



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 27, 2020 – 02:08 PM BST

PDB ID : 6UTV
Title : E. coli sigma-S transcription initiation complex with a 6-nt RNA ("Fresh" crystal soaked with CTP, UTP, GTP, and ddATP for 150 seconds)
Authors : Zuo, Y.; De, S.; Steitz, T.A.
Deposited on : 2019-10-30
Resolution : 3.45 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:

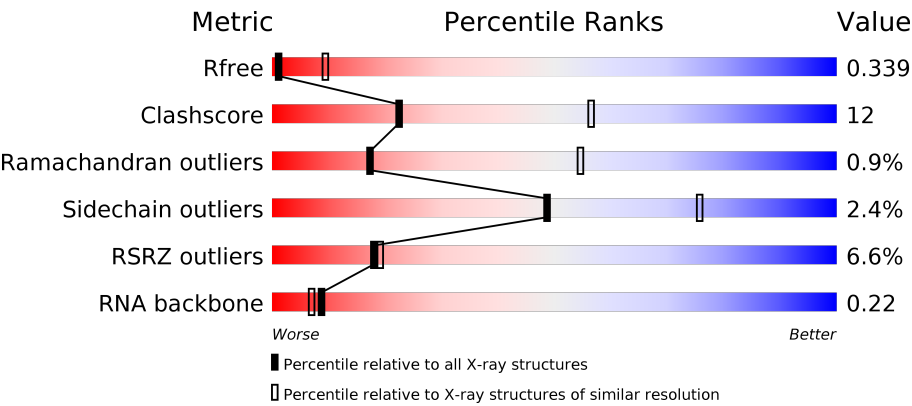
MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, 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 3.45 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	1291 (3.52-3.40)
Clashscore	141614	1372 (3.52-3.40)
Ramachandran outliers	138981	1337 (3.52-3.40)
Sidechain outliers	138945	1338 (3.52-3.40)
RSRZ outliers	127900	1205 (3.52-3.40)
RNA backbone	3102	1036 (3.96-2.96)

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>7%</div><div><div></div><div>70%</div><div>22%</div><div>• 5%</div></div></div>
1	BBB	242	<div><div>11%</div><div><div></div><div>57%</div><div>33%</div><div>• 6%</div></div></div>
2	CCC	1342	<div><div>4%</div><div><div></div><div>81%</div><div>18%</div><div>•</div></div></div>
3	DDD	1407	<div><div>7%</div><div><div></div><div>77%</div><div>19%</div><div>••</div></div></div>

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Mol	Chain	Length	Quality of chain
4	EEE	90	<div><div><div></div><div></div><div></div></div><div><div>7%</div><div>76%</div><div>11%</div><div>•</div><div>12%</div></div></div>
5	FFF	336	<div><div><div></div><div></div><div></div></div><div><div>7%</div><div>60%</div><div>21%</div><div>•</div><div>18%</div></div></div>
6	111	50	<div><div><div></div><div></div><div></div></div><div><div>4%</div><div>26%</div><div>34%</div><div>40%</div></div></div>
7	222	50	<div><div><div></div><div></div><div></div></div><div><div>20%</div><div>38%</div><div>32%</div><div>30%</div></div></div>
8	333	6	<div><div><div></div><div></div><div></div></div><div><div></div><div>50%</div><div>33%</div><div>17%</div></div></div>

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 29063 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	1341	Total	C	N	O	S	0	0	0
			10577	6636	1842	2056	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	30	Total	C	N	O	P	0	0	0
			618	294	111	183	30			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	222	35	Total	C	N	O	P	0	0	0
			716	342	132	208	34			

- Molecule 8 is a RNA chain called RNA 6-mer.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	333	6	Total	C	N	O	P	0	0	0
			137	57	22	50	8			

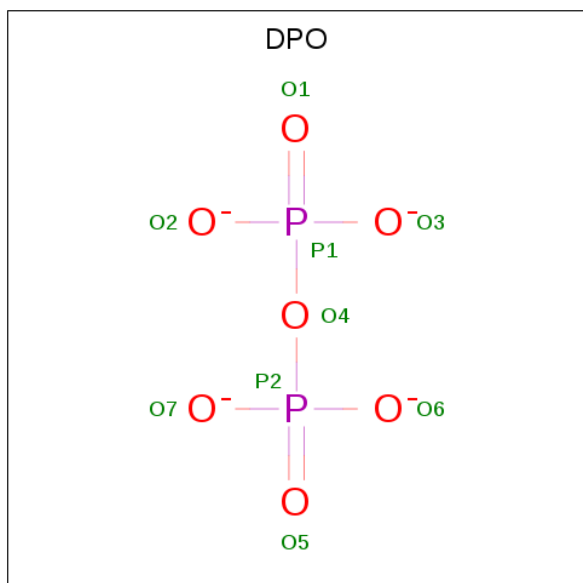
- Molecule 9 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	CCC	1	Total	Mg	0	0
			1	1		
9	DDD	1	Total	Mg	0	0
			1	1		

- Molecule 10 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 11 is DIPHOSPHATE (three-letter code: DPO) (formula: O₇P₂).

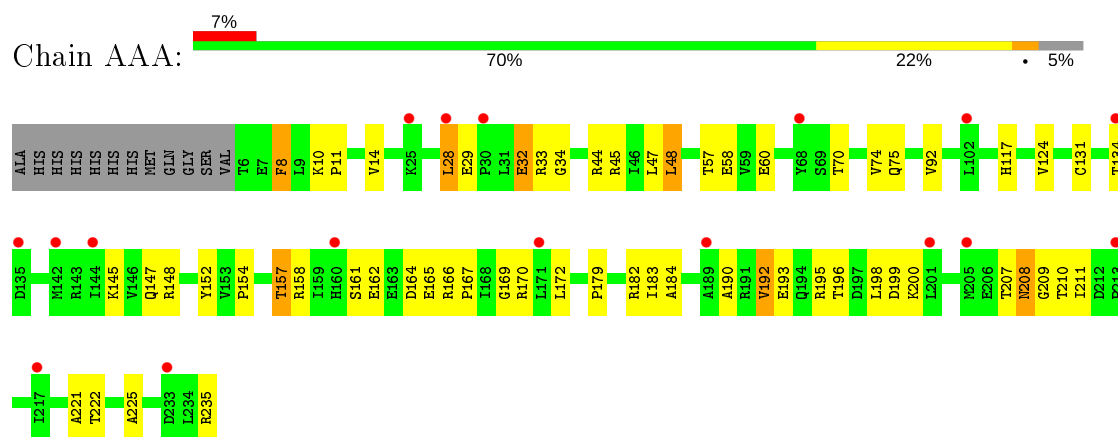


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	DDD	1	Total	O	P	0	0
			9	7	2		

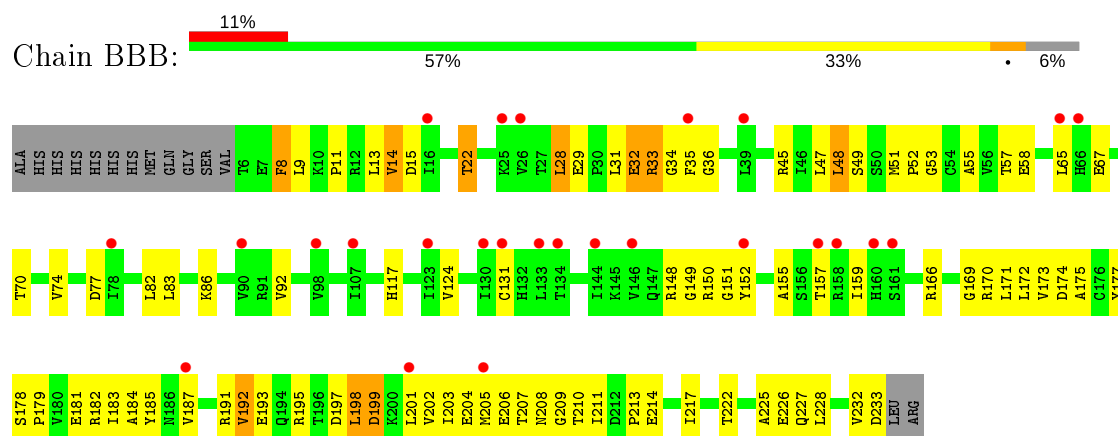
3 Residue-property plots [i](#)

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.

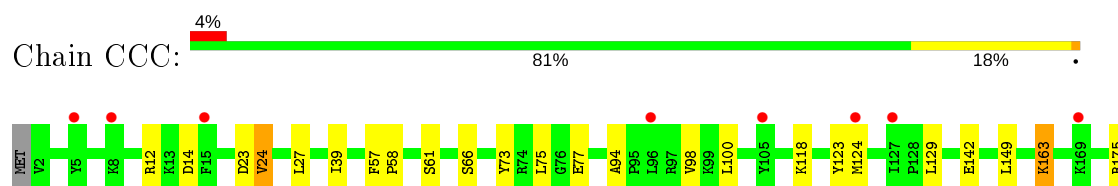
- Molecule 1: DNA-directed RNA polymerase subunit alpha

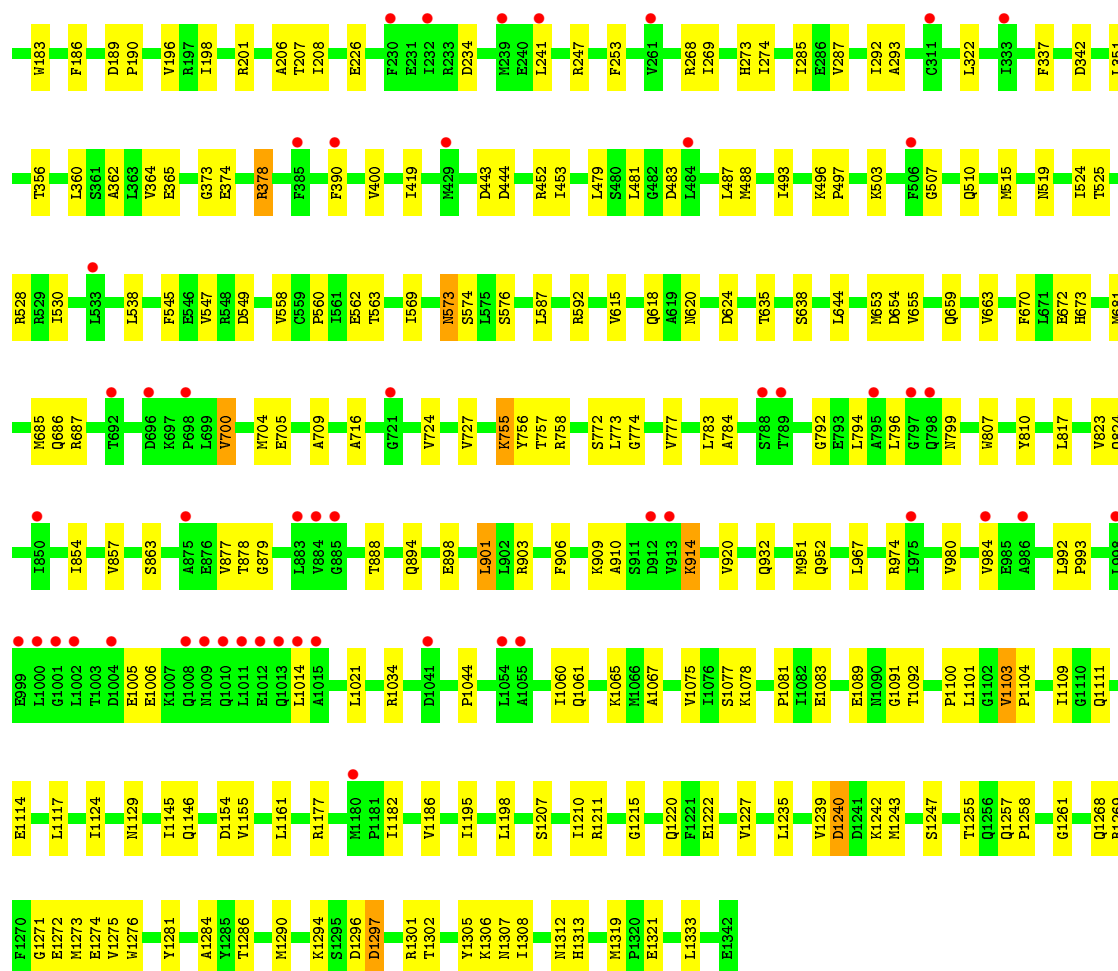


- Molecule 1: DNA-directed RNA polymerase subunit alpha

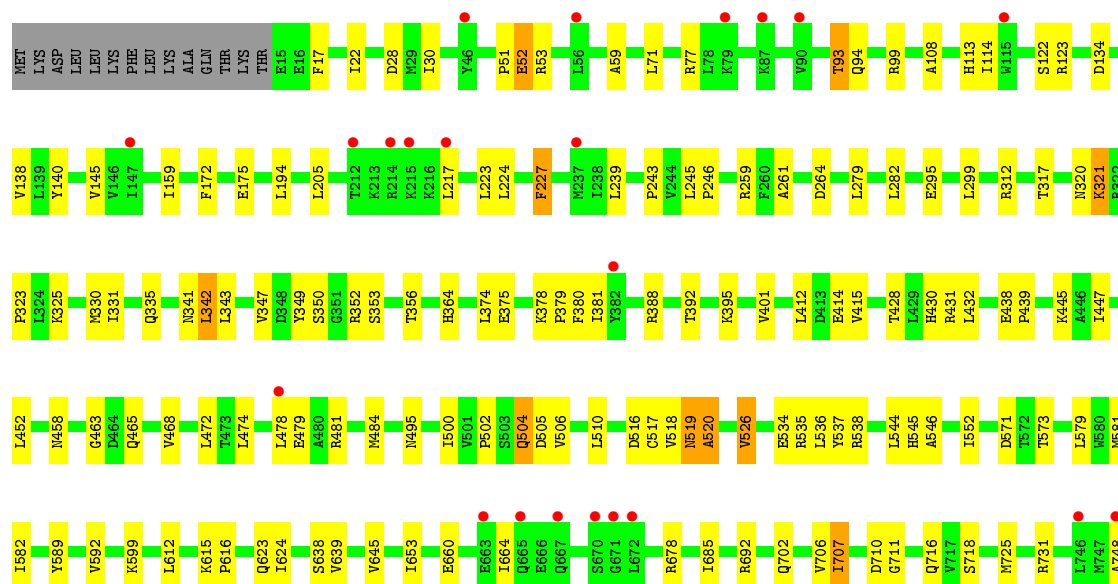
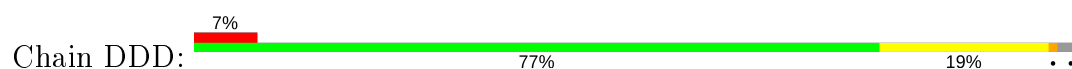


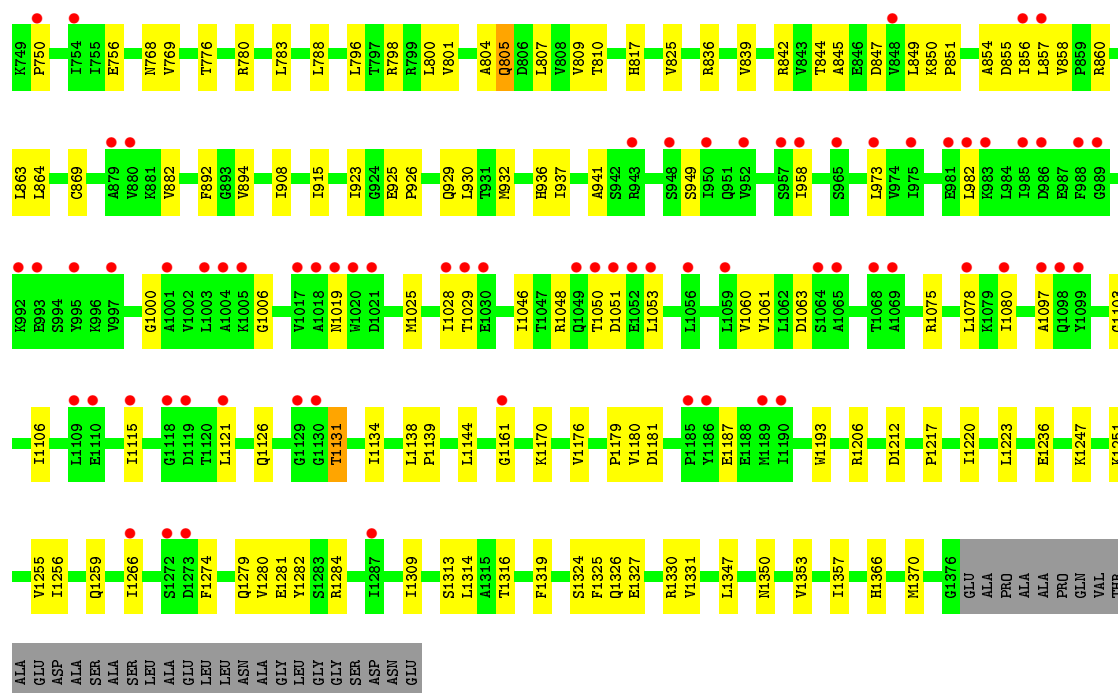
- Molecule 2: DNA-directed RNA polymerase subunit beta



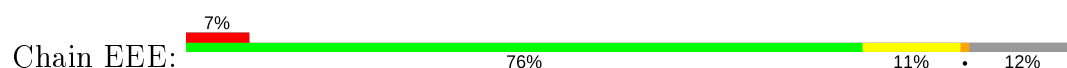


• Molecule 3: DNA-directed RNA polymerase subunit beta'

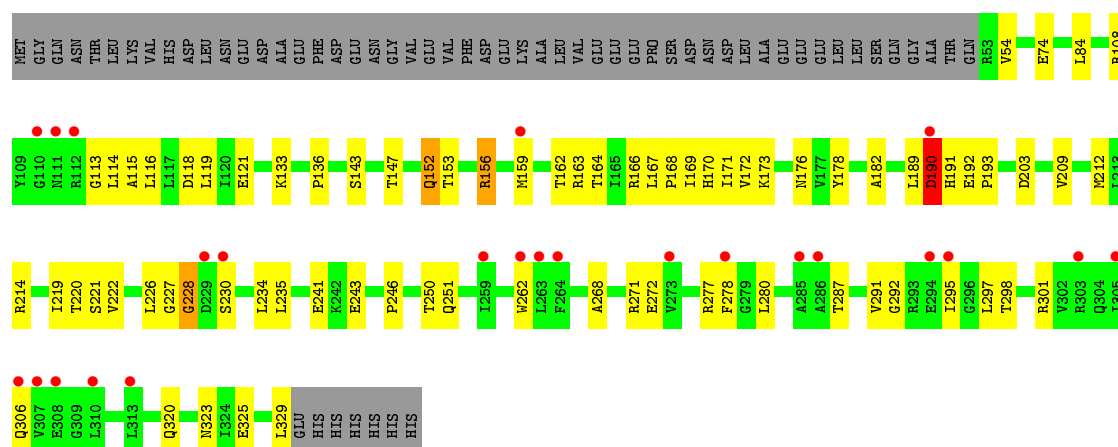




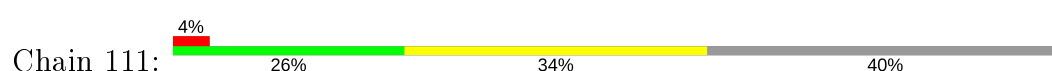
- Molecule 4: DNA-directed RNA polymerase subunit omega



- Molecule 5: RNA polymerase sigma factor RpoS

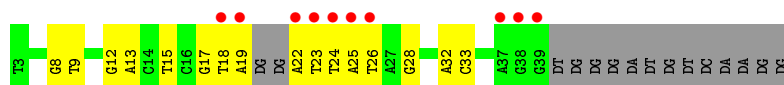


- Molecule 6: Synthetic DNA 50-MER (promoter non-template strand)





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



- Molecule 8: RNA 6-mer



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	132.53Å 155.43Å 232.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.28 – 3.45 49.28 – 3.45	Depositor EDS
% Data completeness (in resolution range)	99.2 (49.28-3.45) 99.3 (49.28-3.45)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.06 (at 3.48Å)	Xtriage
Refinement program	REFMAC 5.8.0257	Depositor
R, R_{free}	0.282 , 0.348 0.277 , 0.339	Depositor DCC
R_{free} test set	3029 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å ²)	121.7	Xtriage
Anisotropy	0.265	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 105.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.36$, $\langle L^2 \rangle = 0.20$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	29063	wwPDB-VP
Average B, all atoms (Å ²)	195.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.32% 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: DPO, GTP, ZN, 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	0.66	0/1809	0.71	0/2450
1	BBB	0.67	0/1789	0.72	0/2425
2	CCC	0.63	0/10746	0.78	0/14499
3	DDD	0.63	0/10729	0.76	0/14487
4	EEE	0.63	0/629	0.75	0/847
5	FFF	0.66	0/2282	0.70	0/3076
6	111	0.41	0/691	0.63	0/1063
7	222	0.41	0/802	0.67	0/1234
8	333	0.32	0/116	0.69	0/178
All	All	0.63	0/29593	0.75	0/40259

There are no bond length outliers.

There are no bond angle outliers.

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	AAA	1787	0	1813	71	0
1	BBB	1767	0	1789	142	0
2	CCC	10577	0	10591	213	0
3	DDD	10568	0	10780	248	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	EEE	627	0	634	14	0
5	FFF	2253	0	2298	72	0
6	111	618	0	341	27	0
7	222	716	0	397	29	1
8	333	137	0	65	5	0
9	CCC	1	0	0	0	0
9	DDD	1	0	0	0	0
10	DDD	2	0	0	0	0
11	DDD	9	0	0	1	0
All	All	29063	0	28708	666	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 12.

All (666) 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:817:HIS:HB3	3:DDD:860:ARG:NH2	1.16	1.40
1:BBB:49:SER:O	1:BBB:151:GLY:HA3	1.38	1.24
6:111:54:DA:H2"	6:111:55:DC:C5	1.75	1.19
3:DDD:817:HIS:CB	3:DDD:860:ARG:NH2	2.05	1.18
1:BBB:179:PRO:HG2	1:BBB:211:ILE:HD12	1.15	1.13
3:DDD:849:LEU:HD12	3:DDD:850:LYS:O	1.47	1.13
1:BBB:179:PRO:HG2	1:BBB:211:ILE:CD1	1.82	1.10
1:BBB:205:MET:CE	1:BBB:217:ILE:HG13	1.81	1.10
1:AAA:60:GLU:HG3	1:AAA:169:GLY:O	1.49	1.09
6:111:54:DA:H2"	6:111:55:DC:C6	1.91	1.06
1:BBB:11:PRO:HG3	1:BBB:31:LEU:HD21	1.39	1.05
1:BBB:67:GLU:HB3	1:BBB:171:LEU:HD22	1.07	1.04
3:DDD:849:LEU:CD1	3:DDD:850:LYS:O	2.10	0.99
1:BBB:67:GLU:HB3	1:BBB:171:LEU:CD2	1.93	0.98
1:BBB:11:PRO:HG3	1:BBB:31:LEU:CD2	1.93	0.97
2:CCC:496:LYS:HB3	7:222:24:DT:OP1	1.66	0.95
1:BBB:86:LYS:HE2	1:BBB:174:ASP:H	1.32	0.95
5:FFF:262:TRP:HE1	5:FFF:320:GLN:HE22	1.06	0.94
3:DDD:817:HIS:HB3	3:DDD:860:ARG:HH21	1.17	0.93
1:BBB:67:GLU:CB	1:BBB:171:LEU:HD22	1.98	0.92
1:BBB:179:PRO:CG	1:BBB:211:ILE:HD12	1.98	0.92
2:CCC:1273:MET:HG3	7:222:12:DG:H4'	1.52	0.92
1:AAA:192:VAL:HG12	1:AAA:193:GLU:H	1.35	0.91
5:FFF:234:LEU:HD21	7:222:19:DA:H61	1.35	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BBB:185:TYR:CB	1:BBB:203:ILE:HG12	2.02	0.90
3:DDD:259:ARG:NH2	7:222:22:DA:OP2	2.04	0.89
1:AAA:45:ARG:NH2	1:BBB:34:GLY:O	2.06	0.87
6:111:54:DA:C2'	6:111:55:DC:C5	2.58	0.87
2:CCC:1313:HIS:HB2	3:DDD:474:LEU:HG	1.57	0.86
1:BBB:205:MET:HE3	1:BBB:217:ILE:HG13	1.56	0.86
1:BBB:11:PRO:HB3	1:BBB:31:LEU:HG	1.57	0.86
1:AAA:184:ALA:HB2	2:CCC:1091:GLY:HA3	1.58	0.85
1:BBB:14:VAL:HG21	1:BBB:29:GLU:HG2	1.56	0.85
3:DDD:844:THR:O	3:DDD:860:ARG:O	1.94	0.85
1:BBB:152:TYR:CZ	3:DDD:536:LEU:HD21	2.11	0.85
1:AAA:192:VAL:HG12	1:AAA:193:GLU:N	1.92	0.85
3:DDD:392:THR:CG2	5:FFF:320:GLN:O	2.24	0.85
1:BBB:86:LYS:HD3	1:BBB:174:ASP:HB2	1.58	0.84
1:BBB:65:LEU:O	1:BBB:169:GLY:HA2	1.76	0.84
1:BBB:33:ARG:HB2	1:BBB:197:ASP:O	1.78	0.84
2:CCC:525:THR:HG21	2:CCC:687:ARG:HD3	1.60	0.84
1:BBB:205:MET:HE1	1:BBB:217:ILE:HG13	1.60	0.83
1:AAA:158:ARG:HB3	1:AAA:172:LEU:HD21	1.59	0.82
1:BBB:82:LEU:HD22	1:BBB:173:VAL:HG22	1.62	0.82
3:DDD:800:LEU:HD23	3:DDD:1309:ILE:CD1	2.09	0.82
3:DDD:817:HIS:CB	3:DDD:860:ARG:HH22	1.80	0.81
1:BBB:51:MET:C	1:BBB:150:ARG:HB2	1.99	0.81
1:BBB:14:VAL:HG21	1:BBB:29:GLU:CG	2.09	0.81
1:BBB:51:MET:O	1:BBB:151:GLY:N	2.13	0.81
5:FFF:133:LYS:HE3	6:111:35:DC:OP1	1.81	0.80
3:DDD:392:THR:HG21	5:FFF:320:GLN:O	1.82	0.80
2:CCC:183:TRP:CH2	6:111:51:DC:H2'	2.16	0.80
1:BBB:83:LEU:HD21	3:DDD:526:VAL:CG2	2.10	0.80
3:DDD:839:VAL:HG12	3:DDD:864:LEU:CD1	2.12	0.80
3:DDD:279:LEU:HD22	3:DDD:299:LEU:CD1	2.12	0.79
1:BBB:205:MET:CE	1:BBB:217:ILE:CG1	2.61	0.79
3:DDD:847:ASP:OD1	3:DDD:860:ARG:HB2	1.83	0.79
1:BBB:67:GLU:N	1:BBB:171:LEU:HD21	1.99	0.78
1:AAA:32:GLU:HA	1:AAA:198:LEU:CD2	2.14	0.78
5:FFF:234:LEU:CD2	7:222:19:DA:H61	1.96	0.78
3:DDD:849:LEU:HD12	3:DDD:850:LYS:N	1.99	0.78
1:BBB:185:TYR:HB2	1:BBB:203:ILE:HG12	1.62	0.78
1:BBB:83:LEU:HD21	3:DDD:526:VAL:HG21	1.65	0.78
2:CCC:1044:PRO:HB2	5:FFF:214:ARG:HG2	1.66	0.77
2:CCC:525:THR:HG21	2:CCC:687:ARG:CD	2.15	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:DDD:415:VAL:O	4:EEE:45:LYS:NZ	2.18	0.76
1:BBB:179:PRO:HG2	1:BBB:211:ILE:CG1	2.14	0.76
1:BBB:51:MET:O	1:BBB:150:ARG:HA	1.85	0.76
2:CCC:528:ARG:NH2	2:CCC:576:SER:O	2.19	0.75
3:DDD:817:HIS:HB3	3:DDD:860:ARG:HH22	0.94	0.75
3:DDD:1266:ILE:HD13	3:DDD:1274:PHE:HB3	1.68	0.75
2:CCC:1124:ILE:HD11	2:CCC:1198:LEU:HD11	1.67	0.74
3:DDD:478:LEU:HG	4:EEE:47:THR:HG23	1.70	0.74
1:BBB:51:MET:O	1:BBB:150:ARG:CA	2.36	0.74
2:CCC:94:ALA:HB2	2:CCC:129:LEU:HD11	1.69	0.74
1:BBB:124:VAL:HG21	1:BBB:210:THR:HG22	1.69	0.74
1:BBB:185:TYR:HA	1:BBB:203:ILE:HA	1.69	0.74
1:AAA:195:ARG:CG	1:AAA:198:LEU:HD12	2.18	0.73
3:DDD:842:ARG:HB3	3:DDD:882:VAL:CG1	2.18	0.73
1:AAA:222:THR:OG1	1:BBB:233:ASP:CB	2.36	0.73
1:BBB:86:LYS:HG2	1:BBB:173:VAL:HG12	1.71	0.73
1:BBB:184:ALA:O	1:BBB:203:ILE:CG2	2.38	0.72
3:DDD:615:LYS:HG2	4:EEE:5:THR:HG21	1.70	0.72
2:CCC:562:GLU:HG2	2:CCC:574:SER:HB2	1.72	0.72
2:CCC:624:ASP:OD1	2:CCC:624:ASP:O	2.08	0.71
2:CCC:100:LEU:HD22	2:CCC:493:ILE:HD11	1.71	0.71
1:BBB:83:LEU:HD11	3:DDD:526:VAL:HB	1.72	0.71
5:FFF:262:TRP:HE1	5:FFF:320:GLN:NE2	1.85	0.71
2:CCC:1306:LYS:HG2	5:FFF:250:THR:OG1	1.91	0.71
2:CCC:1333:LEU:O	3:DDD:113:HIS:NE2	2.18	0.71
5:FFF:170:HIS:NE2	6:111:31:DT:H2'	2.05	0.71
3:DDD:807:LEU:HD11	3:DDD:894:VAL:HG23	1.72	0.71
1:BBB:182:ARG:O	1:BBB:206:GLU:N	2.22	0.71
3:DDD:519:ASN:O	3:DDD:520:ALA:HB3	1.90	0.71
1:BBB:49:SER:O	1:BBB:151:GLY:CA	2.30	0.70
3:DDD:261:ALA:HA	5:FFF:220:THR:O	1.90	0.70
1:BBB:185:TYR:HB3	1:BBB:203:ILE:HG12	1.71	0.70
7:222:17:DG:C2'	7:222:18:DT:O4'	2.40	0.70
2:CCC:560:PRO:HB2	3:DDD:776:THR:HG21	1.72	0.70
1:AAA:222:THR:OG1	1:BBB:233:ASP:HB2	1.92	0.69
1:AAA:29:GLU:HB3	1:AAA:200:LYS:HB3	1.73	0.69
1:BBB:184:ALA:C	1:BBB:203:ILE:HG23	2.12	0.69
1:BBB:33:ARG:CB	1:BBB:197:ASP:O	2.40	0.69
5:FFF:227:GLY:O	8:333:14:GTP:N7	2.25	0.69
1:AAA:28:LEU:O	1:AAA:200:LYS:HB2	1.93	0.69
3:DDD:458:ASN:ND2	3:DDD:929:GLN:OE1	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:DDD:842:ARG:HD3	3:DDD:882:VAL:HG11	1.75	0.69
1:AAA:195:ARG:HB3	1:AAA:198:LEU:HD12	1.75	0.68
1:BBB:86:LYS:CG	1:BBB:173:VAL:HG12	2.23	0.68
1:AAA:75:GLN:HE22	2:CCC:772:SER:HA	1.59	0.68
1:BBB:208:ASN:OD1	1:BBB:209:GLY:N	2.27	0.68
1:AAA:184:ALA:CB	2:CCC:1091:GLY:HA3	2.23	0.68
1:BBB:83:LEU:CD1	3:DDD:526:VAL:HB	2.23	0.68
1:BBB:152:TYR:CE2	3:DDD:536:LEU:HD21	2.28	0.68
1:BBB:184:ALA:O	1:BBB:203:ILE:HG23	1.94	0.68
2:CCC:672:GLU:HG3	2:CCC:673:HIS:CD2	2.29	0.68
1:AAA:154:PRO:HG2	1:AAA:157:THR:HB	1.76	0.68
3:DDD:134:ASP:HB3	3:DDD:159:ILE:HD11	1.76	0.68
3:DDD:279:LEU:HD22	3:DDD:299:LEU:HD11	1.75	0.68
2:CCC:1281:TYR:CD2	3:DDD:484:MET:HG2	2.29	0.67
3:DDD:343:LEU:HD11	3:DDD:1324:SER:HB2	1.76	0.67
3:DDD:800:LEU:HD23	3:DDD:1309:ILE:HD13	1.77	0.67
2:CCC:1242:LYS:HD2	3:DDD:465:GLN:HE22	1.60	0.67
7:222:17:DG:H2'	7:222:18:DT:C6	2.31	0.66
1:BBB:155:ALA:O	1:BBB:159:ILE:HG22	1.96	0.66
2:CCC:906:PHE:HZ	5:FFF:323:ASN:HA	1.61	0.66
1:AAA:184:ALA:HB2	2:CCC:1091:GLY:CA	2.25	0.66
3:DDD:279:LEU:HD22	3:DDD:299:LEU:HD12	1.78	0.65
2:CCC:1154:ASP:OD1	2:CCC:1154:ASP:N	2.29	0.65
5:FFF:162:THR:HG23	5:FFF:163:ARG:HG3	1.77	0.65
1:BBB:182:ARG:H	1:BBB:206:GLU:HB3	1.62	0.65
2:CCC:563:THR:OG1	2:CCC:569:ILE:O	2.12	0.65
1:BBB:205:MET:HE3	1:BBB:217:ILE:CG1	2.25	0.65
1:AAA:32:GLU:HG3	1:AAA:198:LEU:HD21	1.78	0.64
1:AAA:29:GLU:HB3	1:AAA:200:LYS:CB	2.27	0.64
1:BBB:82:LEU:HD22	1:BBB:173:VAL:CG2	2.26	0.64
1:AAA:75:GLN:HE21	2:CCC:727:VAL:HG11	1.61	0.64
2:CCC:1257:GLN:HG2	2:CCC:1296:ASP:OD1	1.97	0.64
1:BBB:184:ALA:O	1:BBB:204:GLU:N	2.30	0.64
2:CCC:755:LYS:O	2:CCC:757:THR:OG1	2.08	0.64
1:AAA:166:ARG:HG3	1:AAA:166:ARG:O	1.98	0.64
2:CCC:906:PHE:CZ	5:FFF:323:ASN:HA	2.32	0.64
3:DDD:849:LEU:HA	3:DDD:857:LEU:HB3	1.79	0.64
3:DDD:295:GLU:OE1	5:FFF:121:GLU:HG3	1.98	0.63
1:AAA:225:ALA:HB2	1:BBB:228:LEU:HD13	1.80	0.63
3:DDD:108:ALA:HB3	3:DDD:279:LEU:HD23	1.80	0.63
5:FFF:189:LEU:O	5:FFF:191:HIS:N	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CCC:1101:LEU:HD23	3:DDD:725:MET:HE2	1.81	0.63
1:BBB:157:THR:O	1:BBB:157:THR:HG22	1.98	0.62
3:DDD:264:ASP:OD1	5:FFF:221:SER:OG	2.14	0.62
3:DDD:395:LYS:HD3	5:FFF:329:LEU:HD13	1.79	0.62
2:CCC:1273:MET:HG3	7:222:12:DG:C4'	2.27	0.62
5:FFF:222:VAL:CG1	5:FFF:235:LEU:HB2	2.29	0.62
3:DDD:122:SER:O	3:DDD:123:ARG:HB2	2.00	0.62
1:AAA:158:ARG:HD2	1:AAA:172:LEU:HD11	1.81	0.62
2:CCC:253:PHE:CZ	2:CCC:287:VAL:HG12	2.34	0.62
5:FFF:227:GLY:O	8:333:14:GTP:C8	2.52	0.62
3:DDD:172:PHE:HB3	3:DDD:175:GLU:HB2	1.79	0.61
1:BBB:181:GLU:N	1:BBB:206:GLU:O	2.27	0.61
2:CCC:980:VAL:HG13	2:CCC:984:VAL:HG23	1.81	0.61
6:111:31:DT:H1'	6:111:32:DA:H5'	1.81	0.61
5:FFF:147:THR:HG21	6:111:40:DA:C6	2.35	0.61
2:CCC:903:ARG:NH1	2:CCC:910:ALA:HB3	2.15	0.61
3:DDD:748:ALA:HB2	3:DDD:941:ALA:HB2	1.81	0.61
1:AAA:195:ARG:HD2	1:AAA:198:LEU:HD12	1.82	0.61
1:BBB:11:PRO:CB	1:BBB:31:LEU:HG	2.29	0.61
2:CCC:1273:MET:CG	7:222:12:DG:H4'	2.29	0.61
1:BBB:52:PRO:CA	1:BBB:150:ARG:HB3	2.31	0.61
2:CCC:903:ARG:HB3	2:CCC:909:LYS:HG2	1.83	0.61
2:CCC:1146:GLN:HB2	2:CCC:1161:LEU:HD12	1.81	0.61
1:AAA:158:ARG:CD	1:AAA:172:LEU:HD11	2.30	0.61
3:DDD:817:HIS:CG	3:DDD:860:ARG:NH2	2.69	0.61
1:AAA:11:PRO:HD3	1:BBB:227:GLN:NE2	2.16	0.60
1:BBB:53:GLY:O	1:BBB:177:TYR:HB3	2.01	0.60
2:CCC:1065:LYS:HG2	2:CCC:1235:LEU:HD12	1.83	0.60
2:CCC:576:SER:OG	2:CCC:659:GLN:O	2.18	0.60
5:FFF:234:LEU:HD21	7:222:19:DA:N6	2.13	0.60
1:BBB:86:LYS:CD	1:BBB:174:ASP:HB2	2.30	0.60
3:DDD:582:ILE:HD12	3:DDD:623:GLN:HB3	1.83	0.60
2:CCC:685:MET:HE2	2:CCC:1067:ALA:CB	2.32	0.60
2:CCC:1101:LEU:HD23	3:DDD:725:MET:CE	2.32	0.60
2:CCC:635:THR:HG22	2:CCC:644:LEU:CD2	2.31	0.60
3:DDD:863:LEU:HD22	3:DDD:908:ILE:HG12	1.83	0.60
1:BBB:11:PRO:CG	1:BBB:31:LEU:CD2	2.76	0.60
3:DDD:1347:LEU:HD22	3:DDD:1357:ILE:HG23	1.84	0.60
3:DDD:134:ASP:CB	3:DDD:159:ILE:HD11	2.31	0.60
3:DDD:335:GLN:NE2	5:FFF:230:SER:HB2	2.16	0.60
1:AAA:74:VAL:HG13	1:AAA:131:CYS:SG	2.42	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BBB:52:PRO:HA	1:BBB:150:ARG:HB3	1.84	0.59
1:BBB:47:LEU:HA	1:BBB:51:MET:HG2	1.83	0.59
2:CCC:292:ILE:HB	2:CCC:322:LEU:HD11	1.85	0.59
3:DDD:707:ILE:HD12	3:DDD:707:ILE:H	1.67	0.59
3:DDD:817:HIS:CB	3:DDD:860:ARG:HH21	1.87	0.59
2:CCC:196:VAL:HG23	2:CCC:206:ALA:HA	1.83	0.59
1:AAA:195:ARG:CB	1:AAA:198:LEU:HD12	2.32	0.59
1:BBB:14:VAL:CG2	1:BBB:29:GLU:HG2	2.28	0.59
1:AAA:222:THR:OG1	1:BBB:233:ASP:HB3	2.02	0.59
3:DDD:664:ILE:HD11	3:DDD:685:ILE:HD11	1.85	0.59
1:AAA:195:ARG:CD	1:AAA:198:LEU:HD12	2.33	0.59
1:BBB:49:SER:C	1:BBB:151:GLY:HA3	2.21	0.59
2:CCC:620:ASN:HD21	3:DDD:768:ASN:HB2	1.67	0.59
1:AAA:34:GLY:O	1:BBB:45:ARG:NH2	2.35	0.58
1:BBB:51:MET:O	1:BBB:150:ARG:HB2	2.01	0.58
3:DDD:807:LEU:HD11	3:DDD:894:VAL:CG2	2.33	0.58
2:CCC:1222:GLU:OE2	3:DDD:537:TYR:OH	2.15	0.58
5:FFF:170:HIS:CE1	6:111:31:DT:C6	2.91	0.58
1:BBB:55:ALA:HB3	1:BBB:175:ALA:HB1	1.84	0.58
3:DDD:817:HIS:CA	3:DDD:860:ARG:HH21	2.16	0.58
1:BBB:11:PRO:HG3	1:BBB:31:LEU:HD23	1.84	0.58
1:BBB:152:TYR:CE2	3:DDD:536:LEU:CD2	2.86	0.58
2:CCC:400:VAL:HG11	2:CCC:452:ARG:HD3	1.86	0.58
2:CCC:247:ARG:HA	2:CCC:274:ILE:HD11	1.84	0.58
2:CCC:1306:LYS:HE2	5:FFF:250:THR:HA	1.85	0.58
2:CCC:685:MET:CE	2:CCC:1067:ALA:CB	2.82	0.57
3:DDD:845:ALA:O	3:DDD:860:ARG:HG3	2.04	0.57
1:BBB:92:VAL:O	1:BBB:148:ARG:NH2	2.37	0.57
1:BBB:52:PRO:HA	1:BBB:150:ARG:HA	1.85	0.57
3:DDD:849:LEU:CD1	3:DDD:850:LYS:N	2.68	0.57
5:FFF:226:LEU:HD22	7:222:18:DT:O4	2.03	0.57
3:DDD:1080:ILE:HB	3:DDD:1097:ALA:HB3	1.87	0.57
2:CCC:510:GLN:HG2	8:333:14:GTP:O1G	2.04	0.57
1:BBB:182:ARG:O	1:BBB:206:GLU:HB3	2.05	0.57
1:BBB:86:LYS:HE2	1:BBB:174:ASP:N	2.13	0.57
6:111:50:DT:H2"	6:111:51:DC:H5"	1.85	0.57
2:CCC:481:LEU:HD11	5:FFF:108:ARG:NH2	2.20	0.57
1:AAA:32:GLU:HA	1:AAA:198:LEU:HD23	1.87	0.56
2:CCC:73:TYR:HB2	2:CCC:98:VAL:HG22	1.87	0.56
3:DDD:378:LYS:N	3:DDD:379:PRO:HD2	2.19	0.56
3:DDD:707:ILE:HD11	3:DDD:716:GLN:HG2	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:EEE:2:ALA:N	4:EEE:5:THR:O	2.37	0.56
1:AAA:11:PRO:HD3	1:BBB:227:GLN:HE22	1.70	0.56
1:AAA:44:ARG:HH22	2:CCC:1215:GLY:HA2	1.69	0.56
5:FFF:133:LYS:CE	6:111:35:DC:OP1	2.52	0.56
3:DDD:842:ARG:HB3	3:DDD:882:VAL:HG11	1.86	0.56
2:CCC:967:LEU:HD21	2:CCC:1021:LEU:HD22	1.87	0.56
3:DDD:500:ILE:HG22	3:DDD:500:ILE:O	2.04	0.56
3:DDD:392:THR:HG21	5:FFF:320:GLN:HB3	1.86	0.56
1:BBB:51:MET:O	1:BBB:150:ARG:CB	2.54	0.56
1:BBB:67:GLU:CB	1:BBB:171:LEU:CD2	2.72	0.56
3:DDD:518:VAL:HG21	3:DDD:707:ILE:HD13	1.87	0.56
2:CCC:1005:GLU:HG2	2:CCC:1006:GLU:H	1.70	0.55
1:BBB:187:VAL:HG23	1:BBB:201:LEU:HA	1.87	0.55
2:CCC:1210:ILE:HD12	2:CCC:1227:VAL:CG1	2.35	0.55
2:CCC:269:ILE:HG23	2:CCC:273:HIS:HB2	1.87	0.55
2:CCC:1268:GLN:OE1	3:DDD:352:ARG:HD2	2.06	0.55
1:BBB:52:PRO:HA	1:BBB:150:ARG:CB	2.37	0.55
2:CCC:226:GLU:HB2	2:CCC:337:PHE:HB3	1.88	0.55
3:DDD:807:LEU:HD13	3:DDD:1259:GLN:HE22	1.71	0.55
3:DDD:320:ASN:O	3:DDD:321:LYS:CB	2.55	0.55
1:BBB:33:ARG:HD3	1:BBB:195:ARG:NH2	2.22	0.55
3:DDD:1144:LEU:HD11	3:DDD:1236:GLU:HG3	1.89	0.55
3:DDD:516:ASP:HB3	3:DDD:573:THR:HG21	1.89	0.55
1:BBB:47:LEU:HD13	1:BBB:183:ILE:CD1	2.36	0.55
1:AAA:57:THR:HG23	1:AAA:158:ARG:CZ	2.36	0.55
1:AAA:92:VAL:O	1:AAA:148:ARG:NH2	2.40	0.54
3:DDD:615:LYS:HE2	4:EEE:5:THR:HB	1.88	0.54
3:DDD:842:ARG:CD	3:DDD:882:VAL:HG11	2.36	0.54
1:AAA:190:ALA:HB2	1:AAA:199:ASP:HA	1.90	0.54
1:BBB:159:ILE:HD12	1:BBB:166:ARG:HH21	1.72	0.54
2:CCC:1294:LYS:HD3	3:DDD:347:VAL:HG13	1.89	0.54
1:AAA:164:ASP:OD1	1:AAA:165:GLU:N	2.35	0.54
2:CCC:1284:ALA:CB	3:DDD:1357:ILE:HB	2.37	0.54
2:CCC:1333:LEU:HD11	3:DDD:331:ILE:HD12	1.90	0.54
2:CCC:1273:MET:HB3	3:DDD:428:THR:HB	1.89	0.54
2:CCC:592:ARG:HG3	2:CCC:655:VAL:HG22	1.89	0.54
1:BBB:74:VAL:HG13	1:BBB:131:CYS:SG	2.48	0.54
2:CCC:1281:TYR:CD1	3:DDD:431:ARG:HD2	2.43	0.54
3:DDD:1314:LEU:HD11	3:DDD:1327:GLU:HG3	1.90	0.54
5:FFF:298:THR:HG21	5:FFF:301:ARG:HD3	1.88	0.54
1:BBB:225:ALA:HA	1:BBB:228:LEU:HD12	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CCC:1296:ASP:HB3	2:CCC:1321:GLU:H	1.73	0.54
5:FFF:176:ASN:OD1	7:222:26:DT:H71	2.07	0.54
3:DDD:518:VAL:O	3:DDD:520:ALA:N	2.40	0.53
2:CCC:1302:THR:HG22	5:FFF:246:PRO:HA	1.90	0.53
2:CCC:241:LEU:HD22	2:CCC:285:ILE:CD1	2.37	0.53
2:CCC:208:ILE:HD11	2:CCC:365:GLU:HG2	1.89	0.53
3:DDD:1080:ILE:HD12	3:DDD:1115:ILE:HD11	1.91	0.53
2:CCC:1257:GLN:HE22	3:DDD:341:ASN:HA	1.74	0.53
2:CCC:118:LYS:HD3	2:CCC:488:MET:SD	2.49	0.53
1:AAA:166:ARG:NH2	2:CCC:863:SER:HB2	2.23	0.53
1:AAA:47:LEU:HD13	1:AAA:183:ILE:CD1	2.39	0.53
3:DDD:941:ALA:HB1	3:DDD:1131:THR:HG21	1.90	0.53
3:DDD:1075:ARG:NH2	3:DDD:1193:TRP:CE3	2.77	0.53
3:DDD:615:LYS:HB2	3:DDD:616:PRO:HD3	1.91	0.53
3:DDD:836:ARG:HG3	3:DDD:869:CYS:HB3	1.89	0.53
3:DDD:949:SER:HB3	3:DDD:1019:ASN:HD22	1.73	0.53
2:CCC:123:TYR:CE2	5:FFF:190:ASP:O	2.61	0.53
1:BBB:22:THR:O	1:BBB:207:THR:HG22	2.08	0.53
1:BBB:36:GLY:O	1:BBB:201:LEU:HD13	2.09	0.52
2:CCC:360:LEU:HD11	2:CCC:378:ARG:HG3	1.90	0.52
5:FFF:262:TRP:CZ2	5:FFF:320:GLN:OE1	2.62	0.52
3:DDD:653:ILE:HG12	3:DDD:692:ARG:HD2	1.91	0.52
2:CCC:685:MET:CE	2:CCC:1067:ALA:HB2	2.38	0.52
5:FFF:156:ARG:NH2	6:111:33:DT:C6	2.78	0.52
3:DDD:1313:SER:O	3:DDD:1316:THR:HG22	2.09	0.52
5:FFF:166:ARG:HH12	5:FFF:168:PRO:HA	1.74	0.52
1:BBB:205:MET:HE3	1:BBB:217:ILE:CD1	2.40	0.52
2:CCC:878:THR:HG22	2:CCC:879:GLY:N	2.25	0.52
1:BBB:205:MET:HE3	1:BBB:213:PRO:O	2.08	0.52
2:CCC:453:ILE:HD12	2:CCC:587:LEU:HD21	1.91	0.52
3:DDD:1063:ASP:HB3	3:DDD:1103:GLY:HA3	1.91	0.52
2:CCC:100:LEU:CD2	2:CCC:493:ILE:HD11	2.40	0.52
2:CCC:1075:VAL:CG2	3:DDD:463:GLY:N	2.73	0.52
2:CCC:1100:PRO:CB	3:DDD:639:VAL:HG23	2.40	0.52
3:DDD:510:LEU:HD11	3:DDD:624:ILE:HG23	1.92	0.52
3:DDD:839:VAL:HG12	3:DDD:864:LEU:HD12	1.89	0.52
7:222:17:DG:H2'	7:222:18:DT:O4'	2.11	0.51
1:AAA:158:ARG:NE	1:AAA:172:LEU:HD11	2.25	0.51
1:BBB:11:PRO:HB2	1:BBB:28:LEU:HD12	1.92	0.51
2:CCC:27:LEU:HD22	2:CCC:663:VAL:HG21	1.91	0.51
3:DDD:844:THR:HG21	3:DDD:858:VAL:HG11	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CCC:183:TRP:CZ3	6:111:51:DC:C2'	2.94	0.51
2:CCC:560:PRO:O	3:DDD:780:ARG:NH2	2.41	0.51
1:AAA:75:GLN:NE2	2:CCC:772:SER:HA	2.25	0.51
2:CCC:1290:MET:HG2	2:CCC:1294:LYS:HD2	1.92	0.51
2:CCC:984:VAL:HG13	2:CCC:984:VAL:O	2.10	0.51
2:CCC:519:ASN:HD21	2:CCC:796:LEU:HD22	1.74	0.51
3:DDD:1217:PRO:HA	3:DDD:1220:ILE:HD12	1.92	0.51
3:DDD:863:LEU:HD22	3:DDD:908:ILE:CG1	2.41	0.51
1:AAA:152:TYR:CD2	2:CCC:824:GLN:HG2	2.45	0.51
2:CCC:1117:LEU:HD11	2:CCC:1182:ILE:HD13	1.93	0.51
3:DDD:1350:ASN:HA	3:DDD:1353:VAL:HG22	1.92	0.51
6:111:29:DC:H2''	6:111:30:DG:C8	2.46	0.51
2:CCC:123:TYR:CZ	5:FFF:190:ASP:O	2.63	0.51
1:BBB:184:ALA:O	1:BBB:203:ILE:HG22	2.11	0.51
3:DDD:1330:ARG:NH2	7:222:8:DG:OP1	2.44	0.51
2:CCC:183:TRP:CZ3	6:111:51:DC:H2''	2.46	0.51
2:CCC:1145:ILE:HG22	2:CCC:1161:LEU:HD11	1.93	0.50
1:BBB:179:PRO:CG	1:BBB:211:ILE:CD1	2.72	0.50
3:DDD:1138:LEU:N	3:DDD:1139:PRO:CD	2.75	0.50
1:BBB:124:VAL:HG21	1:BBB:210:THR:CG2	2.40	0.50
3:DDD:516:ASP:CB	3:DDD:573:THR:HG21	2.41	0.50
1:BBB:53:GLY:C	1:BBB:177:TYR:HB3	2.31	0.50
5:FFF:178:TYR:CE1	5:FFF:209:VAL:HG22	2.47	0.50
3:DDD:194:LEU:HD22	3:DDD:224:LEU:HD23	1.94	0.50
7:222:22:DA:OP1	7:222:22:DA:H3'	2.12	0.50
3:DDD:810:THR:HG21	3:DDD:892:PHE:HB2	1.92	0.50
2:CCC:207:THR:HG21	2:CCC:351:LEU:HG	1.94	0.50
5:FFF:226:LEU:HD21	7:222:19:DA:N6	2.27	0.50
1:AAA:182:ARG:HD2	2:CCC:1092:THR:HG22	1.94	0.50
3:DDD:660:GLU:HG3	3:DDD:685:ILE:HD13	1.93	0.50
2:CCC:1100:PRO:HB3	3:DDD:639:VAL:HG23	1.94	0.49
2:CCC:241:LEU:HD22	2:CCC:285:ILE:HD11	1.93	0.49
3:DDD:478:LEU:CG	4:EEE:47:THR:HG23	2.41	0.49
1:BBB:67:GLU:CA	1:BBB:171:LEU:HD21	2.42	0.49
2:CCC:1247:SER:HB3	3:DDD:375:GLU:O	2.12	0.49
3:DDD:452:LEU:HB3	3:DDD:500:ILE:HG23	1.95	0.49
3:DDD:842:ARG:HB3	3:DDD:882:VAL:HG13	1.91	0.49
5:FFF:163:ARG:CD	5:FFF:167:LEU:HD12	2.43	0.49
2:CCC:724:VAL:O	2:CCC:774:GLY:HA2	2.13	0.49
1:AAA:165:GLU:HG3	1:AAA:165:GLU:O	2.13	0.49
3:DDD:850:LYS:HB2	3:DDD:851:PRO:HD2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AAA:182:ARG:CD	2:CCC:1092:THR:HG22	2.43	0.49
1:BBB:183:ILE:HD12	1:BBB:205:MET:HG3	1.94	0.49
2:CCC:483:ASP:O	2:CCC:487:LEU:HB2	2.13	0.49
2:CCC:142:GLU:OE1	2:CCC:515:MET:HE1	2.13	0.49
2:CCC:1269:ARG:HD3	7:222:13:DA:H5'	1.95	0.49
2:CCC:686:GLN:HG2	2:CCC:796:LEU:HD13	1.94	0.49
2:CCC:894:GLN:HB3	3:DDD:77:ARG:HH22	1.78	0.49
1:AAA:28:LEU:O	1:AAA:200:LYS:HA	2.13	0.48
1:BBB:51:MET:C	1:BBB:150:ARG:CB	2.77	0.48
1:BBB:52:PRO:HA	1:BBB:149:GLY:O	2.13	0.48
5:FFF:171:ILE:HG23	5:FFF:212:MET:SD	2.53	0.48
3:DDD:516:ASP:HB3	3:DDD:573:THR:CG2	2.43	0.48
5:FFF:287:THR:O	5:FFF:291:VAL:HG23	2.13	0.48
1:BBB:184:ALA:O	1:BBB:203:ILE:HA	2.13	0.48
1:BBB:182:ARG:N	1:BBB:206:GLU:HB3	2.27	0.48
2:CCC:888:THR:O	2:CCC:914:LYS:N	2.46	0.48
1:AAA:48:LEU:CD2	1:AAA:183:ILE:HG22	2.43	0.48
1:BBB:185:TYR:CA	1:BBB:203:ILE:HG23	2.44	0.48
4:EEE:41:GLU:HG3	4:EEE:42:GLU:N	2.28	0.48
2:CCC:24:VAL:HG11	2:CCC:704:MET:SD	2.54	0.48
2:CCC:992:LEU:HB3	2:CCC:993:PRO:HD2	1.95	0.48
2:CCC:292:ILE:HG21	2:CCC:322:LEU:HD21	1.96	0.48
2:CCC:1284:ALA:HB1	3:DDD:1357:ILE:HB	1.94	0.48
1:BBB:86:LYS:CE	1:BBB:174:ASP:HB2	2.43	0.48
3:DDD:478:LEU:HG	4:EEE:47:THR:CG2	2.43	0.48
1:AAA:58:GLU:HB2	1:AAA:145:LYS:HB3	1.96	0.48
5:FFF:176:ASN:OD1	7:222:26:DT:C7	2.62	0.48
2:CCC:1129:ASN:OD1	2:CCC:1177:ARG:NH2	2.41	0.48
2:CCC:777:VAL:HG11	2:CCC:783:LEU:HD21	1.94	0.48
3:DDD:519:ASN:O	3:DDD:520:ALA:CB	2.55	0.48
3:DDD:645:VAL:HG23	3:DDD:645:VAL:O	2.14	0.48
2:CCC:705:GLU:HB3	2:CCC:794:LEU:H	1.79	0.47
3:DDD:474:LEU:HD12	4:EEE:28:ARG:HD3	1.95	0.47
1:BBB:152:TYR:HD1	3:DDD:535:ARG:NH1	2.12	0.47
1:BBB:185:TYR:HB3	1:BBB:203:ILE:HG23	1.97	0.47
1:BBB:52:PRO:HA	1:BBB:150:ARG:CA	2.45	0.47
2:CCC:877:VAL:HB	2:CCC:920:VAL:HG21	1.96	0.47
3:DDD:518:VAL:O	3:DDD:519:ASN:C	2.52	0.47
2:CCC:1276:TRP:CE2	3:DDD:801:VAL:HG11	2.49	0.47
1:AAA:167:PRO:HG2	1:AAA:170:ARG:HD2	1.96	0.47
2:CCC:1306:LYS:CE	5:FFF:250:THR:HA	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CCC:481:LEU:HD11	5:FFF:108:ARG:HH22	1.78	0.47
3:DDD:504:GLN:HB3	3:DDD:504:GLN:HE21	1.53	0.47
3:DDD:349:TYR:CD2	3:DDD:472:LEU:HD11	2.50	0.47
1:AAA:158:ARG:HD2	1:AAA:172:LEU:HD21	1.96	0.47
2:CCC:549:ASP:OD2	3:DDD:750:PRO:HB2	2.13	0.47
3:DDD:850:LYS:HB2	3:DDD:851:PRO:CD	2.45	0.47
1:AAA:195:ARG:HD2	1:AAA:198:LEU:CD1	2.43	0.47
2:CCC:496:LYS:N	2:CCC:497:PRO:CD	2.78	0.47
3:DDD:804:ALA:O	3:DDD:805:GLN:C	2.53	0.47
3:DDD:93:THR:HG22	3:DDD:94:GLN:H	1.80	0.47
3:DDD:839:VAL:O	3:DDD:864:LEU:HD12	2.15	0.47
3:DDD:925:GLU:HB3	3:DDD:926:PRO:HD3	1.97	0.47
6:111:32:DA:C2	7:222:32:DA:C2	3.03	0.47
2:CCC:1243:MET:SD	3:DDD:445:LYS:HB3	2.55	0.47
2:CCC:149:LEU:HB2	2:CCC:530:ILE:CG2	2.45	0.46
2:CCC:525:THR:HG21	2:CCC:687:ARG:HD2	1.95	0.46
3:DDD:1280:VAL:HG12	3:DDD:1281:GLU:N	2.30	0.46
3:DDD:430:HIS:CE1	3:DDD:432:LEU:HB2	2.51	0.46
3:DDD:392:THR:HG23	5:FFF:320:GLN:O	2.10	0.46
1:AAA:8:PHE:N	1:AAA:8:PHE:CD1	2.83	0.46
1:BBB:48:LEU:CD2	1:BBB:183:ILE:CG2	2.93	0.46
2:CCC:23:ASP:N	2:CCC:23:ASP:OD1	2.48	0.46
1:BBB:32:GLU:HB3	1:BBB:35:PHE:HD2	1.80	0.46
1:BBB:67:GLU:CA	1:BBB:171:LEU:CD2	2.92	0.46
3:DDD:579:LEU:HB3	3:DDD:592:VAL:HG21	1.97	0.46
3:DDD:825:VAL:HG12	3:DDD:825:VAL:O	2.14	0.46
3:DDD:364:HIS:HB3	4:EEE:4:VAL:HG13	1.98	0.46
5:FFF:173:LYS:CE	7:222:28:DG:N7	2.78	0.46
2:CCC:1077:SER:HA	3:DDD:356:THR:OG1	2.15	0.46
1:AAA:28:LEU:O	1:AAA:200:LYS:CB	2.62	0.46
3:DDD:317:THR:HA	3:DDD:323:PRO:HA	1.97	0.46
6:111:52:DT:C2'	6:111:52:DT:O2	2.64	0.46
1:BBB:55:ALA:HB3	1:BBB:177:TYR:CE1	2.51	0.46
1:BBB:182:ARG:O	1:BBB:206:GLU:CB	2.63	0.46
2:CCC:1103:VAL:HG13	2:CCC:1111:GLN:HE21	1.81	0.46
2:CCC:373:GLY:HA3	5:FFF:54:VAL:HG21	1.97	0.46
2:CCC:268:ARG:HD2	3:DDD:1048:ARG:NH1	2.30	0.46
3:DDD:1206:ARG:NH2	3:DDD:1223:LEU:O	2.46	0.46
3:DDD:1330:ARG:HH21	7:222:8:DG:P	2.39	0.46
3:DDD:849:LEU:C	3:DDD:849:LEU:HD12	2.36	0.46
1:BBB:199:ASP:N	1:BBB:199:ASP:OD1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CCC:175:ARG:NH1	6:111:52:DT:H72	2.31	0.46
2:CCC:253:PHE:CE1	2:CCC:287:VAL:HG12	2.50	0.46
2:CCC:932:GLN:HE22	2:CCC:952:GLN:HE22	1.62	0.46
2:CCC:57:PHE:HB3	2:CCC:58:PRO:HA	1.98	0.46
3:DDD:1266:ILE:HD13	3:DDD:1274:PHE:CB	2.41	0.46
1:BBB:58:GLU:CD	1:BBB:170:ARG:HE	2.18	0.46
2:CCC:1109:ILE:O	2:CCC:1109:ILE:HG22	2.16	0.46
3:DDD:114:ILE:HD11	3:DDD:312:ARG:HB2	1.97	0.46
1:BBB:33:ARG:HA	1:BBB:199:ASP:OD1	2.15	0.45
2:CCC:1319:MET:HE1	3:DDD:17:PHE:HE2	1.81	0.45
3:DDD:381:ILE:HD11	3:DDD:412:LEU:HD13	1.97	0.45
1:AAA:195:ARG:HG3	1:AAA:198:LEU:HD12	1.96	0.45
1:AAA:179:PRO:HG3	1:AAA:211:ILE:HG13	1.98	0.45
1:AAA:28:LEU:O	1:AAA:200:LYS:CA	2.64	0.45
2:CCC:823:VAL:HG22	2:CCC:1060:ILE:HG13	1.98	0.45
2:CCC:1333:LEU:CD1	3:DDD:331:ILE:HD12	2.45	0.45
3:DDD:59:ALA:HB3	3:DDD:71:LEU:HD11	1.99	0.45
1:AAA:48:LEU:HD23	1:AAA:183:ILE:CG2	2.46	0.45
2:CCC:27:LEU:HD22	2:CCC:663:VAL:CG2	2.46	0.45
3:DDD:592:VAL:O	3:DDD:592:VAL:HG22	2.16	0.45
3:DDD:796:LEU:O	3:DDD:800:LEU:HG	2.17	0.45
5:FFF:84:LEU:HD11	5:FFF:136:PRO:HD3	1.96	0.45
6:111:30:DG:H1'	6:111:31:DT:H5'	1.99	0.45
2:CCC:1210:ILE:HD12	2:CCC:1227:VAL:HG11	1.97	0.45
3:DDD:849:LEU:HB3	3:DDD:856:ILE:HA	1.98	0.45
6:111:32:DA:N3	7:222:32:DA:C2	2.85	0.45
2:CCC:163:LYS:NZ	6:111:55:DC:OP2	2.45	0.45
1:BBB:185:TYR:N	1:BBB:203:ILE:HG23	2.31	0.45
2:CCC:1061:GLN:HE22	3:DDD:445:LYS:HD2	1.80	0.45
3:DDD:958:ILE:HG23	3:DDD:982:LEU:HD11	1.99	0.45
1:BBB:8:PHE:CD1	1:BBB:8:PHE:N	2.84	0.45
3:DDD:320:ASN:O	3:DDD:321:LYS:HB2	2.16	0.45
3:DDD:350:SER:HA	3:DDD:468:VAL:O	2.16	0.45
3:DDD:702:GLN:O	3:DDD:718:SER:N	2.45	0.45
2:CCC:183:TRP:CZ3	6:111:51:DC:H2'	2.52	0.45
2:CCC:558:VAL:HG12	2:CCC:573:ASN:ND2	2.31	0.45
3:DDD:1029:THR:HG22	3:DDD:1121:LEU:HD11	1.99	0.45
2:CCC:653:MET:HG2	2:CCC:654:ASP:N	2.32	0.45
3:DDD:923:ILE:HD12	3:DDD:1256:ILE:HD12	1.99	0.45
2:CCC:1261:GLY:HA2	7:222:15:DT:OP1	2.17	0.44
1:AAA:44:ARG:NH2	2:CCC:1215:GLY:HA2	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CCC:1061:GLN:HE21	2:CCC:1239:VAL:CG1	2.30	0.44
3:DDD:51:PRO:HG2	3:DDD:71:LEU:HD21	1.98	0.44
2:CCC:562:GLU:HG2	2:CCC:574:SER:CB	2.44	0.44
5:FFF:268:ALA:O	5:FFF:272:GLU:HG3	2.16	0.44
5:FFF:292:GLY:HA2	5:FFF:297:LEU:H	1.81	0.44
1:AAA:14:VAL:HG21	1:AAA:29:GLU:HG2	1.99	0.44
2:CCC:974:ARG:HD2	2:CCC:1014:LEU:HD11	1.99	0.44
2:CCC:189:ASP:HB2	2:CCC:190:PRO:HD2	1.98	0.44
2:CCC:66:SER:OG	2:CCC:479:LEU:HD22	2.18	0.44
3:DDD:1025:MET:HB2	3:DDD:1126:GLN:HE21	1.82	0.44
1:AAA:158:ARG:HD2	1:AAA:172:LEU:CD1	2.44	0.44
1:BBB:202:VAL:HG12	1:BBB:202:VAL:O	2.17	0.44
2:CCC:1083:GLU:HG2	2:CCC:1083:GLU:H	1.65	0.44
2:CCC:1211:ARG:HB3	2:CCC:1220:GLN:NE2	2.32	0.44
2:CCC:269:ILE:HG23	2:CCC:273:HIS:CB	2.47	0.44
1:AAA:48:LEU:CD2	1:AAA:183:ILE:CG2	2.95	0.44
1:BBB:86:LYS:HG3	1:BBB:173:VAL:HG12	1.98	0.44
2:CCC:573:ASN:HD22	2:CCC:574:SER:N	2.15	0.44
5:FFF:277:ARG:CD	5:FFF:306:GLN:HE21	2.31	0.44
1:AAA:235:ARG:HB3	1:BBB:214:GLU:OE2	2.18	0.44
1:BBB:222:THR:O	1:BBB:226:GLU:HG3	2.18	0.44
2:CCC:14:ASP:O	2:CCC:1155:VAL:HG13	2.18	0.44
2:CCC:360:LEU:O	2:CCC:364:VAL:HG23	2.18	0.44
2:CCC:525:THR:CG2	2:CCC:687:ARG:HD2	2.48	0.44
3:DDD:114:ILE:CD1	3:DDD:312:ARG:HB2	2.47	0.44
3:DDD:1180:VAL:HG23	3:DDD:1181:ASP:N	2.33	0.44
3:DDD:138:VAL:HG22	3:DDD:145:VAL:HG23	2.00	0.44
3:DDD:579:LEU:O	3:DDD:579:LEU:HD23	2.18	0.44
1:BBB:83:LEU:HD11	3:DDD:526:VAL:CG1	2.48	0.44
2:CCC:183:TRP:CH2	6:111:51:DC:C2'	2.96	0.44
2:CCC:898:GLU:OE2	5:FFF:280:LEU:CD1	2.66	0.44
2:CCC:503:LYS:HE2	7:222:22:DA:H4'	2.00	0.44
1:BBB:52:PRO:CA	1:BBB:150:ARG:CB	2.93	0.44
3:DDD:1279:GLN:O	3:DDD:1279:GLN:HG3	2.17	0.44
3:DDD:678:ARG:NH1	3:DDD:756:GLU:OE2	2.51	0.44
3:DDD:1000:GLY:HA2	3:DDD:1028:ILE:HD12	2.00	0.44
5:FFF:164:THR:HB	5:FFF:219:ILE:CD1	2.47	0.44
2:CCC:700:VAL:HG21	2:CCC:1114:GLU:HG3	1.99	0.43
2:CCC:1182:ILE:HD11	2:CCC:1198:LEU:HD21	2.00	0.43
2:CCC:932:GLN:HE22	2:CCC:952:GLN:NE2	2.16	0.43
3:DDD:1161:GLY:HA3	3:DDD:1179:PRO:HA	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:DDD:1326:GLN:CD	7:222:9:DT:H4'	2.38	0.43
3:DDD:392:THR:HG21	5:FFF:320:GLN:C	2.38	0.43
3:DDD:502:PRO:HB3	3:DDD:506:VAL:HG11	1.99	0.43
3:DDD:638:SER:OG	3:DDD:639:VAL:N	2.51	0.43
2:CCC:685:MET:HE1	2:CCC:1067:ALA:CB	2.47	0.43
2:CCC:1308:ILE:HG23	3:DDD:380:PHE:CD1	2.54	0.43
1:BBB:83:LEU:CD2	3:DDD:526:VAL:HB	2.49	0.43
2:CCC:685:MET:HE1	2:CCC:1067:ALA:HB2	2.00	0.43
2:CCC:1271:GLY:O	2:CCC:1275:VAL:HG23	2.19	0.43
2:CCC:810:TYR:CE1	2:CCC:1078:LYS:HD2	2.53	0.43
3:DDD:325:LYS:HE2	3:DDD:330:MET:HG2	2.00	0.43
3:DDD:378:LYS:N	3:DDD:379:PRO:CD	2.82	0.43
2:CCC:854:ILE:HB	2:CCC:857:VAL:HG21	2.00	0.43
3:DDD:22:ILE:HG13	3:DDD:1319:PHE:CZ	2.54	0.43
3:DDD:842:ARG:CB	3:DDD:882:VAL:HG11	2.48	0.43
2:CCC:61:SER:HB3	2:CCC:479:LEU:HB3	2.01	0.43
3:DDD:1050:THR:HG22	3:DDD:1051:ASP:N	2.33	0.43
3:DDD:495:ASN:ND2	3:DDD:1247:LYS:HB2	2.33	0.43
2:CCC:545:PHE:CE1	3:DDD:788:LEU:HD12	2.54	0.43
1:BBB:157:THR:CG2	1:BBB:157:THR:O	2.66	0.43
3:DDD:245:LEU:HD12	3:DDD:246:PRO:HD2	2.00	0.43
3:DDD:809:VAL:CG2	3:DDD:915:ILE:HD11	2.49	0.43
7:222:17:DG:H2''	7:222:18:DT:O4'	2.16	0.43
1:AAA:235:ARG:HB2	1:BBB:13:LEU:HD23	2.00	0.43
2:CCC:1124:ILE:CD1	2:CCC:1198:LEU:HD11	2.45	0.43
3:DDD:800:LEU:CD2	3:DDD:1309:ILE:CD1	2.89	0.43
5:FFF:159:MET:HG2	5:FFF:172:VAL:HG11	2.00	0.43
2:CCC:716:ALA:HB3	2:CCC:784:ALA:HB3	2.01	0.43
2:CCC:27:LEU:HB2	2:CCC:524:ILE:HD11	2.01	0.43
2:CCC:390:PHE:HA	2:CCC:419:ILE:HG23	1.99	0.43
2:CCC:525:THR:CG2	2:CCC:687:ARG:CD	2.94	0.43
2:CCC:757:THR:HG22	2:CCC:758:ARG:N	2.34	0.43
3:DDD:973:LEU:CD2	3:DDD:1006:GLY:HA2	2.49	0.43
3:DDD:1046:ILE:HG22	3:DDD:1061:VAL:HA	2.00	0.43
3:DDD:925:GLU:N	3:DDD:926:PRO:HD2	2.34	0.43
3:DDD:395:LYS:HG2	5:FFF:251:GLN:NE2	2.34	0.43
1:BBB:179:PRO:HG2	1:BBB:211:ILE:HG13	1.99	0.42
1:BBB:83:LEU:HD11	3:DDD:526:VAL:CB	2.42	0.42
2:CCC:1308:ILE:HG23	3:DDD:380:PHE:CE1	2.54	0.42
3:DDD:122:SER:O	3:DDD:123:ARG:CB	2.66	0.42
4:EEE:41:GLU:HG3	4:EEE:42:GLU:H	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CCC:1302:THR:HA	5:FFF:246:PRO:HB3	2.01	0.42
1:BBB:67:GLU:N	1:BBB:171:LEU:CD2	2.75	0.42
3:DDD:52:GLU:HG3	3:DDD:53:ARG:H	1.84	0.42
3:DDD:552:ILE:HG21	3:DDD:589:TYR:CD1	2.55	0.42
3:DDD:863:LEU:CD2	3:DDD:908:ILE:HG13	2.50	0.42
2:CCC:901:LEU:HG	5:FFF:278:PHE:CD2	2.54	0.42
2:CCC:670:PHE:CZ	2:CCC:1195:ILE:HD11	2.54	0.42
2:CCC:686:GLN:HG2	2:CCC:796:LEU:CD1	2.49	0.42
1:AAA:166:ARG:HH21	2:CCC:863:SER:HB2	1.85	0.42
3:DDD:710:ASP:OD1	3:DDD:710:ASP:N	2.52	0.42
3:DDD:474:LEU:CD1	4:EEE:28:ARG:HD3	2.50	0.42
2:CCC:1257:GLN:HB3	2:CCC:1258:PRO:HD2	2.02	0.42
2:CCC:186:PHE:CD1	2:CCC:196:VAL:HG22	2.55	0.42
2:CCC:624:ASP:O	2:CCC:624:ASP:CG	2.58	0.42
1:BBB:31:LEU:O	1:BBB:198:LEU:HD13	2.19	0.42
3:DDD:438:GLU:HA	3:DDD:439:PRO:HD3	1.87	0.42
3:DDD:707:ILE:HD12	3:DDD:707:ILE:N	2.31	0.42
2:CCC:1301:ARG:NH1	5:FFF:243:GLU:OE2	2.52	0.42
1:AAA:124:VAL:HG11	1:AAA:209:GLY:HA3	2.01	0.42
2:CCC:1307:ASN:HB3	2:CCC:1312:ASN:O	2.18	0.42
3:DDD:140:TYR:OH	3:DDD:312:ARG:HD2	2.19	0.42
3:DDD:855:ASP:OD1	3:DDD:855:ASP:O	2.37	0.42
5:FFF:228:GLY:HA3	8:333:14:GTP:O1A	2.20	0.42
2:CCC:1305:TYR:CD2	5:FFF:250:THR:HG21	2.54	0.42
2:CCC:356:THR:HG21	2:CCC:362:ALA:HA	2.01	0.42
3:DDD:282:LEU:HD11	5:FFF:121:GLU:OE1	2.19	0.42
3:DDD:353:SER:HB3	3:DDD:447:ILE:HG13	2.00	0.42
3:DDD:1251:LYS:O	3:DDD:1255:VAL:HG23	2.19	0.42
3:DDD:30:ILE:HG23	3:DDD:243:PRO:HB3	2.02	0.42
2:CCC:1286:THR:N	3:DDD:479:GLU:OE1	2.53	0.42
2:CCC:538:LEU:HD11	2:CCC:547:VAL:HG11	2.02	0.42
3:DDD:1078:LEU:HD12	3:DDD:1121:LEU:HB3	2.02	0.42
2:CCC:615:VAL:HA	2:CCC:638:SER:HB3	2.01	0.42
3:DDD:342:LEU:HD12	3:DDD:342:LEU:HA	1.82	0.42
3:DDD:388:ARG:HH21	3:DDD:414:GLU:HG2	1.85	0.42
5:FFF:163:ARG:HD3	5:FFF:167:LEU:HD12	2.02	0.42
7:222:22:DA:H1'	7:222:23:DT:H5'	2.02	0.41
1:AAA:145:LYS:HD3	1:AAA:147:GLN:HE21	1.85	0.41
2:CCC:360:LEU:HA	2:CCC:360:LEU:HD12	1.88	0.41
1:BBB:159:ILE:HD12	1:BBB:166:ARG:NH2	2.34	0.41
1:BBB:58:GLU:OE1	1:BBB:170:ARG:NE	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BBB:11:PRO:CG	1:BBB:31:LEU:HD23	2.47	0.41
1:BBB:9:LEU:HB2	1:BBB:32:GLU:OE1	2.20	0.41
2:CCC:817:LEU:HD23	2:CCC:817:LEU:HA	1.78	0.41
3:DDD:1212:ASP:N	3:DDD:1212:ASP:OD1	2.53	0.41
3:DDD:937:ILE:HD11	11:DDD:1504:DPO:O6	2.20	0.41
3:DDD:537:TYR:CE1	3:DDD:544:LEU:HG	2.55	0.41
5:FFF:152:GLN:HG3	5:FFF:153:THR:N	2.34	0.41
1:AAA:192:VAL:CG1	1:AAA:193:GLU:N	2.64	0.41
2:CCC:618:GLN:HE21	3:DDD:769:VAL:HB	1.85	0.41
3:DDD:517:CYS:HB3	3:DDD:545:HIS:HB2	2.01	0.41
5:FFF:116:LEU:HA	5:FFF:119:LEU:HD12	2.02	0.41
3:DDD:930:LEU:HB3	3:DDD:1134:ILE:HG13	2.01	0.41
2:CCC:878:THR:CG2	2:CCC:879:GLY:N	2.84	0.41
3:DDD:1134:ILE:HG22	3:DDD:1138:LEU:HG	2.01	0.41
3:DDD:113:HIS:CD2	3:DDD:239:LEU:HD11	2.56	0.41
2:CCC:1274:GLU:HA	3:DDD:428:THR:HG21	2.03	0.41
3:DDD:571:ASP:N	3:DDD:571:ASP:OD1	2.54	0.41
1:BBB:57:THR:O	1:BBB:172:LEU:HD12	2.21	0.41
2:CCC:807:TRP:CD1	2:CCC:817:LEU:CD1	3.04	0.41
3:DDD:612:LEU:HB3	3:DDD:616:PRO:HG2	2.03	0.41
5:FFF:143:SER:CB	6:111:41:DT:H72	2.51	0.41
1:BBB:178:SER:HA	1:BBB:179:PRO:HD3	1.72	0.41
2:CCC:1240:ASP:OD1	2:CCC:1240:ASP:N	2.53	0.41
3:DDD:1281:GLU:HB3	3:DDD:1284:ARG:HG3	2.03	0.41
3:DDD:849:LEU:HD11	3:DDD:850:LYS:O	2.15	0.41
2:CCC:1103:VAL:HB	2:CCC:1104:PRO:HD3	2.02	0.41
3:DDD:1176:VAL:HG22	3:DDD:1187:GLU:HG2	2.01	0.41
3:DDD:1327:GLU:O	3:DDD:1331:VAL:HG23	2.21	0.41
3:DDD:534:GLU:OE1	3:DDD:581:MET:HE1	2.21	0.41
3:DDD:800:LEU:HD22	3:DDD:1256:ILE:HD13	2.03	0.41
5:FFF:277:ARG:HD3	5:FFF:306:GLN:HE21	1.86	0.41
2:CCC:967:LEU:HD21	2:CCC:1021:LEU:HD13	2.03	0.41
2:CCC:1124:ILE:HD11	2:CCC:1198:LEU:CD1	2.43	0.41
3:DDD:1266:ILE:CD1	3:DDD:1274:PHE:HB3	2.47	0.41
3:DDD:864:LEU:HD23	3:DDD:864:LEU:HA	1.79	0.41
5:FFF:114:LEU:HD13	5:FFF:118:ASP:HB3	2.02	0.41
1:BBB:47:LEU:HD13	1:BBB:183:ILE:HD13	2.01	0.41
2:CCC:1284:ALA:HB2	3:DDD:1357:ILE:HB	2.02	0.41
3:DDD:1366:HIS:O	3:DDD:1370:MET:HG2	2.21	0.41
3:DDD:205:LEU:HD13	3:DDD:217:LEU:HD12	2.02	0.41
2:CCC:374:GLU:OE2	6:111:43:DT:H72	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:222:25:DA:H2''	7:222:26:DT:H5''	2.02	0.40
1:AAA:134:THR:HA	2:CCC:773:LEU:HD22	2.03	0.40
1:BBB:33:ARG:HB3	1:BBB:197:ASP:O	2.21	0.40
1:BBB:208:ASN:OD1	1:BBB:208:ASN:C	2.58	0.40
2:CCC:1296:ASP:O	2:CCC:1297:ASP:C	2.60	0.40
2:CCC:992:LEU:HB3	2:CCC:993:PRO:CD	2.50	0.40
3:DDD:374:LEU:HD11	3:DDD:401:VAL:HG13	2.03	0.40
3:DDD:546:ALA:O	3:DDD:573:THR:HA	2.22	0.40
6:111:55:DC:H2''	6:111:56:DG:OP2	2.21	0.40
1:AAA:221:ALA:O	1:BBB:228:LEU:HD22	2.21	0.40
3:DDD:844:THR:HG21	3:DDD:858:VAL:CG1	2.51	0.40
3:DDD:932:MET:SD	8:333:19:U:H2'	2.60	0.40
1:BBB:33:ARG:HH22	2:CCC:1081:PRO:HG3	1.85	0.40
2:CCC:198:ILE:O	2:CCC:201:ARG:CG	2.69	0.40
2:CCC:39:ILE:HG23	2:CCC:75:LEU:HD11	2.03	0.40
2:CCC:709:ALA:HB3	2:CCC:792:GLY:O	2.21	0.40
3:DDD:925:GLU:N	3:DDD:926:PRO:CD	2.85	0.40
3:DDD:481:ARG:NH1	4:EEE:3:ARG:O	2.54	0.40
6:111:37:DA:H4'	6:111:38:DT:OP1	2.21	0.40
7:222:12:DG:H2'	7:222:13:DA:O4'	2.21	0.40
1:AAA:207:THR:OG1	1:AAA:208:ASN:N	2.54	0.40
2:CCC:681:MET:O	2:CCC:685:MET:HG3	2.21	0.40
3:DDD:1060:VAL:HG22	3:DDD:1106:ILE:HG12	2.02	0.40
3:DDD:223:LEU:O	3:DDD:227:PHE:N	2.47	0.40
4:EEE:73:GLN:HA	4:EEE:76:GLU:HB2	2.04	0.40
5:FFF:169:ILE:HG22	5:FFF:173:LYS:HD2	2.03	0.40
5:FFF:182:ALA:HB1	5:FFF:193:PRO:HG3	2.03	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)
3:DDD:1170:LYS:NZ	7:222:33:DC:OP1[3_644]	2.16	0.04

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%)	210 (92%)	12 (5%)	6 (3%)	5	32
1	BBB	226/242 (93%)	203 (90%)	20 (9%)	3 (1%)	12	46
2	CCC	1339/1342 (100%)	1245 (93%)	85 (6%)	9 (1%)	22	60
3	DDD	1360/1407 (97%)	1260 (93%)	91 (7%)	9 (1%)	22	60
4	EEE	77/90 (86%)	75 (97%)	2 (3%)	0	100	100
5	FFF	275/336 (82%)	256 (93%)	14 (5%)	5 (2%)	8	39
All	All	3505/3659 (96%)	3249 (93%)	224 (6%)	32 (1%)	17	54

All (32) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AAA	192	VAL
3	DDD	519	ASN
3	DDD	1053	LEU
5	FFF	190	ASP
1	AAA	210	THR
1	BBB	232	VAL
2	CCC	756	TYR
1	AAA	162	GLU
1	AAA	196	THR
1	AAA	208	ASN
2	CCC	914	LYS
3	DDD	805	GLN
1	AAA	161	SER
2	CCC	234	ASP
2	CCC	293	ALA
2	CCC	342	ASP
2	CCC	1103	VAL
2	CCC	1297	ASP
3	DDD	520	ALA
5	FFF	115	ALA
3	DDD	321	LYS
3	DDD	854	ALA
3	DDD	1325	PHE
3	DDD	342	LEU
3	DDD	711	GLY
5	FFF	113	GLY

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Mol	Chain	Res	Type
2	CCC	507	GLY
2	CCC	1186	VAL
1	BBB	14	VAL
5	FFF	228	GLY
5	FFF	295	ILE
1	BBB	192	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AAA	198/208 (95%)	189 (96%)	9 (4%)	27	60
1	BBB	196/208 (94%)	181 (92%)	15 (8%)	13	42
2	CCC	1156/1157 (100%)	1136 (98%)	20 (2%)	60	82
3	DDD	1135/1168 (97%)	1117 (98%)	18 (2%)	62	83
4	EEE	67/74 (90%)	66 (98%)	1 (2%)	65	84
5	FFF	240/292 (82%)	231 (96%)	9 (4%)	33	64
All	All	2992/3107 (96%)	2920 (98%)	72 (2%)	49	76

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	8	PHE
1	AAA	10	LYS
1	AAA	28	LEU
1	AAA	32	GLU
1	AAA	33	ARG
1	AAA	48	LEU
1	AAA	70	THR
1	AAA	117	HIS
1	AAA	157	THR
1	BBB	8	PHE
1	BBB	15	ASP
1	BBB	22	THR

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Mol	Chain	Res	Type
1	BBB	28	LEU
1	BBB	32	GLU
1	BBB	33	ARG
1	BBB	48	LEU
1	BBB	70	THR
1	BBB	77	ASP
1	BBB	117	HIS
1	BBB	191	ARG
1	BBB	192	VAL
1	BBB	193	GLU
1	BBB	198	LEU
1	BBB	199	ASP
2	CCC	12	ARG
2	CCC	24	VAL
2	CCC	77	GLU
2	CCC	124	MET
2	CCC	163	LYS
2	CCC	378	ARG
2	CCC	443	ASP
2	CCC	444	ASP
2	CCC	573	ASN
2	CCC	700	VAL
2	CCC	755	LYS
2	CCC	799	ASN
2	CCC	901	LEU
2	CCC	951	MET
2	CCC	1034	ARG
2	CCC	1089	GLU
2	CCC	1207	SER
2	CCC	1240	ASP
2	CCC	1255	THR
2	CCC	1272	GLU
3	DDD	28	ASP
3	DDD	52	GLU
3	DDD	93	THR
3	DDD	99	ARG
3	DDD	227	PHE
3	DDD	504	GLN
3	DDD	505	ASP
3	DDD	526	VAL
3	DDD	538	ARG
3	DDD	599	LYS

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Mol	Chain	Res	Type
3	DDD	706	VAL
3	DDD	707	ILE
3	DDD	731	ARG
3	DDD	783	LEU
3	DDD	798	ARG
3	DDD	936	HIS
3	DDD	1131	THR
3	DDD	1282	TYR
4	EEE	45	LYS
5	FFF	74	GLU
5	FFF	152	GLN
5	FFF	156	ARG
5	FFF	190	ASP
5	FFF	192	GLU
5	FFF	203	ASP
5	FFF	241	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 ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
8	333	4/6 (66%)	2 (50%)	0

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	333	18	C
8	333	19	U

There are no RNA pucker outliers to report.

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	$\# Z > 2$
11	DPO	DDD	1504	-	6,8,8	0.76	0	13,13,13	0.79	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
11	DPO	DDD	1504	-	-	1/6/6/6	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	DDD	1504	DPO	P2-O4-P1-O1

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	DDD	1504	DPO	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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%)	0.42	17 (7%) 14 17	159, 207, 265, 284	0
1	BBB	228/242 (94%)	0.44	26 (11%) 5 7	162, 219, 286, 326	0
2	CCC	1341/1342 (99%)	0.16	58 (4%) 35 34	95, 172, 271, 347	0
3	DDD	1362/1407 (96%)	0.30	94 (6%) 16 19	101, 185, 277, 345	0
4	EEE	79/90 (87%)	0.06	6 (7%) 13 16	156, 223, 347, 400	0
5	FFF	277/336 (82%)	0.44	24 (8%) 10 13	136, 210, 288, 306	0
6	111	30/50 (60%)	0.04	2 (6%) 17 19	191, 228, 301, 336	0
7	222	35/50 (70%)	0.83	10 (28%) 0 0	129, 234, 353, 421	0
8	333	5/6 (83%)	-0.06	0 100 100	137, 138, 155, 188	0
All	All	3587/3765 (95%)	0.27	237 (6%) 18 19	95, 191, 283, 421	0

All (237) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	CCC	1002	LEU	7.1
2	CCC	1004	ASP	7.0
3	DDD	1110	GLU	7.0
5	FFF	263	LEU	6.9
3	DDD	1129	GLY	6.0
3	DDD	1130	GLY	6.0
5	FFF	310	LEU	5.8
3	DDD	1030	GLU	5.8
2	CCC	1000	LEU	5.6
5	FFF	273	VAL	5.6
3	DDD	1078	LEU	5.5
7	222	38	DG	5.5
6	111	49	DG	5.5
1	AAA	30	PRO	5.4
3	DDD	880	VAL	5.2

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Mol	Chain	Res	Type	RSRZ
3	DDD	1185	PRO	5.1
4	EEE	78	ALA	5.1
3	DDD	1189	MET	4.9
7	222	18	DT	4.9
3	DDD	1273	ASP	4.8
2	CCC	1055	ALA	4.7
1	BBB	160	HIS	4.7
3	DDD	983	LYS	4.6
1	AAA	142	MET	4.5
5	FFF	229	ASP	4.4
3	DDD	958	ILE	4.4
7	222	37	DA	4.3
3	DDD	982	LEU	4.3
3	DDD	995	TYR	4.3
2	CCC	998	LEU	4.1
2	CCC	975	ILE	4.1
3	DDD	1051	ASP	4.1
3	DDD	1003	LEU	4.1
1	AAA	135	ASP	4.1
3	DDD	1056	LEU	4.1
3	DDD	856	ILE	4.0
3	DDD	1098	GLN	3.9
4	EEE	80	LEU	3.9
3	DDD	1028	ILE	3.9
1	BBB	78	ILE	3.9
3	DDD	973	LEU	3.9
1	BBB	35	PHE	3.9
3	DDD	670	SER	3.9
3	DDD	1065	ALA	3.8
2	CCC	1001	GLY	3.8
2	CCC	230	PHE	3.8
6	111	44	DG	3.8
3	DDD	1019	ASN	3.7
1	BBB	131	CYS	3.7
3	DDD	1050	THR	3.7
1	AAA	144	ILE	3.6
2	CCC	124	MET	3.6
3	DDD	46	TYR	3.6
2	CCC	241	LEU	3.6
3	DDD	879	ALA	3.6
3	DDD	1118	GLY	3.5
2	CCC	885	GLY	3.5

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Mol	Chain	Res	Type	RSRZ
3	DDD	997	VAL	3.5
3	DDD	1190	ILE	3.5
1	AAA	213	PRO	3.4
2	CCC	1013	GLN	3.4
2	CCC	8	LYS	3.4
5	FFF	306	GLN	3.4
3	DDD	382	TYR	3.4
2	CCC	1014	LEU	3.4
3	DDD	957	SER	3.4
3	DDD	989	GLY	3.4
1	AAA	233	ASP	3.3
5	FFF	230	SER	3.3
1	BBB	98	VAL	3.3
2	CCC	1010	GLN	3.3
1	BBB	152	TYR	3.3
3	DDD	671	GLY	3.3
3	DDD	1121	LEU	3.3
2	CCC	239	MET	3.3
1	AAA	171	LEU	3.2
5	FFF	305	ILE	3.2
3	DDD	848	VAL	3.2
3	DDD	1115	ILE	3.2
3	DDD	1029	THR	3.2
2	CCC	913	VAL	3.2
1	BBB	90	VAL	3.2
2	CCC	385	PHE	3.2
3	DDD	1017	VAL	3.2
1	BBB	39	LEU	3.2
7	222	26	DT	3.2
4	EEE	77	ALA	3.2
7	222	39	DG	3.2
2	CCC	261	VAL	3.2
3	DDD	667	GLN	3.2
5	FFF	259	ILE	3.1
1	BBB	123	ILE	3.1
3	DDD	1272	SER	3.1
2	CCC	311	CYS	3.1
2	CCC	333	ILE	3.1
5	FFF	307	VAL	3.1
3	DDD	56	LEU	3.1
2	CCC	696	ASP	3.0
2	CCC	850	ILE	3.0

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Mol	Chain	Res	Type	RSRZ
5	FFF	111	ASN	3.0
7	222	22	DA	3.0
3	DDD	975	ILE	3.0
3	DDD	115	TRP	3.0
5	FFF	303	ARG	3.0
2	CCC	999	GLU	3.0
2	CCC	96	LEU	3.0
3	DDD	981	GLU	3.0
3	DDD	237	MET	3.0
3	DDD	1109	LEU	2.9
2	CCC	797	GLY	2.9
3	DDD	1004	ALA	2.9
1	AAA	160	HIS	2.9
2	CCC	1011	LEU	2.9
5	FFF	295	ILE	2.9
3	DDD	992	LYS	2.9
1	BBB	107	ILE	2.9
3	DDD	1068	THR	2.9
5	FFF	286	ALA	2.9
3	DDD	1049	GLN	2.8
1	BBB	133	LEU	2.8
3	DDD	1099	TYR	2.8
5	FFF	110	GLY	2.8
2	CCC	984	VAL	2.8
2	CCC	5	TYR	2.8
3	DDD	1020	TRP	2.8
3	DDD	988	PHE	2.8
1	BBB	205	MET	2.8
1	BBB	26	VAL	2.8
7	222	19	DA	2.8
5	FFF	285	ALA	2.7
2	CCC	232	ILE	2.7
3	DDD	672	LEU	2.7
1	AAA	28	LEU	2.7
3	DDD	1018	ALA	2.7
1	BBB	144	ILE	2.7
3	DDD	943	ARG	2.7
1	BBB	157	THR	2.7
7	222	23	DT	2.7
2	CCC	390	PHE	2.7
1	BBB	161	SER	2.6
3	DDD	950	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
2	CCC	721	GLY	2.6
2	CCC	105	TYR	2.6
2	CCC	484	LEU	2.6
3	DDD	87	LYS	2.6
3	DDD	754	ILE	2.6
3	DDD	1052	GLU	2.6
2	CCC	533	LEU	2.6
3	DDD	147	ILE	2.6
5	FFF	308	GLU	2.6
2	CCC	692	THR	2.6
1	BBB	16	ILE	2.5
3	DDD	1080	ILE	2.5
5	FFF	278	PHE	2.5
1	BBB	25	LYS	2.5
1	BBB	130	ILE	2.5
3	DDD	986	ASP	2.5
3	DDD	750	PRO	2.5
4	EEE	79	GLU	2.5
5	FFF	159	MET	2.5
3	DDD	665	GLN	2.5
1	BBB	65	LEU	2.5
3	DDD	857	LEU	2.5
1	BBB	146	VAL	2.4
2	CCC	1180	MET	2.4
3	DDD	985	ILE	2.4
3	DDD	217	LEU	2.4
1	AAA	205	MET	2.4
3	DDD	90	VAL	2.4
3	DDD	1097	ALA	2.4
5	FFF	112	ARG	2.4
3	DDD	952	VAL	2.4
1	AAA	68	TYR	2.4
2	CCC	1054	LEU	2.4
3	DDD	746	LEU	2.4
5	FFF	313	LEU	2.4
2	CCC	1041	ASP	2.4
3	DDD	1119	ASP	2.4
2	CCC	127	ILE	2.4
3	DDD	215	LYS	2.3
3	DDD	1059	LEU	2.3
2	CCC	1008	GLN	2.3
1	BBB	134	THR	2.3

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Mol	Chain	Res	Type	RSRZ
3	DDD	1186	TYR	2.3
3	DDD	214	ARG	2.3
3	DDD	212	THR	2.3
3	DDD	1161	GLY	2.3
3	DDD	1069	ALA	2.3
2	CCC	883	LEU	2.3
3	DDD	1053	LEU	2.3
3	DDD	1287	ILE	2.3
1	AAA	189	ALA	2.3
7	222	24	DT	2.2
2	CCC	506	PHE	2.2
2	CCC	795	ALA	2.2
4	EEE	2	ALA	2.2
2	CCC	789	THR	2.2
2	CCC	1009	ASN	2.2
2	CCC	798	GLN	2.2
3	DDD	993	GLU	2.2
1	AAA	102	LEU	2.2
3	DDD	1005	LYS	2.2
3	DDD	663	GLU	2.2
2	CCC	15	PHE	2.2
1	BBB	187	VAL	2.2
7	222	25	DA	2.2
4	EEE	58	LEU	2.2
3	DDD	1064	SER	2.2
5	FFF	190	ASP	2.2
1	AAA	25	LYS	2.2
1	BBB	158	ARG	2.2
1	BBB	201	LEU	2.1
3	DDD	1266	ILE	2.1
1	AAA	134	THR	2.1
3	DDD	1021	ASP	2.1
5	FFF	294	GLU	2.1
1	BBB	66	HIS	2.1
2	CCC	875	ALA	2.1
3	DDD	478	LEU	2.1
2	CCC	986	ALA	2.1
1	AAA	201	LEU	2.1
3	DDD	948	SER	2.1
2	CCC	429	MET	2.1
2	CCC	884	VAL	2.0
3	DDD	748	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
2	CCC	169	LYS	2.0
5	FFF	262	TRP	2.0
1	AAA	217	ILE	2.0
5	FFF	264	PHE	2.0
3	DDD	965	SER	2.0
2	CCC	1015	ALA	2.0
2	CCC	698	PRO	2.0
2	CCC	912	ASP	2.0
2	CCC	1012	GLU	2.0
2	CCC	788	SER	2.0
3	DDD	1001	ALA	2.0
3	DDD	79	LYS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides 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(\AA^2)	Q<0.9
10	ZN	DDD	1501	1/1	0.88	0.04	267,267,267,267	0
9	MG	CCC	1401	1/1	0.96	0.42	156,156,156,156	0
11	DPO	DDD	1504	9/9	0.97	0.57	155,178,196,201	0
9	MG	DDD	1503	1/1	0.98	0.23	93,93,93,93	0
10	ZN	DDD	1502	1/1	0.99	0.20	162,162,162,162	0

6.5 Other polymers [i](#)

There are no such residues in this entry.