (82%)	0.04	20 (7%) 15 12	236, 355, 483, 528	0
6	111	32/50 (64%)	0.13	4 (12%) 3 5	336, 381, 469, 537	0
7	222	34/50 (68%)	0.27	2 (5%) 22 18	241, 395, 529, 560	0
All	All	3582/3759 (95%)	-0.07	121 (3%) 45 36	146, 314, 442, 560	0

All (121) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	CCC	911	SER	7.1
2	CCC	1003	THR	6.1
3	DDD	1203	ARG	6.0
2	CCC	983	GLY	5.8
3	DDD	1110	GLU	5.7
3	DDD	1109	LEU	5.6
3	DDD	732	GLY	5.3
2	CCC	1004	ASP	4.6
3	DDD	855	ASP	4.6
3	DDD	1188	GLU	4.5
2	CCC	982	GLY	4.5
1	AAA	27	THR	4.4
5	FFF	312	ARG	4.2
2	CCC	912	ASP	4.1
6	111	46	DG	4.1
3	DDD	1107	VAL	4.0

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Mol	Chain	Res	Type	RSRZ
1	BBB	164	ASP	4.0
1	BBB	165	GLU	3.9
3	DDD	856	ILE	3.8
2	CCC	906	PHE	3.7
5	FFF	310	LEU	3.7
2	CCC	984	VAL	3.6
1	AAA	201	LEU	3.6
3	DDD	1112	GLY	3.6
5	FFF	263	LEU	3.5
3	DDD	854	ALA	3.4
3	DDD	1066	GLU	3.4
5	FFF	306	GLN	3.4
3	DDD	1078	LEU	3.3
5	FFF	53	ARG	3.3
2	CCC	1055	ALA	3.2
3	DDD	1113	VAL	3.2
3	DDD	1068	THR	3.2
3	DDD	878	ASP	3.1
5	FFF	311	ARG	3.0
3	DDD	1186	TYR	3.0
3	DDD	877	VAL	3.0
1	AAA	28	LEU	3.0
3	DDD	87	LYS	2.9
1	BBB	25	LYS	2.9
3	DDD	1204	VAL	2.9
5	FFF	301	ARG	2.9
7	222	23	DT	2.8
5	FFF	308	GLU	2.8
3	DDD	1130	GLY	2.8
7	222	22	DA	2.8
5	FFF	281	LEU	2.8
3	DDD	853	THR	2.7
2	CCC	385	PHE	2.7
3	DDD	1059	LEU	2.7
1	AAA	171	LEU	2.7
5	FFF	305	ILE	2.7
5	FFF	324	ILE	2.7
5	FFF	327	LEU	2.7
3	DDD	1185	PRO	2.7
5	FFF	294	GLU	2.6
2	CCC	696	ASP	2.6
3	DDD	1108	GLN	2.6

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Mol	Chain	Res	Type	RSRZ
5	FFF	217	GLU	2.6
1	AAA	213	PRO	2.6
2	CCC	703	GLY	2.6
3	DDD	993	GLU	2.6
2	CCC	927	THR	2.6
3	DDD	1129	GLY	2.6
1	AAA	107	ILE	2.5
1	AAA	30	PRO	2.5
2	CCC	905	ILE	2.5
2	CCC	1054	LEU	2.5
3	DDD	879	ALA	2.5
2	CCC	1180	MET	2.4
6	111	47	DC	2.4
1	BBB	109	PRO	2.4
3	DDD	1017	VAL	2.4
2	CCC	124	MET	2.3
3	DDD	1101	LEU	2.3
1	BBB	26	VAL	2.3
2	CCC	243	PRO	2.3
5	FFF	326	ALA	2.3
5	FFF	111	ASN	2.3
1	BBB	231	PHE	2.3
5	FFF	216	ASN	2.3
3	DDD	1159	ILE	2.2
1	AAA	172	LEU	2.2
2	CCC	169	LYS	2.2
1	BBB	205	MET	2.2
3	DDD	1266	ILE	2.2
3	DDD	1271	SER	2.2
3	DDD	972	LYS	2.2
3	DDD	1069	ALA	2.2
2	CCC	215	TYR	2.2
5	FFF	198	ILE	2.2
1	AAA	205	MET	2.2
3	DDD	849	LEU	2.2
3	DDD	1177	ILE	2.2
5	FFF	259	ILE	2.2
3	DDD	79	LYS	2.2
3	DDD	1376	GLY	2.1
3	DDD	857	LEU	2.1
3	DDD	731	ARG	2.1
2	CCC	125	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
2	CCC	777	VAL	2.1
3	DDD	974	VAL	2.1
6	111	45	DT	2.1
1	AAA	135	ASP	2.1
2	CCC	1009	ASN	2.1
3	DDD	1187	GLU	2.1
6	111	49	DG	2.1
3	DDD	1202	GLU	2.1
3	DDD	91	GLU	2.1
3	DDD	751	ASP	2.1
3	DDD	1028	ILE	2.0
2	CCC	1005	GLU	2.0
2	CCC	103	VAL	2.0
2	CCC	650	VAL	2.0
2	CCC	230	PHE	2.0
3	DDD	1161	GLY	2.0
4	EEE	78	ALA	2.0
5	FFF	54	VAL	2.0
4	EEE	80	LEU	2.0
3	DDD	747	MET	2.0
3	DDD	671	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 monosaccharides in this entry.

6.4 Ligands ⓘ

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.

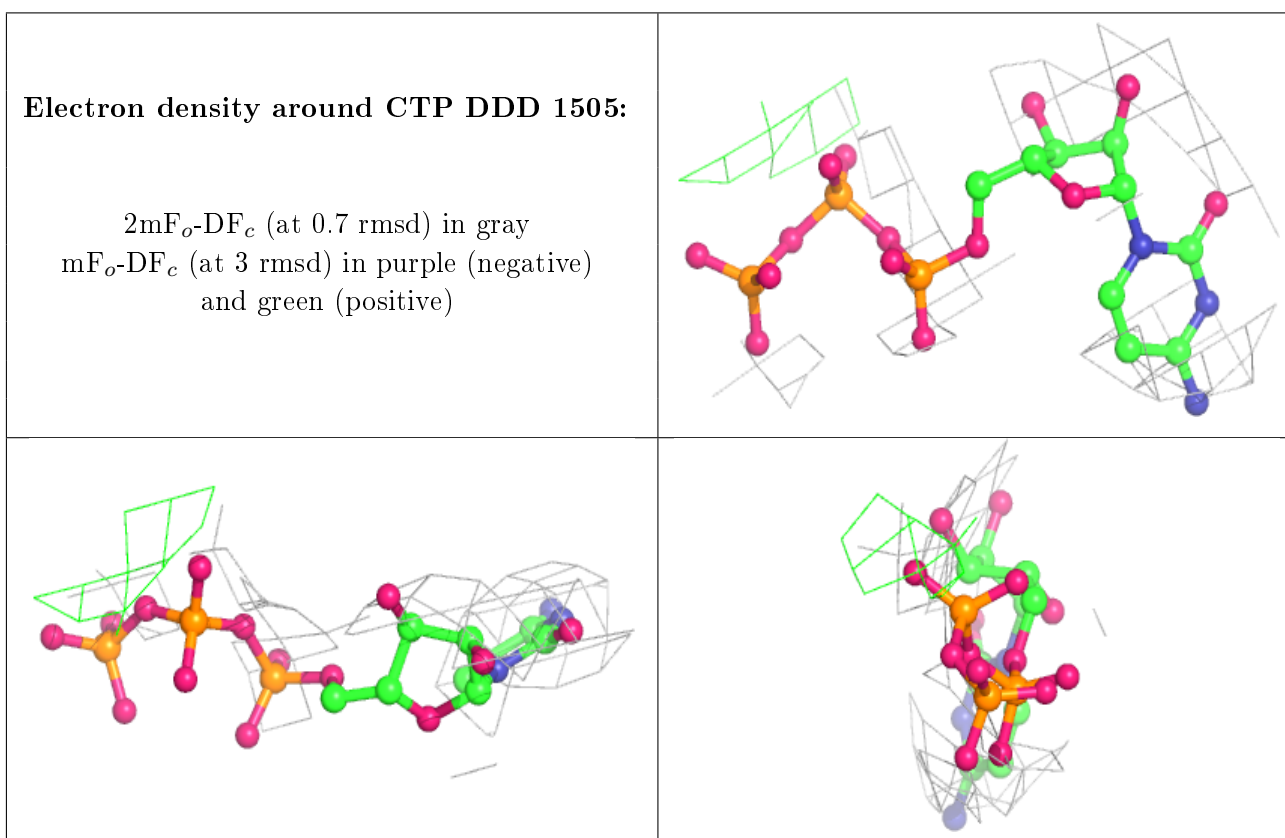
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
10	CTP	DDD	1505	29/29	0.87	0.36	174,233,332,344	0
8	ZN	DDD	1501	1/1	0.88	0.14	585,585,585,585	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
9	MG	DDD	1503	1/1	0.92	0.25	240,240,240,240	0
9	MG	DDD	1504	1/1	0.97	0.28	204,204,204,204	0
8	ZN	DDD	1502	1/1	0.98	0.18	324,324,324,324	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.