



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:10 PM UTC

PDB ID : 2NYG / pdb_00002nyg
Title : Crystal structure of YokD protein from Bacillus subtilis
Authors : Madegowda, M.; Eswaramoorthy, S.; Burley, S.K.; Swaminathan, S.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2006-11-20
Resolution : 2.60 Å(reported)

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

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A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

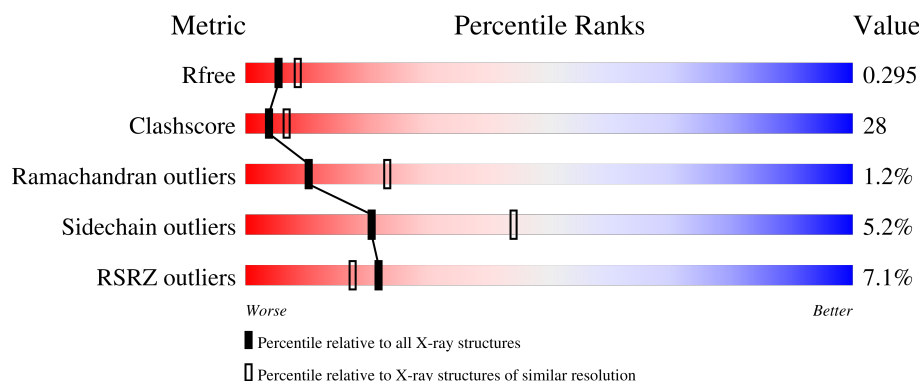
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

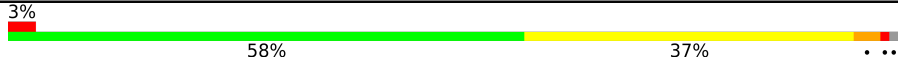
The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	273	
1	B	273	
1	C	273	
1	D	273	
1	E	273	

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Mol	Chain	Length	Quality of chain
1	F	273	

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
2	COA	A	301	X	-	-	-
2	COA	B	302	X	-	-	-
2	COA	C	303	X	-	-	-
2	COA	D	304	X	-	-	-
2	COA	E	305	X	-	-	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12534 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.

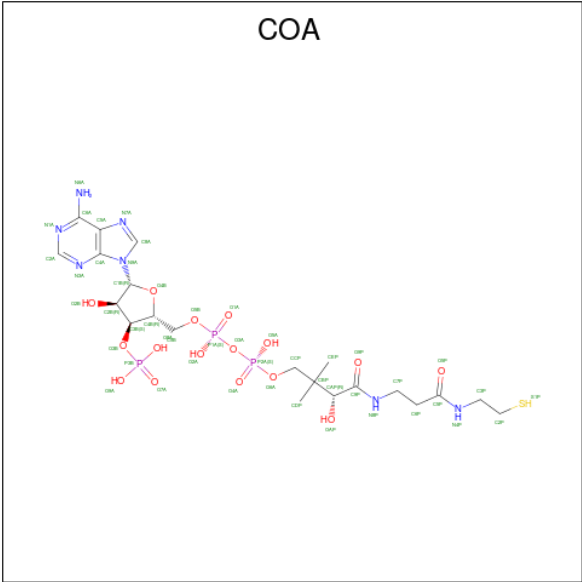
- Molecule 1 is a protein called YokD protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	270	Total	C	N	O	S	0	0	0
			2119	1359	358	395	7			
1	B	251	Total	C	N	O	S	0	0	0
			1942	1250	322	364	6			
1	C	270	Total	C	N	O	S	0	0	0
			2104	1351	348	398	7			
1	D	268	Total	C	N	O	S	0	0	0
			2089	1342	344	396	7			
1	E	260	Total	C	N	O	S	0	0	0
			2018	1295	341	375	7			
1	F	248	Total	C	N	O	S	0	0	0
			1829	1177	307	339	6			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	-	cloning artifact	UNP O32003
A	2	LEU	-	cloning artifact	UNP O32003
B	1	SER	-	cloning artifact	UNP O32003
B	2	LEU	-	cloning artifact	UNP O32003
C	1	SER	-	cloning artifact	UNP O32003
C	2	LEU	-	cloning artifact	UNP O32003
D	1	SER	-	cloning artifact	UNP O32003
D	2	LEU	-	cloning artifact	UNP O32003
E	1	SER	-	cloning artifact	UNP O32003
E	2	LEU	-	cloning artifact	UNP O32003
F	1	SER	-	cloning artifact	UNP O32003
F	2	LEU	-	cloning artifact	UNP O32003

- Molecule 2 is COENZYME A (CCD ID: COA) (formula: $C_{21}H_{36}N_7O_{16}P_3S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			42	18	6	15	3		
2	B	1	Total	C	N	O	P	0	0
			42	18	6	15	3		
2	C	1	Total	C	N	O	P	0	0
			42	18	6	15	3		
2	D	1	Total	C	N	O	P	0	0
			42	18	6	15	3		
2	E	1	Total	C	N	O	P	0	0
			42	18	6	15	3		

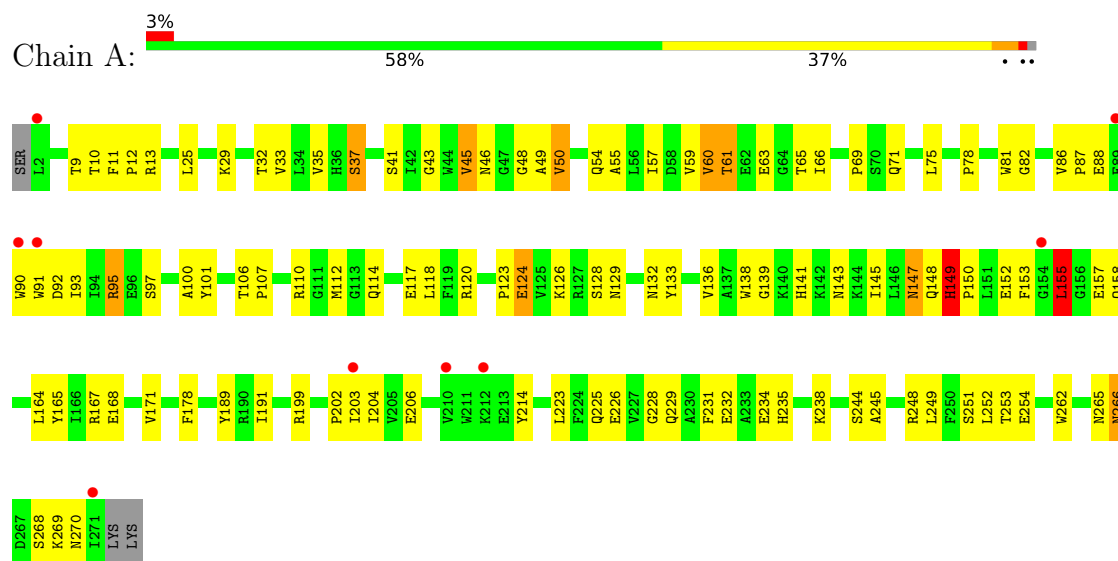
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	39	Total	O	0	0
			39	39		
3	B	28	Total	O	0	0
			28	28		
3	C	41	Total	O	0	0
			41	41		
3	D	34	Total	O	0	0
			34	34		
3	E	43	Total	O	0	0
			43	43		
3	F	38	Total	O	0	0
			38	38		

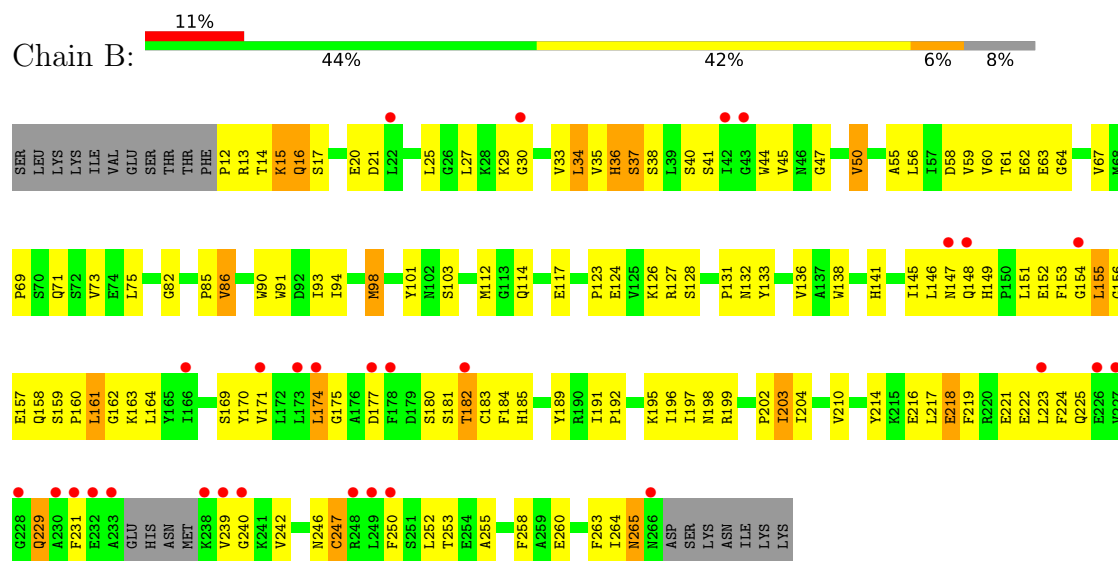
3 Residue-property plots [i](#)

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.

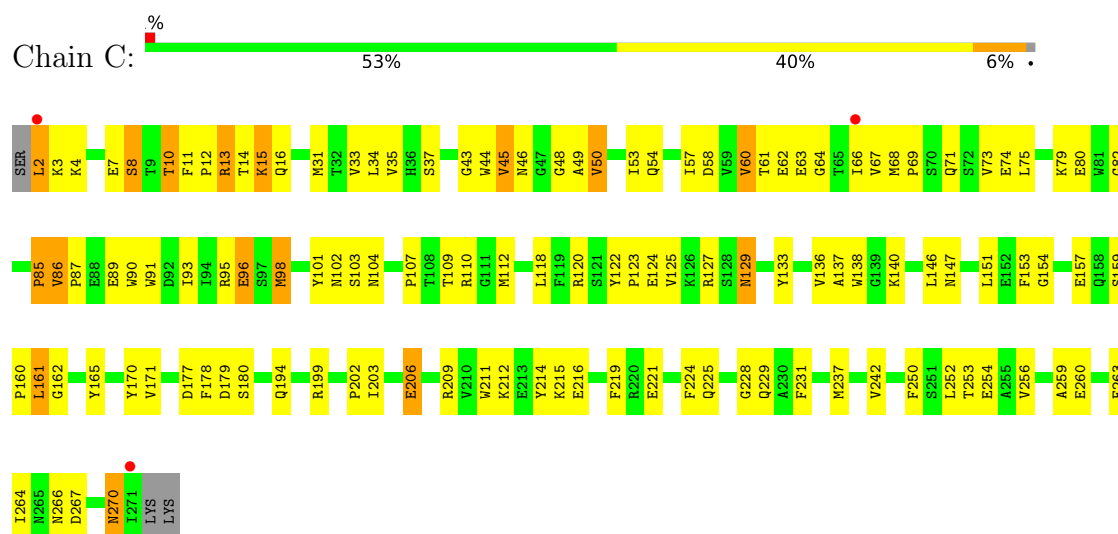
• Molecule 1: YokD protein



• Molecule 1: YokD protein



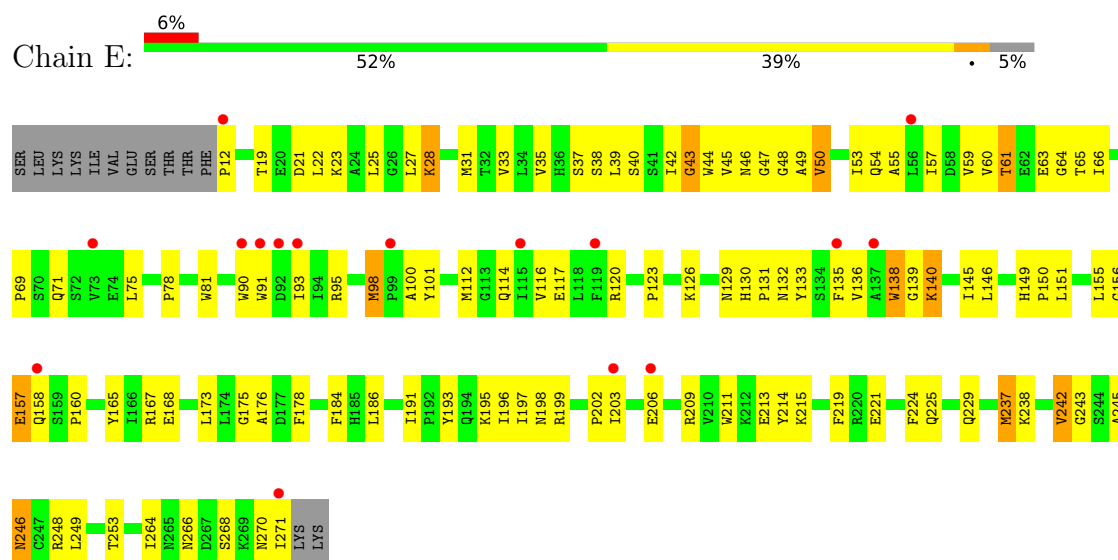
• Molecule 1: YokD protein



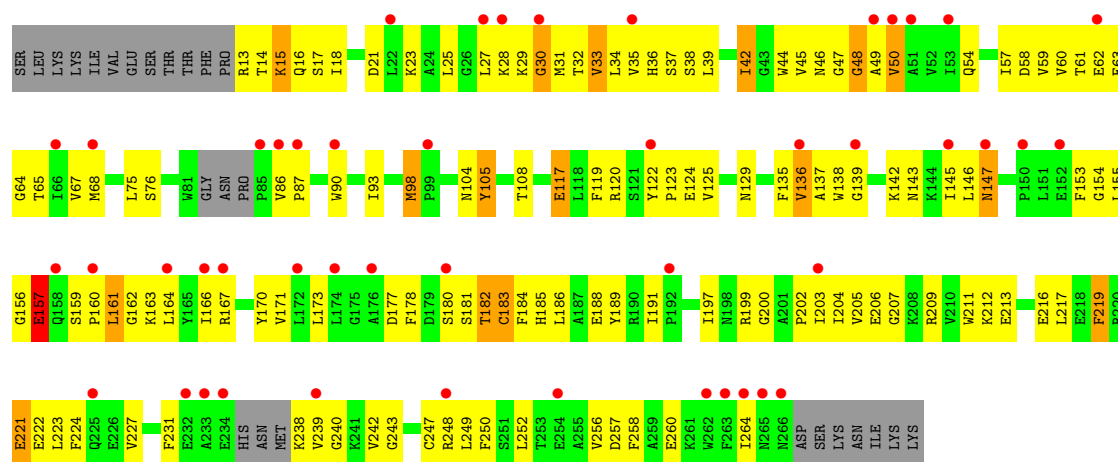
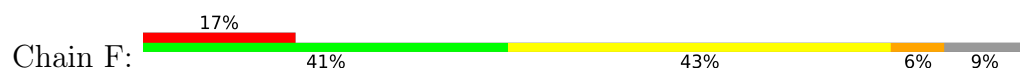
• Molecule 1: YokD protein



• Molecule 1: YokD protein



• Molecule 1: YokD protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	73.02Å 132.39Å 185.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.04 – 2.60 49.04 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.6 (49.04-2.60) 99.6 (49.04-2.60)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.03 (at 2.37Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.257 , 0.296 0.255 , 0.295	Depositor DCC
R_{free} test set	1434 reflections (2.01%)	wwPDB-VP
Wilson B-factor (Å ²)	48.5	Xtriage
Anisotropy	0.486	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 49.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	12534	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.84% 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: COA

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.59	0/2172	1.09	17/2951 (0.6%)
1	B	0.47	1/1993 (0.1%)	0.98	8/2716 (0.3%)
1	C	0.57	1/2158 (0.0%)	1.10	16/2938 (0.5%)
1	D	0.58	2/2143 (0.1%)	1.12	19/2917 (0.7%)
1	E	0.51	0/2069	1.07	16/2812 (0.6%)
1	F	0.47	0/1872	0.98	6/2555 (0.2%)
All	All	0.53	4/12407 (0.0%)	1.06	82/16889 (0.5%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	98	MET	SD-CE	-5.82	1.65	1.79
1	C	98	MET	SD-CE	-5.48	1.65	1.79
1	D	112	MET	SD-CE	-5.11	1.66	1.79
1	B	98	MET	SD-CE	-5.06	1.66	1.79

All (82) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	148	GLN	N-CA-C	10.68	122.68	111.14
1	D	155	LEU	N-CA-C	-10.51	93.25	110.17
1	A	129	ASN	N-CA-C	8.61	122.10	112.97
1	A	43	GLY	N-CA-C	-8.24	102.36	112.33
1	E	129	ASN	N-CA-C	8.06	121.96	112.93
1	C	140	LYS	N-CA-C	7.84	120.81	111.33
1	D	43	GLY	N-CA-C	-7.62	101.95	111.70
1	D	129	ASN	N-CA-C	7.53	120.95	112.97
1	F	35	VAL	N-CA-C	7.38	118.44	108.11
1	E	43	GLY	N-CA-C	-7.38	101.02	112.45
1	E	35	VAL	N-CA-C	6.97	117.93	108.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	37	SER	N-CA-C	6.86	119.84	109.41
1	C	154	GLY	N-CA-C	6.79	122.13	113.24
1	D	149	HIS	CA-C-N	6.77	126.74	119.76
1	D	149	HIS	C-N-CA	6.77	126.74	119.76
1	E	98	MET	CA-C-N	6.76	127.14	119.83
1	E	98	MET	C-N-CA	6.76	127.14	119.83
1	F	37	SER	N-CA-C	6.71	120.00	110.14
1	D	156	GLY	CA-C-N	6.68	129.54	120.38
1	D	156	GLY	C-N-CA	6.68	129.54	120.38
1	C	43	GLY	N-CA-C	-6.66	102.95	112.81
1	C	129	ASN	N-CA-C	6.48	119.89	112.57
1	E	243	GLY	N-CA-C	-6.36	100.13	110.95
1	C	60	VAL	N-CA-C	6.31	117.05	110.62
1	D	15	LYS	N-CA-C	-6.30	104.47	111.71
1	B	37	SER	N-CA-C	6.21	117.67	108.60
1	D	242	VAL	N-CA-C	-6.21	96.43	109.34
1	C	33	VAL	N-CA-C	6.16	116.73	108.11
1	C	242	VAL	N-CA-C	-6.08	97.61	107.28
1	E	37	SER	N-CA-C	6.06	117.45	108.60
1	A	37	SER	N-CA-C	6.04	119.06	109.81
1	A	95	ARG	N-CA-C	-6.03	104.64	112.23
1	C	15	LYS	N-CA-C	-6.02	104.80	111.36
1	C	8	SER	N-CA-C	-5.97	105.73	114.39
1	B	91	TRP	N-CA-C	5.96	118.26	111.11
1	A	149	HIS	N-CA-C	5.96	122.97	109.81
1	C	37	SER	N-CA-C	5.96	118.47	109.41
1	A	33	VAL	N-CA-C	5.93	116.83	108.17
1	C	35	VAL	N-CA-C	5.85	117.42	108.71
1	E	130	HIS	CA-C-N	5.83	125.51	119.56
1	E	130	HIS	C-N-CA	5.83	125.51	119.56
1	A	155	LEU	N-CA-C	-5.82	98.42	110.80
1	E	140	LYS	N-CA-C	5.82	117.70	111.36
1	A	93	ILE	N-CA-C	-5.76	104.50	112.50
1	E	28	LYS	N-CA-C	5.73	119.02	109.96
1	A	139	GLY	N-CA-C	5.72	118.71	111.85
1	F	243	GLY	N-CA-C	-5.70	104.44	111.45
1	F	33	VAL	N-CA-C	5.68	118.34	108.90
1	F	219	PHE	N-CA-C	5.67	117.84	110.53
1	A	141	HIS	N-CA-C	5.65	119.87	112.92
1	A	35	VAL	N-CA-C	5.64	116.71	108.53
1	C	96	GLU	N-CA-C	5.63	119.88	112.89
1	D	3	LYS	N-CA-C	-5.60	105.18	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	40	SER	N-CA-C	5.59	117.37	111.28
1	B	15	LYS	N-CA-C	-5.58	104.22	111.02
1	B	34	LEU	N-CA-C	-5.50	99.77	108.73
1	A	147	ASN	N-CA-C	5.45	122.41	110.80
1	A	49	ALA	N-CA-C	5.45	117.22	111.28
1	D	159	SER	CA-C-N	5.36	126.55	119.84
1	D	159	SER	C-N-CA	5.36	126.55	119.84
1	C	219	PHE	N-CA-C	5.34	117.76	110.55
1	E	138	TRP	N-CA-C	-5.33	102.31	110.14
1	A	191	ILE	N-CA-C	5.32	113.75	107.84
1	C	110	ARG	N-CA-C	5.31	116.75	111.07
1	D	33	VAL	N-CA-C	5.28	116.33	108.46
1	F	15	LYS	N-CA-C	-5.24	104.99	111.33
1	E	242	VAL	N-CA-C	-5.20	98.53	109.34
1	C	13	ARG	N-CA-C	-5.17	101.29	109.76
1	C	85	PRO	N-CA-C	-5.15	103.74	111.57
1	E	33	VAL	N-CA-C	5.15	115.89	108.48
1	D	35	VAL	N-CA-C	5.14	115.99	108.53
1	B	247	CYS	N-CA-C	5.10	116.84	108.52
1	D	267	ASP	N-CA-C	-5.10	105.42	111.69
1	E	175	GLY	N-CA-C	-5.09	108.22	115.30
1	B	36	HIS	N-CA-C	-5.09	100.74	109.24
1	E	91	TRP	N-CA-C	5.09	117.21	111.11
1	D	32	THR	N-CA-C	-5.06	99.02	108.02
1	D	157	GLU	CA-C-O	-5.06	115.17	120.63
1	A	191	ILE	CA-C-N	5.04	124.65	119.05
1	A	191	ILE	C-N-CA	5.04	124.65	119.05
1	B	35	VAL	N-CA-C	5.00	115.79	108.53
1	B	169	SER	N-CA-C	5.00	117.40	109.50

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2119	0	2067	94	0
1	B	1942	0	1846	139	0
1	C	2104	0	2015	111	0
1	D	2089	0	2002	99	0
1	E	2018	0	1953	116	0
1	F	1829	0	1699	136	0
2	A	42	0	24	7	0
2	B	42	0	24	6	0
2	C	42	0	24	1	0
2	D	42	0	24	5	0
2	E	42	0	24	8	0
3	A	39	0	0	7	0
3	B	28	0	0	4	0
3	C	41	0	0	6	0
3	D	34	0	0	3	0
3	E	43	0	0	7	0
3	F	38	0	0	6	0
All	All	12534	0	11702	683	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 28.

All (683) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:14:THR:HG22	1:D:16:GLN:H	1.18	1.07
1:B:98:MET:HE2	1:B:202:PRO:HG3	1.35	1.06
1:E:71:GLN:H	1:E:112:MET:HE2	1.19	1.05
1:A:61:THR:HG23	1:A:63:GLU:H	1.25	1.01
1:F:13:ARG:HB2	1:F:45:VAL:HG12	1.44	0.95
1:A:225:GLN:HE21	1:A:229:GLN:HE21	0.99	0.95
1:B:75:LEU:HA	1:B:98:MET:HE1	1.47	0.94
1:E:28:LYS:H	1:E:31:MET:HE2	1.33	0.94
1:E:27:LEU:HD12	1:E:31:MET:CE	1.99	0.93
1:F:156:GLY:HA2	1:F:186:LEU:HD13	1.50	0.93
1:A:71:GLN:H	1:A:112:MET:HE2	1.33	0.91
1:B:153:PHE:HB3	1:B:189:TYR:HE2	1.35	0.91
1:D:71:GLN:H	1:D:112:MET:HE2	1.36	0.90
1:A:225:GLN:HE21	1:A:229:GLN:NE2	1.68	0.90
1:D:98:MET:HE2	1:D:202:PRO:HG3	1.52	0.90
1:F:98:MET:HG2	1:F:202:PRO:HG3	1.53	0.90
1:B:155:LEU:HD11	1:B:219:PHE:CZ	2.08	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:14:THR:HG22	1:C:16:GLN:H	1.38	0.88
1:A:266:ASN:O	1:A:270:ASN:HB2	1.75	0.87
1:B:40:SER:HB3	2:B:302:COA:H4B	1.57	0.87
1:F:203:ILE:HG22	1:F:204:ILE:H	1.41	0.86
1:B:155:LEU:HD13	1:B:185:HIS:HB3	1.56	0.86
1:A:225:GLN:NE2	1:A:229:GLN:HE21	1.74	0.84
1:C:75:LEU:HA	1:C:98:MET:HE3	1.61	0.83
1:D:225:GLN:HE21	1:D:229:GLN:NE2	1.75	0.83
1:E:123:PRO:HA	3:E:340:HOH:O	1.80	0.82
1:F:25:LEU:HD23	1:F:240:GLY:HA3	1.63	0.81
1:F:14:THR:H	1:F:17:SER:HB3	1.44	0.81
1:B:221:GLU:O	1:B:224:PHE:HB2	1.80	0.80
1:F:14:THR:HG22	1:F:16:GLN:H	1.45	0.80
1:F:203:ILE:HG22	1:F:204:ILE:N	1.95	0.80
1:B:161:LEU:HD12	1:B:183:CYS:HA	1.63	0.80
1:B:29:LYS:HE3	1:B:61:THR:HG21	1.64	0.80
1:A:71:GLN:H	1:A:112:MET:CE	1.95	0.80
1:B:75:LEU:HA	1:B:98:MET:CE	2.12	0.79
1:D:38:SER:HB2	2:D:304:COA:H122	1.65	0.78
1:E:225:GLN:HE21	1:E:229:GLN:HE21	1.31	0.78
1:C:75:LEU:HA	1:C:98:MET:CE	2.13	0.78
1:B:60:VAL:HG13	1:B:64:GLY:HA3	1.66	0.77
1:B:148:GLN:HG3	1:B:163:LYS:HZ1	1.47	0.77
1:B:47:GLY:O	1:B:50:VAL:HG13	1.85	0.77
1:D:69:PRO:HB2	1:D:112:MET:HE1	1.66	0.76
1:C:60:VAL:HG13	1:C:64:GLY:HA3	1.68	0.76
1:B:69:PRO:HB2	1:B:112:MET:HE1	1.68	0.76
1:E:42:ILE:HD13	1:E:245:ALA:HB2	1.67	0.75
1:F:86:VAL:HG13	1:F:87:PRO:HD2	1.67	0.75
1:D:71:GLN:N	1:D:112:MET:HE2	2.01	0.75
1:B:191:ILE:HB	1:B:192:PRO:HD2	1.68	0.74
1:B:252:LEU:HA	3:B:321:HOH:O	1.87	0.74
1:D:161:LEU:HD21	1:D:186:LEU:HB2	1.70	0.74
1:B:98:MET:HE2	1:B:202:PRO:CG	2.16	0.74
1:B:239:VAL:HG12	1:B:240:GLY:H	1.53	0.74
1:A:60:VAL:O	1:A:61:THR:HG22	1.89	0.73
1:C:79:LYS:HG3	1:C:80:GLU:HG3	1.70	0.73
1:F:67:VAL:HG22	1:F:137:ALA:HB2	1.68	0.73
1:E:28:LYS:N	1:E:31:MET:HE2	2.03	0.73
1:E:50:VAL:O	1:E:54:GLN:HG3	1.89	0.73
1:B:75:LEU:CA	1:B:98:MET:HE1	2.18	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:38:SER:HB2	2:B:302:COA:O5A	1.88	0.72
1:B:265:ASN:CG	1:B:265:ASN:O	2.32	0.72
1:D:10:THR:HG23	1:D:11:PHE:N	2.04	0.72
1:D:174:LEU:HD11	1:D:242:VAL:HG11	1.71	0.72
1:C:98:MET:HE2	1:C:202:PRO:CD	2.20	0.71
1:D:53:ILE:HD12	1:D:118:LEU:HD23	1.73	0.71
1:B:171:VAL:HB	1:B:250:PHE:CE1	2.26	0.71
1:F:47:GLY:O	1:F:50:VAL:HG13	1.89	0.71
1:D:123:PRO:O	1:D:124:GLU:HG2	1.90	0.71
1:A:50:VAL:O	1:A:54:GLN:HG3	1.91	0.70
1:E:197:ILE:HG23	3:E:323:HOH:O	1.90	0.70
1:F:191:ILE:HB	3:F:284:HOH:O	1.90	0.70
1:A:71:GLN:N	1:A:112:MET:HE2	2.05	0.70
1:C:14:THR:HG22	1:C:15:LYS:N	2.05	0.70
2:A:301:COA:H71	3:A:302:HOH:O	1.90	0.70
1:F:156:GLY:CA	1:F:186:LEU:HD13	2.20	0.70
1:E:165:TYR:CE1	1:E:253:THR:HG23	2.27	0.69
1:A:45:VAL:HG22	1:A:48:GLY:HA2	1.72	0.69
1:C:120:ARG:NH1	3:C:306:HOH:O	2.26	0.69
1:E:69:PRO:O	1:E:112:MET:HE3	1.92	0.69
1:F:45:VAL:HG23	1:F:48:GLY:HA2	1.73	0.69
1:F:205:VAL:HG12	1:F:206:GLU:HG2	1.74	0.69
1:E:60:VAL:O	1:E:61:THR:HB	1.93	0.68
1:E:98:MET:CA	1:F:46:ASN:HD21	2.07	0.68
1:E:38:SER:HB2	2:E:305:COA:O5A	1.94	0.68
1:C:61:THR:HG22	1:C:63:GLU:H	1.58	0.68
1:C:2:LEU:HD23	1:D:84:PRO:HD3	1.74	0.68
1:D:14:THR:HG22	1:D:16:GLN:N	2.01	0.68
1:E:98:MET:CE	1:E:202:PRO:HD3	2.24	0.68
1:C:225:GLN:HE21	1:C:229:GLN:HE21	1.40	0.67
1:E:98:MET:HA	1:F:46:ASN:HD21	1.58	0.67
1:E:57:ILE:HG23	1:E:138:TRP:CH2	2.30	0.67
1:D:180:SER:HB3	3:D:312:HOH:O	1.94	0.67
1:E:178:PHE:HE1	1:E:248:ARG:NH1	1.92	0.67
1:F:166:ILE:HG13	1:F:167:ARG:N	2.10	0.67
1:E:69:PRO:O	1:E:116:VAL:HG11	1.95	0.66
1:B:239:VAL:HG12	1:B:240:GLY:N	2.10	0.66
1:B:13:ARG:HG2	1:B:44:TRP:O	1.96	0.66
1:A:157:GLU:O	1:A:158:GLN:HB2	1.95	0.66
1:C:203:ILE:HD11	3:C:321:HOH:O	1.94	0.66
1:E:60:VAL:HG12	1:E:64:GLY:HA3	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:174:LEU:HD13	1:B:247:CYS:SG	2.36	0.66
1:F:60:VAL:CG1	1:F:64:GLY:HA3	2.26	0.66
1:F:122:TYR:CD2	1:F:123:PRO:HD2	2.31	0.66
1:D:161:LEU:CD2	1:D:186:LEU:HD13	2.25	0.65
1:A:29:LYS:HG3	1:A:61:THR:HG21	1.77	0.65
1:C:127:ARG:HG3	1:C:136:VAL:HG12	1.78	0.65
1:F:50:VAL:O	1:F:54:GLN:HG3	1.96	0.65
1:A:13:ARG:NH2	1:A:244:SER:HB3	2.12	0.65
1:F:14:THR:HG23	3:F:295:HOH:O	1.96	0.65
1:A:90:TRP:CD2	1:B:12:PRO:HD3	2.31	0.65
1:B:14:THR:HG22	1:B:15:LYS:N	2.12	0.65
1:E:266:ASN:O	1:E:270:ASN:HB2	1.96	0.65
1:C:98:MET:HE2	1:C:202:PRO:HD3	1.78	0.65
1:F:203:ILE:CG2	1:F:204:ILE:H	2.11	0.64
1:D:237:MET:HE2	1:D:250:PHE:CD2	2.32	0.64
1:E:21:ASP:HB3	1:E:242:VAL:HA	1.79	0.64
1:F:163:LYS:O	1:F:166:ILE:HG12	1.98	0.64
1:A:97:SER:HB2	1:B:14:THR:HG23	1.79	0.64
1:F:31:MET:HE2	1:F:170:TYR:CE1	2.33	0.63
1:B:14:THR:HG22	1:B:16:GLN:HG3	1.78	0.63
1:B:171:VAL:HG21	3:B:321:HOH:O	1.98	0.63
1:A:100:ALA:HA	1:A:202:PRO:HB2	1.81	0.63
1:C:31:MET:HE2	1:C:170:TYR:CE1	2.34	0.63
1:D:61:THR:HG22	1:D:62:GLU:N	2.14	0.63
1:F:42:ILE:N	1:F:42:ILE:HD12	2.14	0.63
1:F:125:VAL:HG22	1:F:138:TRP:HB2	1.81	0.63
1:B:221:GLU:HA	1:B:224:PHE:CD1	2.34	0.62
1:E:266:ASN:ND2	1:E:270:ASN:OD1	2.31	0.62
1:F:13:ARG:CB	1:F:45:VAL:HG12	2.26	0.62
1:F:13:ARG:HG2	1:F:44:TRP:O	1.99	0.62
1:F:33:VAL:HG22	1:F:34:LEU:N	2.13	0.62
1:F:98:MET:HE2	1:F:211:TRP:CZ3	2.33	0.62
1:E:98:MET:N	1:F:46:ASN:HD21	1.97	0.62
1:C:98:MET:HE2	1:C:202:PRO:HG3	1.82	0.62
1:C:237:MET:HE2	1:C:250:PHE:CD2	2.35	0.62
1:D:98:MET:HE2	1:D:202:PRO:CG	2.26	0.62
1:E:71:GLN:HG3	1:E:112:MET:CE	2.30	0.62
1:B:14:THR:H	1:B:17:SER:HB3	1.64	0.62
1:D:161:LEU:HD21	1:D:186:LEU:HD13	1.80	0.62
1:D:50:VAL:O	1:D:54:GLN:HG3	2.00	0.62
1:A:203:ILE:HG22	1:A:204:ILE:N	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:61:THR:HG22	1:E:63:GLU:H	1.65	0.61
1:F:184:PHE:HB2	1:F:224:PHE:CE2	2.34	0.61
1:E:90:TRP:O	1:E:93:ILE:HG22	2.00	0.61
1:E:27:LEU:HD12	1:E:31:MET:HE1	1.82	0.61
1:F:98:MET:HE2	1:F:202:PRO:HD3	1.82	0.61
1:C:91:TRP:O	1:C:95:ARG:HG3	2.01	0.61
1:E:45:VAL:HG12	2:E:305:COA:N1A	2.16	0.61
1:F:14:THR:HG22	1:F:15:LYS:N	2.14	0.61
1:C:69:PRO:HB2	1:C:112:MET:HE1	1.82	0.61
1:F:14:THR:CG2	1:F:15:LYS:N	2.64	0.61
1:A:71:GLN:CB	1:A:112:MET:HE2	2.30	0.61
1:A:262:TRP:O	1:A:266:ASN:HB2	2.00	0.60
1:F:108:THR:OG1	1:F:117:GLU:HG2	2.00	0.60
1:E:100:ALA:HA	1:E:202:PRO:HB2	1.82	0.60
1:F:120:ARG:HB3	1:F:136:VAL:HG11	1.81	0.60
1:C:3:LYS:O	1:C:7:GLU:HG2	2.02	0.60
1:D:117:GLU:OE1	1:D:120:ARG:HD3	2.01	0.60
1:E:246:ASN:HD22	1:E:246:ASN:N	1.99	0.60
1:E:27:LEU:HD12	1:E:31:MET:HE3	1.81	0.60
1:E:27:LEU:HA	1:E:31:MET:HE1	1.84	0.60
1:F:67:VAL:HG22	1:F:137:ALA:CB	2.30	0.60
1:B:196:ILE:HD13	1:B:217:LEU:HD23	1.83	0.60
1:F:76:SER:O	1:F:98:MET:HE1	2.02	0.60
1:B:14:THR:CG2	1:B:16:GLN:HG3	2.31	0.60
1:B:253:THR:HB	3:B:313:HOH:O	2.00	0.60
1:D:203:ILE:HG23	3:D:311:HOH:O	2.02	0.60
1:F:61:THR:HG22	1:F:62:GLU:N	2.16	0.60
1:E:78:PRO:HD2	1:E:95:ARG:HH12	1.67	0.59
1:C:60:VAL:O	1:C:61:THR:HB	2.03	0.59
1:D:10:THR:CG2	1:D:11:PHE:N	2.66	0.59
1:F:178:PHE:C	1:F:180:SER:H	2.11	0.59
1:E:184:PHE:HB2	1:E:224:PHE:CE2	2.37	0.59
1:A:50:VAL:HG12	1:A:118:LEU:HD21	1.84	0.59
1:B:114:GLN:OE1	2:B:302:COA:H51A	2.01	0.59
1:D:69:PRO:O	1:D:112:MET:HE3	2.03	0.59
1:E:42:ILE:HD13	1:E:245:ALA:CB	2.32	0.59
1:E:71:GLN:N	1:E:112:MET:HE2	2.03	0.59
1:A:71:GLN:HB2	1:A:112:MET:HE2	1.83	0.59
1:D:123:PRO:C	1:D:124:GLU:HG2	2.28	0.59
1:E:57:ILE:HG23	1:E:138:TRP:CZ2	2.38	0.59
1:B:222:GLU:HG2	1:B:223:LEU:N	2.18	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:82:GLY:HA2	1:C:85:PRO:HG3	1.85	0.59
1:E:156:GLY:HA2	1:E:186:LEU:CD1	2.32	0.59
1:C:14:THR:CG2	1:C:15:LYS:N	2.66	0.59
1:F:31:MET:HE2	1:F:170:TYR:CZ	2.38	0.59
1:F:145:ILE:HD13	1:F:164:LEU:HD21	1.85	0.58
1:B:153:PHE:HA	1:B:216:GLU:OE2	2.03	0.58
1:D:161:LEU:HD21	1:D:186:LEU:CB	2.32	0.58
1:E:98:MET:HA	1:F:46:ASN:ND2	2.18	0.58
1:B:157:GLU:O	1:B:158:GLN:HB2	2.02	0.58
1:E:155:LEU:HD12	1:E:219:PHE:CZ	2.38	0.58
1:E:98:MET:HE2	1:E:211:TRP:HZ3	1.69	0.58
1:A:117:GLU:O	1:A:120:ARG:HG2	2.04	0.58
1:E:133:TYR:O	1:E:149:HIS:HE1	1.86	0.58
1:D:10:THR:CG2	1:D:11:PHE:H	2.16	0.58
1:D:155:LEU:O	1:D:189:TYR:CZ	2.56	0.58
1:B:30:GLY:HA2	1:B:64:GLY:N	2.19	0.58
1:B:36:HIS:CD2	1:B:180:SER:O	2.56	0.58
1:A:147:ASN:C	1:A:147:ASN:OD1	2.46	0.58
1:C:86:VAL:HG13	1:C:87:PRO:HD2	1.86	0.58
1:D:75:LEU:HA	1:D:98:MET:HE1	1.86	0.58
1:E:98:MET:HE3	1:E:202:PRO:CD	2.34	0.58
1:F:239:VAL:HG12	1:F:240:GLY:N	2.19	0.58
1:E:69:PRO:HB2	1:E:112:MET:HE1	1.85	0.57
1:F:147:ASN:HA	3:F:307:HOH:O	2.03	0.57
1:C:151:LEU:CD2	1:C:212:LYS:HD2	2.34	0.57
1:E:98:MET:HE3	1:E:202:PRO:HD3	1.86	0.57
1:F:171:VAL:HB	1:F:250:PHE:CE1	2.39	0.57
1:C:50:VAL:HG12	1:C:118:LEU:HD21	1.85	0.57
1:C:153:PHE:HA	1:C:216:GLU:OE1	2.04	0.57
1:D:11:PHE:CD1	1:D:12:PRO:HD2	2.39	0.57
1:A:61:THR:HG23	1:A:63:GLU:N	2.09	0.57
1:B:155:LEU:HD13	1:B:185:HIS:CB	2.33	0.57
1:B:69:PRO:CB	1:B:112:MET:HE1	2.35	0.57
1:B:191:ILE:HG21	1:B:263:PHE:HB2	1.87	0.57
1:E:21:ASP:CB	1:E:242:VAL:HA	2.34	0.57
1:F:252:LEU:O	1:F:256:VAL:HG23	2.04	0.57
1:C:171:VAL:HB	1:C:250:PHE:CE1	2.40	0.57
1:D:156:GLY:H	1:D:161:LEU:HD22	1.70	0.57
1:A:132:ASN:ND2	1:A:199:ARG:HH21	2.02	0.57
1:D:10:THR:HG23	1:D:11:PHE:H	1.67	0.57
1:E:150:PRO:HG2	3:E:328:HOH:O	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:30:GLY:HA2	1:F:63:GLU:C	2.30	0.57
1:B:128:SER:HB3	1:B:146:LEU:HD22	1.86	0.56
1:C:75:LEU:HD23	1:C:101:TYR:HB2	1.86	0.56
1:C:98:MET:HE2	1:C:202:PRO:CG	2.35	0.56
1:A:45:VAL:HG22	1:A:48:GLY:CA	2.35	0.56
1:B:218:GLU:O	1:B:218:GLU:HG3	2.05	0.56
1:E:191:ILE:HG22	1:E:264:ILE:HG13	1.85	0.56
1:F:34:LEU:HD12	1:F:67:VAL:O	2.05	0.56
1:A:132:ASN:ND2	1:A:214:TYR:OH	2.38	0.56
1:B:151:LEU:HD11	1:B:214:TYR:CE2	2.40	0.56
1:B:265:ASN:O	1:B:265:ASN:ND2	2.38	0.56
1:C:13:ARG:HG2	1:C:44:TRP:O	2.05	0.56
1:A:128:SER:HB2	1:A:149:HIS:HD2	1.71	0.56
1:A:165:TYR:CE1	1:A:253:THR:HG23	2.41	0.56
1:D:11:PHE:CG	1:D:12:PRO:HD2	2.40	0.56
1:B:148:GLN:CG	1:B:163:LYS:HZ1	2.14	0.56
1:C:71:GLN:HG2	1:C:133:TYR:HA	1.87	0.56
1:A:128:SER:CB	1:A:149:HIS:HD2	2.19	0.56
1:E:78:PRO:HA	1:E:81:TRP:CE2	2.41	0.56
1:E:178:PHE:CE1	1:E:248:ARG:NH1	2.73	0.56
1:F:135:PHE:CZ	1:F:161:LEU:HD13	2.40	0.56
1:F:223:LEU:O	1:F:227:VAL:HG23	2.05	0.56
1:C:86:VAL:HG13	1:C:90:TRP:CE3	2.41	0.55
1:C:123:PRO:C	1:C:124:GLU:HG2	2.32	0.55
1:D:114:GLN:HG3	2:D:304:COA:O2A	2.06	0.55
1:E:43:GLY:O	2:E:305:COA:H2A	2.06	0.55
1:A:251:SER:HB3	1:A:254:GLU:HB3	1.89	0.55
1:B:61:THR:HG22	1:B:62:GLU:N	2.22	0.55
1:E:95:ARG:HB2	1:E:95:ARG:NH1	2.22	0.55
1:D:83:ASN:OD1	1:D:83:ASN:O	2.25	0.55
1:D:19:THR:HG23	1:D:59:VAL:HG23	1.88	0.55
1:A:114:GLN:NE2	2:A:301:COA:H51A	2.22	0.54
1:E:19:THR:HG23	1:E:59:VAL:CG2	2.36	0.54
1:F:166:ILE:HG13	1:F:167:ARG:H	1.70	0.54
1:C:61:THR:HG22	1:C:63:GLU:HG2	1.90	0.54
1:C:61:THR:HG22	1:C:62:GLU:N	2.21	0.54
1:B:171:VAL:CG2	3:B:321:HOH:O	2.54	0.54
1:D:75:LEU:HA	1:D:98:MET:CE	2.37	0.54
1:D:252:LEU:O	1:D:256:VAL:HG23	2.08	0.54
1:F:33:VAL:CG2	1:F:34:LEU:N	2.70	0.54
1:A:145:ILE:HD13	1:A:164:LEU:HD23	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:90:TRP:O	1:C:93:ILE:HG22	2.08	0.54
1:D:69:PRO:C	1:D:112:MET:HE3	2.33	0.54
1:D:125:VAL:HG22	1:D:138:TRP:HB2	1.89	0.54
1:E:98:MET:HE2	1:E:211:TRP:CZ3	2.41	0.54
1:A:110:ARG:HD2	1:A:110:ARG:N	2.22	0.54
1:F:21:ASP:HB3	1:F:242:VAL:HA	1.88	0.54
1:D:18:ILE:O	1:D:22:LEU:HG	2.08	0.54
1:E:95:ARG:HB2	1:E:95:ARG:HH11	1.72	0.54
1:A:95:ARG:NH1	3:A:315:HOH:O	2.40	0.54
1:D:144:LYS:HA	1:D:147:ASN:HB2	1.88	0.54
1:F:156:GLY:O	1:F:157:GLU:C	2.50	0.54
1:E:156:GLY:HA2	1:E:186:LEU:HD13	1.88	0.53
1:E:221:GLU:HA	1:E:224:PHE:CD1	2.43	0.53
1:B:151:LEU:HD11	1:B:214:TYR:CD2	2.43	0.53
1:B:184:PHE:HB2	1:B:224:PHE:CE2	2.44	0.53
1:B:197:ILE:HG22	1:B:198:ASN:N	2.22	0.53
1:C:90:TRP:CD2	1:D:12:PRO:HD3	2.44	0.53
1:C:123:PRO:O	1:C:124:GLU:HG2	2.07	0.53
1:F:25:LEU:HD11	1:F:249:LEU:HB2	1.89	0.53
1:B:153:PHE:HB3	1:B:189:TYR:CE2	2.27	0.53
1:F:155:LEU:HD12	1:F:219:PHE:CZ	2.43	0.53
1:A:78:PRO:O	1:A:81:TRP:HB2	2.08	0.53
1:A:97:SER:HB2	1:B:14:THR:CG2	2.39	0.53
1:A:145:ILE:HD13	1:A:164:LEU:CD2	2.39	0.53
1:B:14:THR:CG2	1:B:15:LYS:N	2.72	0.53
1:B:33:VAL:HA	1:B:170:TYR:O	2.09	0.53
1:B:156:GLY:O	1:B:157:GLU:C	2.51	0.53
1:D:174:LEU:HD12	1:D:247:CYS:SG	2.49	0.53
1:A:143:ASN:O	1:A:147:ASN:HB2	2.08	0.53
1:F:242:VAL:HG23	1:F:247:CYS:SG	2.49	0.53
1:A:203:ILE:HG22	1:A:204:ILE:H	1.73	0.52
1:C:74:GLU:OE2	1:C:109:THR:HG23	2.09	0.52
1:C:127:ARG:HG3	1:C:136:VAL:CG1	2.39	0.52
1:E:135:PHE:CD2	1:E:160:PRO:HG2	2.43	0.52
1:C:45:VAL:HG22	1:C:48:GLY:HA2	1.92	0.52
1:D:14:THR:HG22	1:D:15:LYS:N	2.24	0.52
1:D:41:SER:C	1:D:245:ALA:HB2	2.34	0.52
1:F:36:HIS:CE1	1:F:181:SER:HA	2.44	0.52
1:F:200:GLY:HA2	1:F:212:LYS:O	2.08	0.52
1:C:177:ASP:HB3	1:C:179:ASP:OD1	2.09	0.52
1:F:98:MET:HE2	1:F:211:TRP:HZ3	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:195:LYS:HE2	1:B:197:ILE:HD11	1.92	0.52
1:E:65:THR:HA	1:E:139:GLY:HA3	1.92	0.52
1:E:46:ASN:HD21	1:F:98:MET:HA	1.75	0.52
1:B:94:ILE:O	1:B:98:MET:HB2	2.09	0.52
1:C:57:ILE:HG23	1:C:138:TRP:CH2	2.45	0.52
1:C:73:VAL:HG12	1:C:73:VAL:O	2.09	0.52
1:B:71:GLN:HG2	1:B:133:TYR:HA	1.92	0.52
1:D:161:LEU:CD2	1:D:186:LEU:HB2	2.38	0.52
1:A:29:LYS:HG3	1:A:61:THR:CG2	2.39	0.51
1:B:73:VAL:HG12	1:B:73:VAL:O	2.11	0.51
1:B:13:ARG:HB2	1:B:45:VAL:HA	1.91	0.51
1:C:75:LEU:HA	1:C:98:MET:HE1	1.92	0.51
1:B:27:LEU:HB3	1:B:59:VAL:HG11	1.91	0.51
1:C:61:THR:CG2	1:C:63:GLU:HG2	2.41	0.51
1:F:222:GLU:HG2	1:F:223:LEU:HD23	1.92	0.51
1:B:85:PRO:O	1:B:86:VAL:HG23	2.10	0.51
1:D:225:GLN:NE2	1:D:229:GLN:NE2	2.53	0.51
1:F:238:LYS:HD2	1:F:249:LEU:HD23	1.92	0.51
1:D:13:ARG:HG2	1:D:44:TRP:O	2.11	0.51
1:A:117:GLU:CD	1:A:120:ARG:HH11	2.19	0.51
1:A:128:SER:HB2	1:A:149:HIS:CD2	2.46	0.51
1:B:44:TRP:HA	2:B:302:COA:N1A	2.26	0.51
1:C:90:TRP:CE2	1:D:12:PRO:HD3	2.46	0.51
1:B:17:SER:O	1:B:20:GLU:HB3	2.11	0.51
1:E:199:ARG:O	1:E:213:GLU:HA	2.11	0.51
1:A:57:ILE:HG23	1:A:138:TRP:CH2	2.47	0.50
1:B:152:GLU:HG2	1:B:153:PHE:CD1	2.47	0.50
1:E:197:ILE:CG2	1:E:198:ASN:N	2.74	0.50
1:F:155:LEU:HB2	1:F:189:TYR:OH	2.11	0.50
1:B:103:SER:HB2	1:B:127:ARG:HB3	1.93	0.50
1:F:60:VAL:HG12	1:F:64:GLY:HA3	1.91	0.50
1:E:71:GLN:HG3	1:E:112:MET:HE2	1.93	0.50
1:F:159:SER:O	1:F:162:GLY:N	2.33	0.50
1:F:177:ASP:CG	1:F:178:PHE:H	2.20	0.50
1:C:270:ASN:N	1:C:270:ASN:HD22	2.08	0.50
1:E:27:LEU:HA	1:E:31:MET:CE	2.42	0.50
1:F:32:THR:HG23	1:F:65:THR:HB	1.93	0.50
1:C:10:THR:CG2	1:C:11:PHE:N	2.75	0.50
1:C:225:GLN:HB3	3:C:317:HOH:O	2.11	0.50
1:E:75:LEU:CD2	1:E:101:TYR:HB2	2.42	0.50
1:F:90:TRP:O	1:F:93:ILE:HG22	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:98:MET:CE	1:F:202:PRO:HD3	2.42	0.50
1:A:117:GLU:OE1	1:A:120:ARG:HD3	2.11	0.49
1:D:203:ILE:HG22	1:D:204:ILE:H	1.77	0.49
1:E:19:THR:HG23	1:E:59:VAL:HG23	1.93	0.49
1:E:60:VAL:CG1	1:E:64:GLY:HA3	2.42	0.49
1:B:41:SER:OG	1:B:175:GLY:HA3	2.11	0.49
1:B:90:TRP:O	1:B:93:ILE:HG22	2.11	0.49
1:B:156:GLY:HA3	1:B:189:TYR:CD2	2.46	0.49
1:C:34:LEU:HD11	1:C:69:PRO:HD3	1.94	0.49
1:F:68:MET:SD	1:F:119:PHE:CD2	3.05	0.49
1:B:101:TYR:CD1	1:B:131:PRO:HA	2.48	0.49
1:E:237:MET:HE1	1:E:248:ARG:HD3	1.94	0.49
1:F:161:LEU:O	1:F:186:LEU:HD22	2.11	0.49
1:B:203:ILE:HG23	1:B:204:ILE:N	2.27	0.49
1:C:137:ALA:HB3	1:C:146:LEU:HD11	1.95	0.49
1:C:266:ASN:O	1:C:270:ASN:HB2	2.12	0.49
1:A:37:SER:O	2:A:301:COA:H142	2.13	0.49
1:C:15:LYS:HE2	1:C:58:ASP:OD2	2.13	0.49
1:E:78:PRO:HD2	1:E:95:ARG:NH1	2.26	0.49
1:A:78:PRO:HA	1:A:81:TRP:CD2	2.48	0.49
1:B:164:LEU:HB3	1:B:252:LEU:HD13	1.95	0.49
1:D:60:VAL:CG1	1:D:64:GLY:HA3	2.43	0.49
2:E:305:COA:H52A	3:E:313:HOH:O	2.13	0.49
1:A:10:THR:HG22	3:A:323:HOH:O	2.12	0.49
1:A:71:GLN:HG2	1:A:133:TYR:HA	1.95	0.49
1:F:75:LEU:HA	1:F:98:MET:HE3	1.94	0.49
1:F:238:LYS:NZ	3:F:287:HOH:O	2.45	0.49
1:D:179:ASP:HB3	3:D:315:HOH:O	2.13	0.49
1:F:61:THR:HG22	1:F:62:GLU:H	1.77	0.49
1:F:142:LYS:HG3	1:F:143:ASN:N	2.27	0.49
1:F:221:GLU:HA	1:F:224:PHE:CD1	2.48	0.49
1:B:34:LEU:CD1	1:B:67:VAL:HG12	2.43	0.49
1:C:61:THR:CG2	1:C:62:GLU:N	2.75	0.49
1:C:209:ARG:HH11	1:C:209:ARG:HG2	1.78	0.49
1:E:209:ARG:HH11	1:E:209:ARG:HG2	1.78	0.49
1:B:37:SER:HA	1:B:174:LEU:O	2.12	0.48
1:B:181:SER:O	1:B:183:CYS:N	2.46	0.48
1:D:43:GLY:O	2:D:304:COA:H2A	2.13	0.48
1:D:251:SER:HB3	1:D:254:GLU:HB2	1.95	0.48
1:E:46:ASN:ND2	1:F:98:MET:HA	2.28	0.48
1:A:171:VAL:O	1:A:249:LEU:HD12	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:163:LYS:HG2	3:F:296:HOH:O	2.12	0.48
1:E:101:TYR:CG	1:E:131:PRO:HA	2.48	0.48
1:F:42:ILE:HD12	1:F:42:ILE:H	1.79	0.48
1:F:27:LEU:HB3	1:F:59:VAL:HG11	1.96	0.48
1:D:209:ARG:HG2	1:D:209:ARG:HH11	1.79	0.48
1:E:49:ALA:O	1:E:53:ILE:HG13	2.13	0.48
1:E:155:LEU:HD12	1:E:219:PHE:CE1	2.49	0.48
1:B:252:LEU:C	1:B:252:LEU:HD23	2.39	0.48
1:C:215:LYS:HA	1:C:215:LYS:HD3	1.71	0.48
1:D:75:LEU:HD23	1:D:101:TYR:HB2	1.94	0.48
1:D:88:GLU:HA	1:D:91:TRP:CE2	2.48	0.48
1:C:87:PRO:HD2	1:C:90:TRP:CE3	2.48	0.48
1:F:29:LYS:C	1:F:31:MET:H	2.22	0.48
1:D:57:ILE:HG23	1:D:138:TRP:CH2	2.49	0.48
1:B:60:VAL:O	1:B:61:THR:HB	2.14	0.47
1:C:50:VAL:O	1:C:54:GLN:HG3	2.13	0.47
1:C:157:GLU:O	1:C:162:GLY:HA3	2.13	0.47
1:D:14:THR:CG2	1:D:15:LYS:N	2.77	0.47
1:F:25:LEU:C	1:F:25:LEU:HD13	2.39	0.47
1:A:100:ALA:HA	1:A:202:PRO:CB	2.44	0.47
1:B:145:ILE:O	1:B:145:ILE:HG22	2.14	0.47
1:D:47:GLY:O	1:D:50:VAL:HG13	2.14	0.47
1:A:10:THR:HG23	1:A:11:PHE:H	1.80	0.47
1:A:55:ALA:O	1:A:59:VAL:HG23	2.14	0.47
1:B:21:ASP:HB3	1:B:242:VAL:HA	1.96	0.47
1:B:260:GLU:O	1:B:264:ILE:HG13	2.15	0.47
1:C:14:THR:HG22	1:C:16:GLN:N	2.19	0.47
1:D:129:ASN:O	1:D:129:ASN:CG	2.58	0.47
1:B:124:GLU:HA	1:B:124:GLU:OE2	2.14	0.47
1:D:60:VAL:O	1:D:61:THR:HB	2.15	0.47
1:F:209:ARG:HG2	1:F:209:ARG:HH11	1.80	0.47
1:B:124:GLU:HB2	1:B:138:TRP:CD1	2.50	0.47
1:B:132:ASN:ND2	1:B:199:ARG:HH21	2.12	0.47
1:C:199:ARG:HG2	1:C:199:ARG:HH11	1.79	0.47
1:D:165:TYR:CE1	1:D:253:THR:HG23	2.50	0.47
1:E:195:LYS:HE2	3:E:316:HOH:O	2.13	0.47
1:B:34:LEU:HD13	1:B:67:VAL:HG12	1.96	0.47
1:C:10:THR:HG23	1:C:11:PHE:N	2.29	0.47
1:E:47:GLY:O	1:E:50:VAL:CG1	2.62	0.47
1:F:231:PHE:HB2	1:F:258:PHE:CD2	2.49	0.47
1:B:55:ALA:O	1:B:58:ASP:N	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:246:ASN:N	1:E:246:ASN:ND2	2.63	0.47
1:F:76:SER:N	1:F:98:MET:HE1	2.30	0.47
1:C:71:GLN:HG3	3:C:312:HOH:O	2.13	0.47
1:C:178:PHE:CG	1:C:228:GLY:HA3	2.50	0.47
1:A:60:VAL:HG11	1:A:66:ILE:HG23	1.97	0.47
1:B:239:VAL:CG1	1:B:240:GLY:H	2.25	0.47
1:C:153:PHE:CA	1:C:216:GLU:OE1	2.62	0.47
1:E:193:TYR:CD2	1:E:193:TYR:C	2.93	0.47
1:C:14:THR:CG2	1:C:15:LYS:H	2.29	0.46
1:A:86:VAL:HG13	1:A:87:PRO:HD2	1.97	0.46
1:B:160:PRO:C	1:B:162:GLY:H	2.23	0.46
1:B:174:LEU:C	1:B:174:LEU:HD12	2.40	0.46
1:F:156:GLY:O	1:F:157:GLU:O	2.32	0.46
1:B:231:PHE:CZ	1:B:255:ALA:HA	2.50	0.46
1:F:67:VAL:HA	1:F:136:VAL:O	2.15	0.46
1:F:257:ASP:O	1:F:260:GLU:HB3	2.15	0.46
1:B:154:GLY:O	1:B:159:SER:HB2	2.15	0.46
1:C:46:ASN:ND2	1:D:98:MET:HA	2.30	0.46
1:E:151:LEU:HD13	1:E:203:ILE:HD11	1.97	0.46
1:A:117:GLU:OE1	1:A:117:GLU:HA	2.16	0.46
1:F:178:PHE:C	1:F:180:SER:N	2.74	0.46
1:D:61:THR:CG2	1:D:62:GLU:N	2.79	0.46
1:A:232:GLU:OE2	1:A:248:ARG:NH1	2.49	0.46
1:B:225:GLN:HG3	1:B:229:GLN:OE1	2.15	0.46
1:C:125:VAL:HG22	1:C:138:TRP:HB2	1.98	0.46
1:D:143:ASN:O	1:D:147:ASN:N	2.48	0.46
1:E:28:LYS:H	1:E:31:MET:CE	2.14	0.46
1:E:238:LYS:HB2	1:E:249:LEU:HB3	1.96	0.46
1:B:183:CYS:O	1:B:184:PHE:C	2.57	0.46
1:F:239:VAL:CG1	1:F:240:GLY:N	2.79	0.46
1:F:57:ILE:HG23	1:F:138:TRP:CH2	2.51	0.46
1:A:157:GLU:O	1:A:158:GLN:CB	2.63	0.46
1:B:114:GLN:HB2	2:B:302:COA:O2A	2.16	0.46
1:B:146:LEU:O	1:B:147:ASN:C	2.59	0.46
1:E:69:PRO:C	1:E:112:MET:HE3	2.41	0.46
1:F:14:THR:O	1:F:18:ILE:HG13	2.15	0.46
1:F:145:ILE:HD13	1:F:164:LEU:CD2	2.46	0.46
1:A:75:LEU:CD2	1:A:101:TYR:HB2	2.46	0.45
1:C:209:ARG:HG2	1:C:209:ARG:NH1	2.31	0.45
1:C:66:ILE:HG12	1:C:138:TRP:HB3	1.99	0.45
1:C:75:LEU:CD2	1:C:101:TYR:HB2	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:203:ILE:HG22	1:D:204:ILE:N	2.30	0.45
1:E:120:ARG:HB3	1:E:136:VAL:HG11	1.98	0.45
1:F:39:LEU:HD22	1:F:49:ALA:HB2	1.98	0.45
1:A:9:THR:HA	3:A:323:HOH:O	2.15	0.45
1:B:155:LEU:CD1	1:B:185:HIS:HB3	2.38	0.45
1:D:101:TYR:CG	1:D:131:PRO:HA	2.52	0.45
1:F:139:GLY:O	1:F:142:LYS:HG2	2.16	0.45
1:F:156:GLY:N	1:F:159:SER:OG	2.50	0.45
1:A:152:GLU:O	1:A:153:PHE:HB2	2.16	0.45
1:B:40:SER:HB3	2:B:302:COA:C4B	2.37	0.45
1:D:26:GLY:O	1:D:28:LYS:HG3	2.16	0.45
1:D:237:MET:O	1:D:239:VAL:HG23	2.16	0.45
1:F:122:TYR:CG	1:F:123:PRO:HD2	2.51	0.45
1:A:69:PRO:HB2	1:A:112:MET:HE1	1.98	0.45
1:B:126:LYS:O	1:B:136:VAL:HA	2.17	0.45
1:B:222:GLU:OE1	1:B:222:GLU:N	2.36	0.45
1:F:173:LEU:O	1:F:247:CYS:HA	2.17	0.45
1:F:14:THR:HG22	1:F:16:GLN:N	2.23	0.45
1:F:222:GLU:HG2	1:F:223:LEU:CD2	2.46	0.45
1:B:86:VAL:HG13	1:B:90:TRP:CE3	2.51	0.45
1:C:13:ARG:HB2	1:C:45:VAL:HB	1.99	0.45
1:E:40:SER:HB3	2:E:305:COA:H4B	1.99	0.45
1:F:28:LYS:O	1:F:31:MET:HB3	2.17	0.45
1:A:167:ARG:O	1:A:168:GLU:C	2.59	0.45
1:B:221:GLU:O	1:B:224:PHE:CB	2.60	0.45
1:F:166:ILE:CG1	1:F:167:ARG:N	2.80	0.45
1:A:123:PRO:O	1:A:124:GLU:HB2	2.17	0.45
1:F:182:THR:O	1:F:184:PHE:N	2.49	0.45
1:B:30:GLY:HA2	1:B:63:GLU:C	2.41	0.45
1:C:151:LEU:HD23	1:C:212:LYS:HD2	1.99	0.45
1:C:151:LEU:HG	1:C:214:TYR:CG	2.52	0.45
1:D:61:THR:HG22	1:D:62:GLU:H	1.81	0.45
1:C:267:ASP:HA	3:C:331:HOH:O	2.17	0.44
1:E:61:THR:HG22	1:E:63:GLU:N	2.31	0.44
1:E:133:TYR:O	1:E:149:HIS:CE1	2.68	0.44
1:B:197:ILE:CG2	1:B:198:ASN:N	2.80	0.44
1:D:53:ILE:CD1	1:D:118:LEU:HD23	2.42	0.44
1:E:151:LEU:HD13	1:E:203:ILE:CD1	2.47	0.44
1:F:23:LYS:HG2	1:F:59:VAL:HG13	1.98	0.44
1:C:14:THR:HG23	1:D:97:SER:HB2	1.98	0.44
1:C:170:TYR:CD1	1:C:170:TYR:N	2.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:89:GLU:CD	1:D:89:GLU:H	2.18	0.44
1:D:101:TYR:CD1	1:D:131:PRO:HA	2.53	0.44
1:D:189:TYR:OH	1:D:216:GLU:OE2	2.29	0.44
1:F:60:VAL:HG13	1:F:64:GLY:HA3	1.99	0.44
1:F:212:LYS:HE2	1:F:213:GLU:O	2.16	0.44
1:B:141:HIS:O	1:B:145:ILE:HD12	2.17	0.44
1:C:122:TYR:CG	1:C:123:PRO:HD2	2.52	0.44
1:D:69:PRO:C	1:D:112:MET:CE	2.91	0.44
1:D:117:GLU:O	1:D:120:ARG:HG2	2.17	0.44
1:E:47:GLY:O	1:E:50:VAL:HG13	2.17	0.44
1:A:206:GLU:HA	1:F:129:ASN:CG	2.43	0.44
1:A:238:LYS:O	1:A:248:ARG:HA	2.17	0.44
1:B:149:HIS:NE2	1:B:154:GLY:O	2.50	0.44
1:D:154:GLY:N	1:D:216:GLU:OE1	2.41	0.44
1:A:114:GLN:HG3	2:A:301:COA:O2A	2.17	0.44
1:A:266:ASN:ND2	1:A:270:ASN:HD21	2.16	0.44
1:D:191:ILE:HG22	1:D:264:ILE:HG13	2.00	0.44
1:E:42:ILE:O	1:E:42:ILE:HG22	2.17	0.44
1:E:55:ALA:O	1:E:59:VAL:HG23	2.17	0.44
1:A:69:PRO:C	1:A:112:MET:HE3	2.42	0.44
1:E:12:PRO:HB3	1:E:44:TRP:CZ3	2.53	0.44
1:E:156:GLY:O	1:E:157:GLU:C	2.60	0.44
1:C:165:TYR:CE1	1:C:253:THR:HG23	2.52	0.43
1:D:41:SER:O	1:D:245:ALA:HB2	2.18	0.43
1:B:141:HIS:O	1:B:145:ILE:HG13	2.18	0.43
1:B:152:GLU:O	1:B:153:PHE:HB2	2.18	0.43
1:C:161:LEU:HD12	1:C:161:LEU:HA	1.83	0.43
1:F:161:LEU:HD21	1:F:183:CYS:HA	2.00	0.43
1:A:41:SER:O	1:A:245:ALA:HB2	2.18	0.43
1:B:145:ILE:HG21	1:B:164:LEU:HD21	2.00	0.43
1:C:122:TYR:CD2	1:C:123:PRO:HD2	2.53	0.43
1:B:101:TYR:CG	1:B:131:PRO:HA	2.54	0.43
1:A:266:ASN:ND2	1:A:270:ASN:ND2	2.66	0.43
1:C:31:MET:HE2	1:C:170:TYR:CD1	2.53	0.43
1:E:145:ILE:HG22	1:E:146:LEU:HD23	2.00	0.43
1:F:25:LEU:CD1	1:F:249:LEU:HD22	2.49	0.43
1:A:126:LYS:O	1:A:136:VAL:HA	2.19	0.43
2:A:301:COA:C6P	3:A:302:HOH:O	2.67	0.43
1:C:259:ALA:O	1:C:263:PHE:CD2	2.71	0.43
1:E:173:LEU:HB3	1:E:176:ALA:O	2.19	0.43
1:F:38:SER:O	1:F:42:ILE:CD1	2.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:75:LEU:HD12	1:F:75:LEU:N	2.34	0.43
1:B:55:ALA:O	1:B:56:LEU:C	2.62	0.43
1:E:135:PHE:HD2	1:E:160:PRO:HG2	1.83	0.43
1:A:178:PHE:CG	1:A:228:GLY:HA3	2.54	0.43
1:C:4:LYS:O	1:C:8:SER:HB3	2.19	0.43
1:F:159:SER:O	1:F:160:PRO:C	2.61	0.43
1:A:265:ASN:O	1:A:269:LYS:HB2	2.18	0.43
1:B:131:PRO:HG3	1:B:203:ILE:HD11	2.01	0.43
1:B:246:ASN:N	1:B:246:ASN:ND2	2.64	0.43
1:D:129:ASN:O	1:D:129:ASN:ND2	2.52	0.43
1:E:117:GLU:OE1	1:E:120:ARG:NH1	2.48	0.43
1:C:69:PRO:C	1:C:112:MET:HE2	2.43	0.43
1:D:225:GLN:HE21	1:D:229:GLN:HE21	1.63	0.43
1:E:126:LYS:O	1:E:136:VAL:HA	2.18	0.43
1:F:260:GLU:O	1:F:264:ILE:HG13	2.19	0.43
1:A:25:LEU:HD11	1:A:249:LEU:HB2	2.01	0.42
1:B:189:TYR:CD1	1:B:217:LEU:HD12	2.54	0.42
1:C:73:VAL:O	1:C:73:VAL:CG1	2.67	0.42
1:C:102:ASN:O	1:C:104:ASN:N	2.52	0.42
1:E:114:GLN:HG3	2:E:305:COA:O2A	2.19	0.42
1:E:225:GLN:HG3	1:E:229:GLN:NE2	2.34	0.42
1:B:16:GLN:HE21	1:B:16:GLN:HB2	1.60	0.42
1:B:75:LEU:HG	1:B:98:MET:HE3	2.00	0.42
1:C:206:GLU:HA	1:C:206:GLU:OE1	2.19	0.42
1:D:45:VAL:HG12	2:D:304:COA:N1A	2.34	0.42
1:F:247:CYS:C	1:F:248:ARG:HG2	2.45	0.42
1:B:123:PRO:O	1:B:124:GLU:HB2	2.18	0.42
1:C:171:VAL:HG11	1:C:250:PHE:CZ	2.54	0.42
1:E:209:ARG:HG2	1:E:209:ARG:NH1	2.34	0.42
1:F:216:GLU:HG3	1:F:217:LEU:N	2.34	0.42
1:A:12:PRO:HG3	1:B:90:TRP:CE3	2.55	0.42
1:A:114:GLN:CD	2:A:301:COA:H51A	2.44	0.42
1:B:15:LYS:HE2	1:B:58:ASP:OD2	2.19	0.42
1:B:160:PRO:O	1:B:164:LEU:HG	2.19	0.42
1:D:41:SER:OG	1:D:175:GLY:HA3	2.19	0.42
1:A:46:ASN:OD1	1:B:98:MET:HG3	2.20	0.42
1:A:128:SER:OG	1:A:149:HIS:HD2	2.03	0.42
1:A:203:ILE:CG2	1:A:204:ILE:N	2.83	0.42
1:B:69:PRO:CG	1:B:112:MET:HE1	2.50	0.42
1:E:157:GLU:O	1:E:158:GLN:HB2	2.20	0.42
1:D:154:GLY:O	1:D:159:SER:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:42:ILE:N	1:F:42:ILE:CD1	2.81	0.42
1:C:231:PHE:HZ	1:C:254:GLU:HB3	1.85	0.42
2:A:301:COA:C7P	3:A:302:HOH:O	2.60	0.42
1:C:107:PRO:HA	1:C:120:ARG:NH1	2.35	0.42
1:C:159:SER:HB2	1:C:160:PRO:CD	2.50	0.42
1:E:167:ARG:O	1:E:168:GLU:C	2.63	0.42
1:B:160:PRO:C	1:B:162:GLY:N	2.78	0.42
1:B:182:THR:O	1:B:183:CYS:C	2.61	0.42
1:B:231:PHE:HD1	1:B:258:PHE:CB	2.33	0.42
1:C:2:LEU:HA	1:C:2:LEU:HD12	1.81	0.42
1:C:95:ARG:O	1:C:209:ARG:NH2	2.52	0.42
1:D:98:MET:HE2	1:D:202:PRO:CD	2.50	0.42
1:A:251:SER:HB3	1:A:254:GLU:CB	2.50	0.42
1:D:184:PHE:HB2	1:D:224:PHE:CE2	2.55	0.42
1:F:199:ARG:O	1:F:213:GLU:HA	2.19	0.42
1:F:209:ARG:HG2	1:F:209:ARG:NH1	2.35	0.42
1:F:221:GLU:H	1:F:221:GLU:HG2	1.69	0.42
1:A:223:LEU:O	1:A:226:GLU:N	2.53	0.41
1:B:155:LEU:HD11	1:B:219:PHE:CE1	2.54	0.41
1:C:49:ALA:O	1:C:53:ILE:HG13	2.19	0.41
1:C:202:PRO:HD3	1:C:211:TRP:CZ3	2.55	0.41
1:D:38:SER:CB	2:D:304:COA:H122	2.44	0.41
1:D:161:LEU:HD23	1:D:186:LEU:HD13	2.01	0.41
1:E:23:LYS:HG2	3:E:329:HOH:O	2.20	0.41
1:E:140:LYS:HB2	1:E:140:LYS:HE3	1.88	0.41
1:B:156:GLY:HA3	1:B:189:TYR:CE2	2.56	0.41
1:C:11:PHE:CG	1:C:12:PRO:HD2	2.55	0.41
1:E:114:GLN:OE1	2:E:305:COA:H51A	2.21	0.41
1:F:205:VAL:C	1:F:207:GLY:N	2.78	0.41
1:B:222:GLU:HG2	1:B:223:LEU:H	1.83	0.41
1:D:241:LYS:HA	1:D:245:ALA:O	2.20	0.41
1:F:153:PHE:O	1:F:155:LEU:N	2.53	0.41
1:B:191:ILE:HD13	1:B:263:PHE:HB3	2.01	0.41
1:C:91:TRP:CD1	1:C:91:TRP:N	2.87	0.41
1:E:69:PRO:C	1:E:112:MET:CE	2.94	0.41
1:A:234:GLU:N	3:A:321:HOH:O	2.45	0.41
1:C:75:LEU:N	1:C:75:LEU:HD12	2.36	0.41
1:D:94:ILE:O	1:D:98:MET:HB2	2.21	0.41
1:D:197:ILE:HD12	1:D:218:GLU:OE1	2.20	0.41
1:F:31:MET:HG3	1:F:170:TYR:CE1	2.56	0.41
1:C:60:VAL:HG12	1:C:61:THR:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:39:LEU:HG	2:E:305:COA:N3A	2.35	0.41
1:F:14:THR:CG2	1:F:15:LYS:H	2.32	0.41
1:B:60:VAL:HG12	1:B:61:THR:O	2.20	0.41
1:B:156:GLY:H	1:B:159:SER:HB3	1.85	0.41
1:E:12:PRO:HB3	1:E:44:TRP:HZ3	1.86	0.41
1:F:123:PRO:O	1:F:124:GLU:HG2	2.20	0.41
1:C:260:GLU:O	1:C:264:ILE:HG13	2.21	0.41
1:F:204:ILE:HD11	3:F:292:HOH:O	2.20	0.41
1:C:87:PRO:HB3	1:C:89:GLU:OE1	2.21	0.41
1:D:83:ASN:HA	1:D:84:PRO:HA	1.46	0.41
1:E:156:GLY:HA2	1:E:186:LEU:HD12	2.00	0.41
1:F:185:HIS:HD2	1:F:188:GLU:OE1	2.03	0.41
1:A:29:LYS:HE3	1:A:61:THR:HG21	2.03	0.41
1:A:149:HIS:HA	1:A:150:PRO:HD2	2.01	0.41
1:C:221:GLU:HA	1:C:224:PHE:CD1	2.56	0.41
1:C:252:LEU:O	1:C:256:VAL:HG23	2.21	0.41
1:D:123:PRO:O	1:D:124:GLU:CG	2.66	0.41
1:E:197:ILE:HG22	1:E:198:ASN:N	2.36	0.41
1:F:173:LEU:HD12	1:F:248:ARG:HB2	2.03	0.41
1:A:231:PHE:O	1:A:235:HIS:HB2	2.20	0.40
1:B:218:GLU:O	1:B:218:GLU:CG	2.64	0.40
2:C:303:COA:P3B	3:C:309:HOH:O	2.78	0.40
1:D:98:MET:CE	1:D:202:PRO:HG3	2.35	0.40
1:F:86:VAL:CG1	1:F:87:PRO:HD2	2.43	0.40
1:A:110:ARG:HD2	1:A:110:ARG:H	1.85	0.40
1:A:123:PRO:O	1:A:124:GLU:CB	2.68	0.40
1:C:86:VAL:HG13	1:C:87:PRO:CD	2.51	0.40
1:B:161:LEU:CD1	1:B:183:CYS:HA	2.44	0.40
1:B:239:VAL:CG1	1:B:240:GLY:N	2.79	0.40
1:C:178:PHE:C	1:C:180:SER:H	2.30	0.40
1:E:22:LEU:HD22	1:E:27:LEU:HD22	2.03	0.40
1:E:132:ASN:ND2	1:E:214:TYR:OH	2.54	0.40
1:F:15:LYS:HE2	1:F:58:ASP:OD2	2.21	0.40
1:F:137:ALA:HB3	1:F:146:LEU:HD11	2.04	0.40
1:A:88:GLU:HA	1:A:91:TRP:CE2	2.56	0.40
1:A:106:THR:HA	1:A:107:PRO:HD2	1.95	0.40
1:C:159:SER:HB2	1:C:160:PRO:HD2	2.03	0.40
1:D:38:SER:OG	1:D:41:SER:HB3	2.21	0.40
1:F:104:ASN:O	1:F:105:TYR:HB3	2.21	0.40
1:A:32:THR:HG23	1:A:65:THR:HB	2.03	0.40
1:A:155:LEU:HB3	1:A:189:TYR:OH	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:252:LEU:C	1:A:252:LEU:HD23	2.46	0.40
1:B:16:GLN:HG3	1:B:16:GLN:H	1.52	0.40
1:B:181:SER:O	1:B:182:THR:C	2.64	0.40
1:B:231:PHE:CD1	1:B:258:PHE:CB	3.04	0.40
1:C:67:VAL:HG12	1:C:68:MET:N	2.36	0.40
1:C:129:ASN:CG	1:C:129:ASN:O	2.65	0.40
1:E:132:ASN:ND2	3:E:324:HOH:O	2.47	0.40
1:E:196:ILE:HG23	1:E:215:LYS:CG	2.51	0.40
1:E:237:MET:HE3	1:E:237:MET:HB3	1.56	0.40
1:F:155:LEU:HD13	1:F:185:HIS:CB	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	268/273 (98%)	243 (91%)	21 (8%)	4 (2%)	8	18
1	B	247/273 (90%)	204 (83%)	41 (17%)	2 (1%)	16	34
1	C	268/273 (98%)	247 (92%)	19 (7%)	2 (1%)	18	38
1	D	266/273 (97%)	248 (93%)	17 (6%)	1 (0%)	30	51
1	E	258/273 (94%)	226 (88%)	29 (11%)	3 (1%)	10	23
1	F	242/273 (89%)	198 (82%)	37 (15%)	7 (3%)	3	6
All	All	1549/1638 (95%)	1366 (88%)	164 (11%)	19 (1%)	10	23

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	182	THR
1	C	103	SER

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Mol	Chain	Res	Type
1	E	206	GLU
1	F	157	GLU
1	A	155	LEU
1	C	147	ASN
1	F	105	TYR
1	F	154	GLY
1	F	183	CYS
1	A	61	THR
1	A	82	GLY
1	D	147	ASN
1	E	48	GLY
1	F	147	ASN
1	E	157	GLU
1	F	30	GLY
1	A	149	HIS
1	B	82	GLY
1	F	48	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	227/240 (95%)	219 (96%)	8 (4%)	32	59
1	B	202/240 (84%)	188 (93%)	14 (7%)	14	32
1	C	223/240 (93%)	213 (96%)	10 (4%)	24	50
1	D	222/240 (92%)	206 (93%)	16 (7%)	13	30
1	E	213/240 (89%)	205 (96%)	8 (4%)	29	56
1	F	179/240 (75%)	169 (94%)	10 (6%)	19	40
All	All	1266/1440 (88%)	1200 (95%)	66 (5%)	21	44

All (66) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	VAL

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Mol	Chain	Res	Type
1	A	50	VAL
1	A	60	VAL
1	A	92	ASP
1	A	124	GLU
1	A	149	HIS
1	A	266	ASN
1	A	268	SER
1	B	16	GLN
1	B	25	LEU
1	B	50	VAL
1	B	86	VAL
1	B	117	GLU
1	B	155	LEU
1	B	161	LEU
1	B	174	LEU
1	B	177	ASP
1	B	203	ILE
1	B	210	VAL
1	B	218	GLU
1	B	229	GLN
1	B	265	ASN
1	C	2	LEU
1	C	10	THR
1	C	45	VAL
1	C	50	VAL
1	C	86	VAL
1	C	96	GLU
1	C	161	LEU
1	C	194	GLN
1	C	206	GLU
1	C	270	ASN
1	D	7	GLU
1	D	20	GLU
1	D	25	LEU
1	D	45	VAL
1	D	50	VAL
1	D	66	ILE
1	D	73	VAL
1	D	84	PRO
1	D	89	GLU
1	D	96	GLU
1	D	117	GLU

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Mol	Chain	Res	Type
1	D	160	PRO
1	D	161	LEU
1	D	197	ILE
1	D	221	GLU
1	D	229	GLN
1	E	25	LEU
1	E	50	VAL
1	E	61	THR
1	E	66	ILE
1	E	237	MET
1	E	246	ASN
1	E	268	SER
1	E	271	ILE
1	F	42	ILE
1	F	50	VAL
1	F	98	MET
1	F	117	GLU
1	F	136	VAL
1	F	157	GLU
1	F	161	LEU
1	F	182	THR
1	F	197	ILE
1	F	221	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (50) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	GLN
1	A	114	GLN
1	A	129	ASN
1	A	132	ASN
1	A	143	ASN
1	A	149	HIS
1	A	194	GLN
1	A	225	GLN
1	A	235	HIS
1	A	266	ASN
1	B	16	GLN
1	B	36	HIS
1	B	54	GLN
1	B	71	GLN
1	B	132	ASN

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Mol	Chain	Res	Type
1	B	148	GLN
1	B	194	GLN
1	B	246	ASN
1	B	265	ASN
1	C	36	HIS
1	C	46	ASN
1	C	114	GLN
1	C	132	ASN
1	C	143	ASN
1	C	198	ASN
1	C	229	GLN
1	C	266	ASN
1	C	270	ASN
1	D	114	GLN
1	D	129	ASN
1	D	147	ASN
1	D	194	GLN
1	D	225	GLN
1	D	229	GLN
1	E	54	GLN
1	E	104	ASN
1	E	114	GLN
1	E	132	ASN
1	E	141	HIS
1	E	143	ASN
1	E	229	GLN
1	E	246	ASN
1	E	266	ASN
1	E	270	ASN
1	F	46	ASN
1	F	104	ASN
1	F	132	ASN
1	F	147	ASN
1	F	194	GLN
1	F	246	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

5 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	COA	B	302	-	42,44,50	2.20	11 (26%)	62,68,75	1.83	13 (20%)
2	COA	C	303	-	42,44,50	1.68	5 (11%)	62,68,75	1.87	12 (19%)
2	COA	A	301	-	42,44,50	1.85	10 (23%)	62,68,75	1.98	14 (22%)
2	COA	D	304	-	42,44,50	1.83	5 (11%)	62,68,75	1.88	13 (20%)
2	COA	E	305	-	42,44,50	1.97	9 (21%)	62,68,75	1.86	14 (22%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	COA	B	302	-	1/1/10/13	17/41/57/64	0/3/3/3
2	COA	C	303	-	1/1/10/13	23/41/57/64	0/3/3/3
2	COA	A	301	-	1/1/10/13	20/41/57/64	0/3/3/3
2	COA	D	304	-	1/1/10/13	20/41/57/64	0/3/3/3
2	COA	E	305	-	1/1/10/13	21/41/57/64	0/3/3/3

All (40) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	305	COA	O9P-C9P	8.69	1.40	1.23
2	B	302	COA	O9P-C9P	7.72	1.38	1.23
2	D	304	COA	O9P-C9P	7.26	1.37	1.23
2	C	303	COA	O9P-C9P	6.93	1.36	1.23
2	A	301	COA	O9P-C9P	6.92	1.36	1.23
2	B	302	COA	P1A-O3A	-5.79	1.53	1.59
2	D	304	COA	P1A-O3A	-4.28	1.54	1.59
2	E	305	COA	C2A-N1A	4.14	1.41	1.33
2	B	302	COA	C8A-N7A	3.99	1.39	1.31
2	B	302	COA	C2A-N1A	3.96	1.41	1.33
2	A	301	COA	P1A-O3A	-3.79	1.55	1.59
2	A	301	COA	C2A-N1A	3.71	1.40	1.33
2	B	302	COA	P3B-O3B	3.51	1.65	1.59
2	D	304	COA	C2A-N1A	3.45	1.40	1.33
2	C	303	COA	C2A-N3A	3.35	1.39	1.33
2	C	303	COA	C2A-N1A	3.14	1.39	1.33
2	D	304	COA	C2A-N3A	2.94	1.39	1.33
2	B	302	COA	C4A-N3A	2.93	1.39	1.34
2	B	302	COA	C2A-N3A	2.91	1.39	1.33
2	D	304	COA	C8A-N7A	2.88	1.37	1.31
2	A	301	COA	C8A-N7A	2.79	1.37	1.31
2	E	305	COA	C8A-N7A	2.77	1.37	1.31
2	B	302	COA	C8A-N9A	2.73	1.42	1.37
2	B	302	COA	OAP-CAP	2.70	1.47	1.42
2	E	305	COA	CCP-CBP	2.67	1.57	1.52
2	C	303	COA	P1A-O3A	-2.66	1.56	1.59
2	E	305	COA	C2A-N3A	2.66	1.38	1.33
2	A	301	COA	C2A-N3A	2.54	1.38	1.33
2	A	301	COA	C6A-N1A	2.48	1.42	1.35
2	A	301	COA	P3B-O3B	2.47	1.63	1.59
2	B	302	COA	C5A-C4A	2.45	1.43	1.39
2	E	305	COA	C8A-N9A	2.35	1.41	1.37
2	A	301	COA	C8A-N9A	2.32	1.41	1.37
2	B	302	COA	C6A-N1A	2.32	1.42	1.35
2	C	303	COA	C8A-N7A	2.31	1.36	1.31
2	E	305	COA	C4A-N3A	2.23	1.38	1.34
2	A	301	COA	CCP-CBP	2.21	1.56	1.52
2	E	305	COA	C4A-N9A	-2.11	1.33	1.37
2	A	301	COA	C4A-N3A	2.09	1.38	1.34
2	E	305	COA	C6A-N1A	2.06	1.41	1.35

All (66) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	303	COA	N3A-C2A-N1A	-6.60	118.60	128.58
2	A	301	COA	N3A-C2A-N1A	-6.35	118.97	128.58
2	E	305	COA	N3A-C2A-N1A	-6.06	119.41	128.58
2	D	304	COA	N3A-C2A-N1A	-5.83	119.75	128.58
2	B	302	COA	N3A-C2A-N1A	-5.69	119.97	128.58
2	E	305	COA	O4B-C1B-N9A	5.20	118.08	108.09
2	A	301	COA	CAP-C9P-N8P	5.19	126.33	116.48
2	D	304	COA	O4B-C1B-N9A	5.16	118.01	108.09
2	A	301	COA	O4B-C1B-N9A	4.80	117.30	108.09
2	B	302	COA	O4B-C1B-N9A	4.67	117.06	108.09
2	D	304	COA	CAP-C9P-N8P	4.49	125.00	116.48
2	E	305	COA	N9A-C8A-N7A	-4.26	107.90	113.94
2	C	303	COA	O4B-C1B-N9A	4.24	116.23	108.09
2	D	304	COA	N9A-C8A-N7A	-4.01	108.24	113.94
2	B	302	COA	N9A-C8A-N7A	-3.95	108.34	113.94
2	C	303	COA	CAP-C9P-N8P	3.92	123.92	116.48
2	A	301	COA	N9A-C8A-N7A	-3.89	108.41	113.94
2	C	303	COA	N9A-C8A-N7A	-3.88	108.43	113.94
2	B	302	COA	CEP-CBP-CAP	3.85	115.33	108.77
2	C	303	COA	C2A-N3A-C4A	3.67	120.80	111.83
2	A	301	COA	CEP-CBP-CAP	3.67	115.02	108.77
2	A	301	COA	C2A-N3A-C4A	3.63	120.70	111.83
2	B	302	COA	CAP-C9P-N8P	3.57	123.27	116.48
2	B	302	COA	C5A-C4A-N3A	-3.57	121.81	126.72
2	D	304	COA	C2A-N3A-C4A	3.55	120.51	111.83
2	C	303	COA	CDP-CBP-CAP	-3.53	102.75	108.77
2	D	304	COA	CEP-CBP-CAP	3.47	114.69	108.77
2	C	303	COA	C5A-C4A-N3A	-3.46	121.95	126.72
2	C	303	COA	CEP-CBP-CAP	3.43	114.61	108.77
2	E	305	COA	C2A-N3A-C4A	3.38	120.09	111.83
2	A	301	COA	O6A-CCP-CBP	3.31	115.86	110.55
2	E	305	COA	CAP-C9P-N8P	3.29	122.73	116.48
2	B	302	COA	C2A-N3A-C4A	3.27	119.82	111.83
2	A	301	COA	C5A-C4A-N3A	-3.25	122.24	126.72
2	D	304	COA	C5A-C4A-N3A	-3.23	122.26	126.72
2	E	305	COA	CEP-CBP-CAP	3.22	114.25	108.77
2	E	305	COA	C5A-C4A-N3A	-3.11	122.43	126.72
2	B	302	COA	C5A-N7A-C8A	3.07	108.27	103.45
2	C	303	COA	C5A-N7A-C8A	3.01	108.18	103.45
2	E	305	COA	C5A-N7A-C8A	2.88	107.97	103.45
2	C	303	COA	O3B-C3B-C2B	-2.81	101.58	111.68
2	A	301	COA	CDP-CBP-CAP	-2.79	104.01	108.77
2	D	304	COA	C5A-N7A-C8A	2.78	107.81	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	305	COA	C4A-C5A-N7A	-2.75	107.43	110.58
2	B	302	COA	C4A-C5A-N7A	-2.67	107.53	110.58
2	A	301	COA	C5A-N7A-C8A	2.63	107.58	103.45
2	E	305	COA	C5A-C4A-N9A	2.62	108.67	105.81
2	D	304	COA	CDP-CBP-CAP	-2.55	104.42	108.77
2	B	302	COA	C5A-C4A-N9A	2.49	108.53	105.81
2	D	304	COA	O3B-C3B-C2B	-2.46	102.85	111.68
2	D	304	COA	O5A-P2A-O3A	2.43	113.84	107.27
2	D	304	COA	C4A-N9A-C8A	2.39	108.25	105.74
2	A	301	COA	O5A-P2A-O3A	2.39	113.72	107.27
2	E	305	COA	CDP-CBP-CAP	-2.37	104.73	108.77
2	E	305	COA	C4A-N9A-C1B	-2.28	121.29	126.63
2	B	302	COA	C2B-C1B-N9A	2.28	118.96	113.30
2	B	302	COA	C4A-N9A-C1B	-2.24	121.39	126.63
2	C	303	COA	C4A-C5A-N7A	-2.20	108.06	110.58
2	A	301	COA	O3B-C3B-C2B	-2.19	103.83	111.68
2	E	305	COA	C4A-N9A-C8A	2.17	108.02	105.74
2	A	301	COA	O9P-C9P-N8P	-2.17	118.38	122.98
2	B	302	COA	CDP-CBP-CAP	-2.10	105.18	108.77
2	D	304	COA	C4A-C5A-N7A	-2.07	108.22	110.58
2	E	305	COA	O6A-CCP-CBP	2.04	113.83	110.55
2	A	301	COA	O9P-C9P-CAP	-2.01	115.28	120.89
2	C	303	COA	O6A-CCP-CBP	2.00	113.76	110.55

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	301	COA	CAP
2	B	302	COA	CAP
2	C	303	COA	CAP
2	D	304	COA	CAP
2	E	305	COA	CAP

All (101) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	COA	CCP-O6A-P2A-O3A
2	A	301	COA	CCP-O6A-P2A-O5A
2	A	301	COA	CDP-CBP-CCP-O6A
2	A	301	COA	CEP-CBP-CCP-O6A
2	A	301	COA	CAP-CBP-CCP-O6A
2	A	301	COA	OAP-CAP-CBP-CCP

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Mol	Chain	Res	Type	Atoms
2	A	301	COA	C9P-CAP-CBP-CCP
2	A	301	COA	OAP-CAP-CBP-CDP
2	A	301	COA	C9P-CAP-CBP-CDP
2	A	301	COA	OAP-CAP-CBP-CEP
2	A	301	COA	C9P-CAP-CBP-CEP
2	A	301	COA	O9P-C9P-CAP-CBP
2	A	301	COA	N8P-C9P-CAP-CBP
2	A	301	COA	N8P-C9P-CAP-OAP
2	B	302	COA	CCP-O6A-P2A-O3A
2	B	302	COA	CCP-O6A-P2A-O4A
2	B	302	COA	CCP-O6A-P2A-O5A
2	B	302	COA	OAP-CAP-CBP-CCP
2	B	302	COA	C9P-CAP-CBP-CCP
2	B	302	COA	OAP-CAP-CBP-CDP
2	B	302	COA	C9P-CAP-CBP-CDP
2	B	302	COA	OAP-CAP-CBP-CEP
2	B	302	COA	C9P-CAP-CBP-CEP
2	B	302	COA	O9P-C9P-CAP-CBP
2	B	302	COA	N8P-C9P-CAP-CBP
2	B	302	COA	N8P-C9P-CAP-OAP
2	C	303	COA	CCP-O6A-P2A-O3A
2	C	303	COA	CCP-O6A-P2A-O4A
2	C	303	COA	CCP-O6A-P2A-O5A
2	C	303	COA	CDP-CBP-CCP-O6A
2	C	303	COA	CEP-CBP-CCP-O6A
2	C	303	COA	CAP-CBP-CCP-O6A
2	C	303	COA	OAP-CAP-CBP-CCP
2	C	303	COA	C9P-CAP-CBP-CCP
2	C	303	COA	OAP-CAP-CBP-CDP
2	C	303	COA	C9P-CAP-CBP-CDP
2	C	303	COA	OAP-CAP-CBP-CEP
2	C	303	COA	C9P-CAP-CBP-CEP
2	C	303	COA	O9P-C9P-CAP-CBP
2	C	303	COA	N8P-C9P-CAP-CBP
2	C	303	COA	N8P-C9P-CAP-OAP
2	D	304	COA	CCP-O6A-P2A-O3A
2	D	304	COA	CCP-O6A-P2A-O4A
2	D	304	COA	CCP-O6A-P2A-O5A
2	D	304	COA	CAP-CBP-CCP-O6A
2	D	304	COA	OAP-CAP-CBP-CCP
2	D	304	COA	C9P-CAP-CBP-CCP
2	D	304	COA	OAP-CAP-CBP-CDP

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Mol	Chain	Res	Type	Atoms
2	D	304	COA	C9P-CAP-CBP-CDP
2	D	304	COA	OAP-CAP-CBP-CEP
2	D	304	COA	C9P-CAP-CBP-CEP
2	D	304	COA	O9P-C9P-CAP-CBP
2	D	304	COA	N8P-C9P-CAP-CBP
2	D	304	COA	N8P-C9P-CAP-OAP
2	E	305	COA	CCP-O6A-P2A-O3A
2	E	305	COA	CCP-O6A-P2A-O4A
2	E	305	COA	CCP-O6A-P2A-O5A
2	E	305	COA	CAP-CBP-CCP-O6A
2	E	305	COA	OAP-CAP-CBP-CCP
2	E	305	COA	C9P-CAP-CBP-CCP
2	E	305	COA	OAP-CAP-CBP-CDP
2	E	305	COA	C9P-CAP-CBP-CDP
2	E	305	COA	OAP-CAP-CBP-CEP
2	E	305	COA	C9P-CAP-CBP-CEP
2	E	305	COA	O9P-C9P-CAP-CBP
2	E	305	COA	N8P-C9P-CAP-CBP
2	E	305	COA	N8P-C9P-CAP-OAP
2	B	302	COA	C2B-C1B-N9A-C4A
2	B	302	COA	C2B-C1B-N9A-C8A
2	E	305	COA	C2B-C1B-N9A-C8A
2	E	305	COA	C2B-C1B-N9A-C4A
2	C	303	COA	C2B-C1B-N9A-C8A
2	A	301	COA	C2B-C1B-N9A-C8A
2	D	304	COA	C2B-C1B-N9A-C8A
2	A	301	COA	P1A-O3A-P2A-O5A
2	B	302	COA	P1A-O3A-P2A-O5A
2	C	303	COA	P1A-O3A-P2A-O5A
2	D	304	COA	P1A-O3A-P2A-O5A
2	E	305	COA	P1A-O3A-P2A-O5A
2	D	304	COA	CDP-CBP-CCP-O6A
2	D	304	COA	CEP-CBP-CCP-O6A
2	E	305	COA	CDP-CBP-CCP-O6A
2	E	305	COA	CEP-CBP-CCP-O6A
2	B	302	COA	CAP-CBP-CCP-O6A
2	A	301	COA	CCP-O6A-P2A-O4A
2	C	303	COA	CAP-C9P-N8P-C7P
2	A	301	COA	C2B-C1B-N9A-C4A
2	C	303	COA	C2B-C1B-N9A-C4A
2	D	304	COA	C2B-C1B-N9A-C4A
2	C	303	COA	O9P-C9P-N8P-C7P

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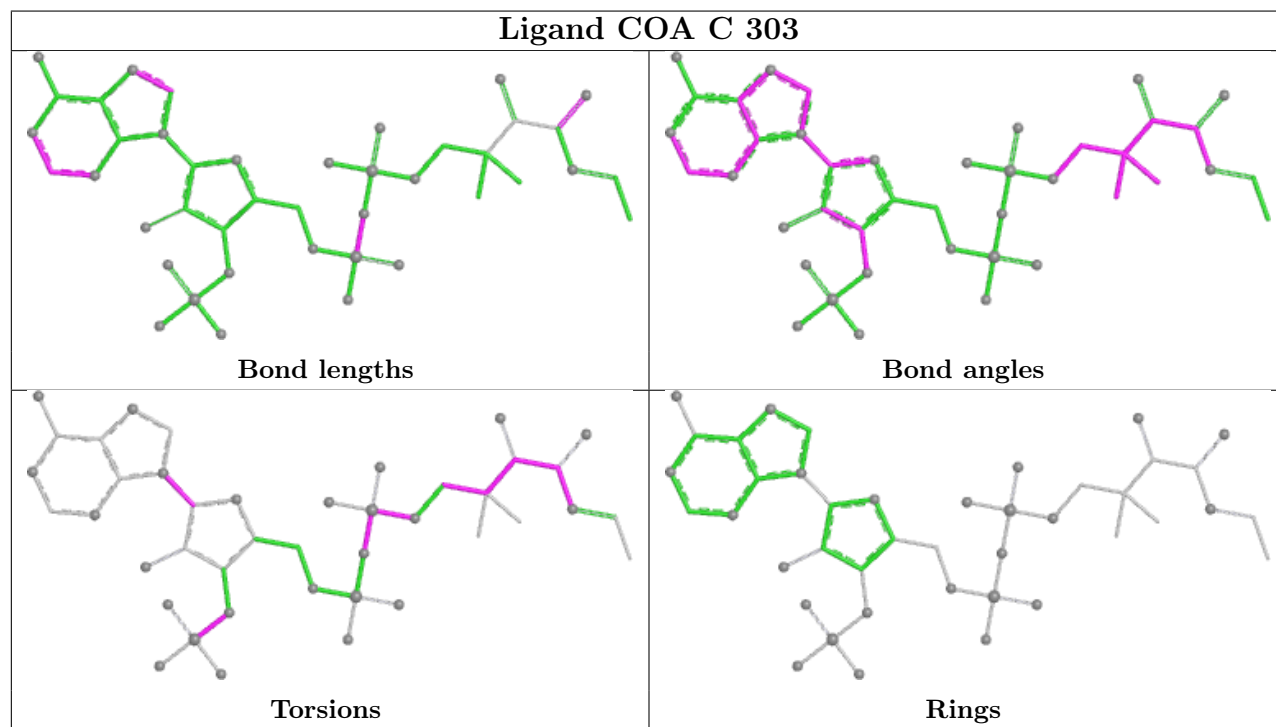
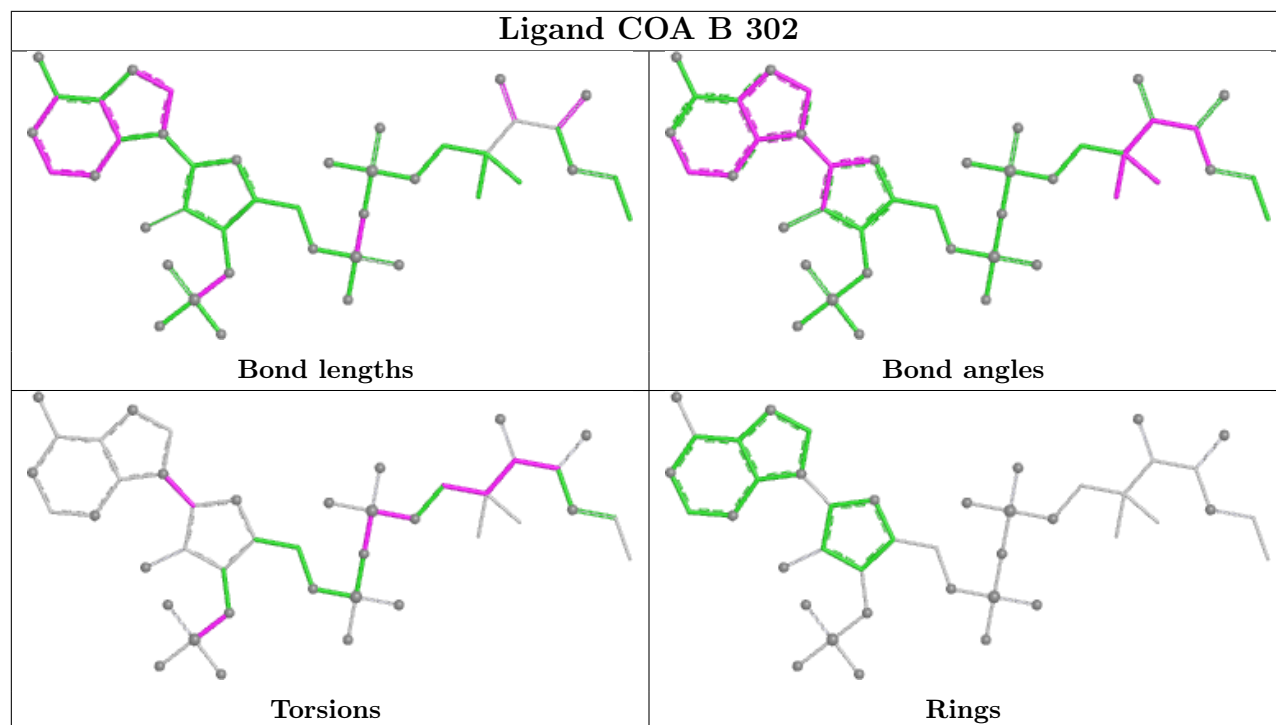
Mol	Chain	Res	Type	Atoms
2	E	305	COA	CAP-C9P-N8P-C7P
2	C	303	COA	P1A-O3A-P2A-O4A
2	E	305	COA	P1A-O3A-P2A-O4A
2	A	301	COA	O4B-C1B-N9A-C8A
2	C	303	COA	O4B-C1B-N9A-C8A
2	D	304	COA	O4B-C1B-N9A-C8A
2	A	301	COA	C3B-O3B-P3B-O7A
2	B	302	COA	C3B-O3B-P3B-O7A
2	C	303	COA	C3B-O3B-P3B-O7A
2	D	304	COA	C3B-O3B-P3B-O7A
2	E	305	COA	C3B-O3B-P3B-O7A

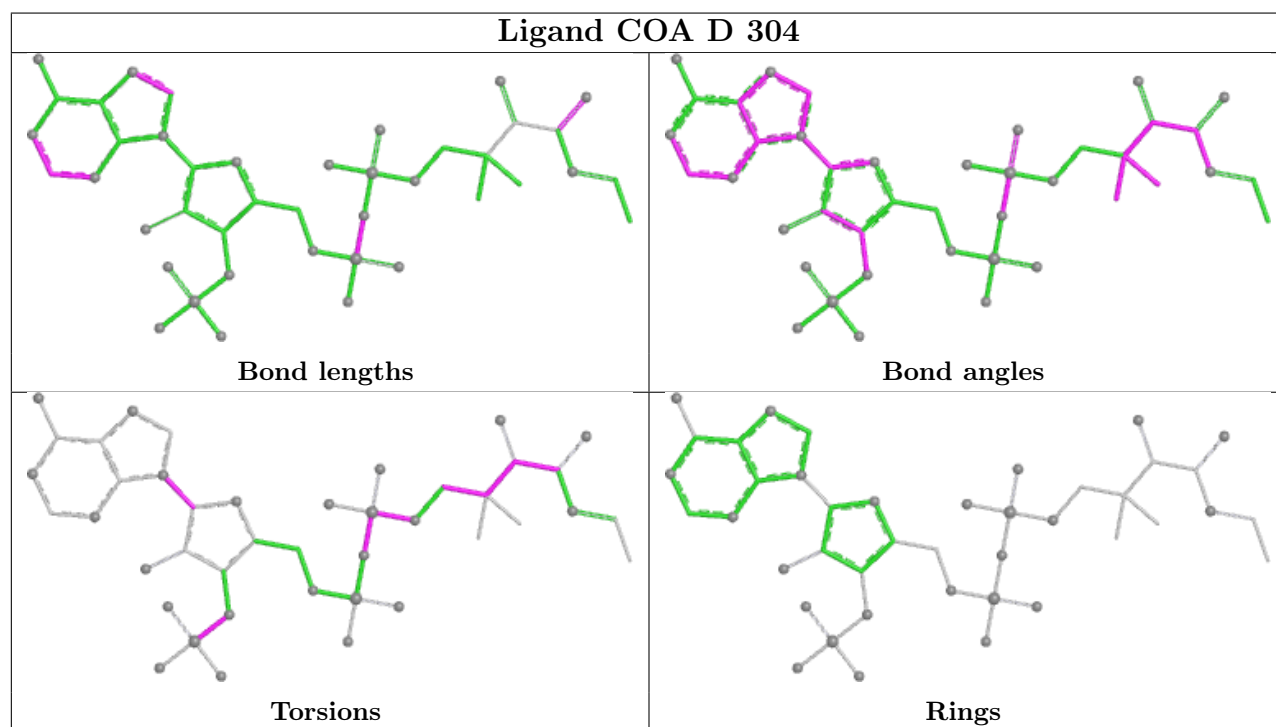
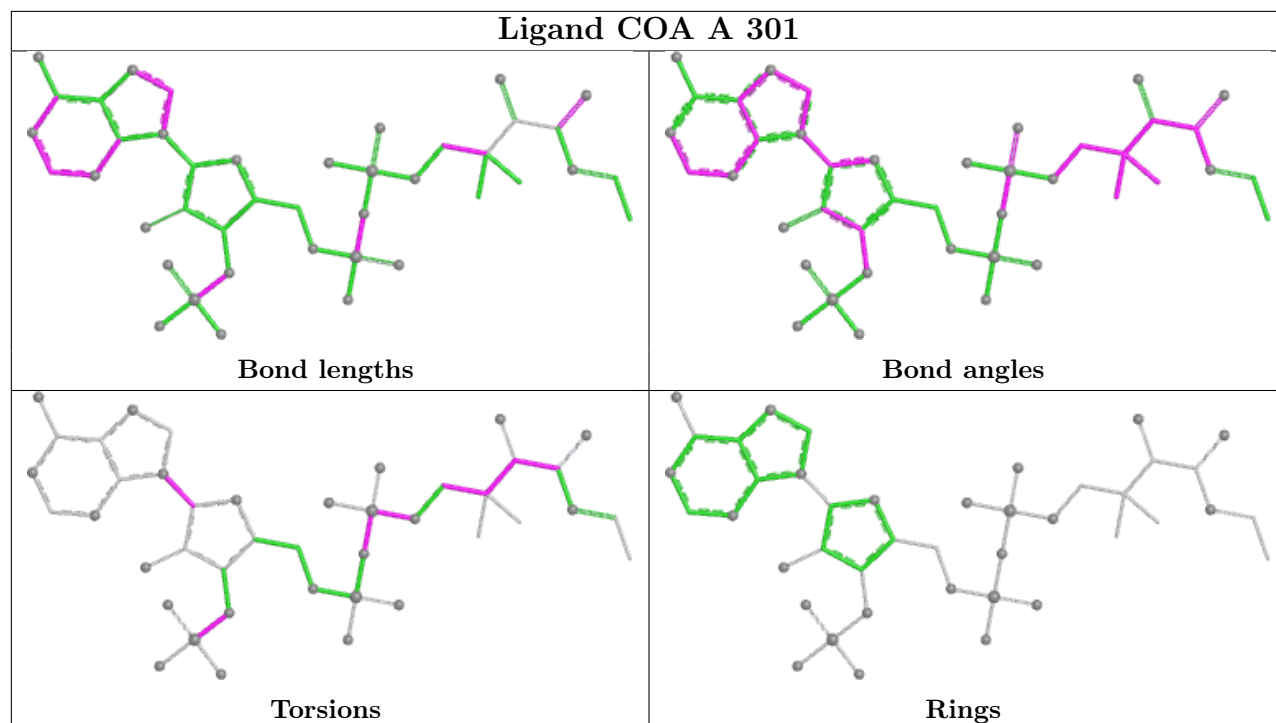
There are no ring outliers.

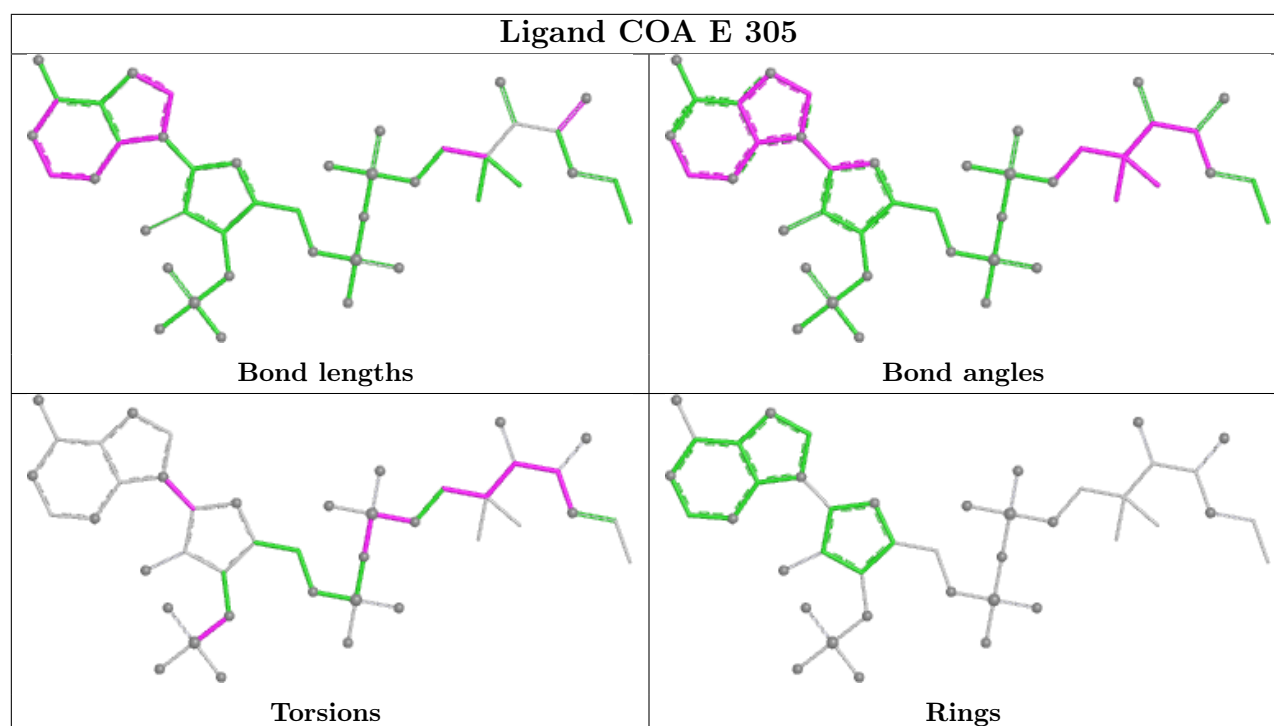
5 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	302	COA	6	0
2	C	303	COA	1	0
2	A	301	COA	7	0
2	D	304	COA	5	0
2	E	305	COA	8	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	270/273 (98%)	0.13	9 (3%) 49 43	26, 40, 67, 92	0
1	B	251/273 (91%)	0.92	29 (11%) 9 7	33, 62, 79, 85	0
1	C	270/273 (98%)	0.13	3 (1%) 78 74	30, 43, 59, 67	0
1	D	268/273 (98%)	0.22	8 (2%) 52 47	26, 42, 64, 72	0
1	E	260/273 (95%)	0.58	16 (6%) 26 21	33, 53, 74, 92	0
1	F	248/273 (90%)	1.30	47 (18%) 3 2	54, 71, 85, 94	0
All	All	1567/1638 (95%)	0.53	112 (7%) 22 17	26, 51, 79, 94	0

All (112) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	227	VAL	5.8
1	F	266	ASN	5.7
1	B	178	PHE	4.8
1	B	248	ARG	4.1
1	F	174	LEU	4.1
1	B	266	ASN	3.9
1	B	233	ALA	3.7
1	F	49	ALA	3.6
1	E	203	ILE	3.5
1	F	85	PRO	3.4
1	F	172	LEU	3.4
1	E	90	TRP	3.3
1	B	230	ALA	3.3
1	F	176	ALA	3.2
1	D	154	GLY	3.2
1	F	264	ILE	3.2
1	F	233	ALA	3.1
1	A	212	LYS	3.0
1	B	238	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	2	LEU	3.0
1	B	228	GLY	3.0
1	B	173	LEU	2.9
1	C	2	LEU	2.9
1	F	234	GLU	2.9
1	A	203	ILE	2.9
1	F	203	ILE	2.9
1	E	92	ASP	2.8
1	F	265	ASN	2.8
1	B	43	GLY	2.8
1	F	158	GLN	2.7
1	E	12	PRO	2.7
1	B	30	GLY	2.7
1	B	154	GLY	2.7
1	B	174	LEU	2.7
1	A	89	GLU	2.7
1	A	90	TRP	2.7
1	F	35	VAL	2.6
1	F	239	VAL	2.6
1	F	68	MET	2.6
1	F	262	TRP	2.6
1	F	263	PHE	2.6
1	B	42	ILE	2.6
1	B	177	ASP	2.5
1	A	271	ILE	2.5
1	D	2	LEU	2.5
1	F	160	PRO	2.5
1	E	93	ILE	2.4
1	F	139	GLY	2.4
1	B	166	ILE	2.4
1	C	271	ILE	2.4
1	F	50	VAL	2.4
1	F	122	TYR	2.4
1	B	182	THR	2.4
1	D	84	PRO	2.4
1	F	150	PRO	2.4
1	A	210	VAL	2.4
1	F	166	ILE	2.3
1	F	147	ASN	2.3
1	E	206	GLU	2.3
1	F	254	GLU	2.3
1	D	269	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	91	TRP	2.3
1	F	28	LYS	2.3
1	B	240	GLY	2.3
1	E	158	GLN	2.3
1	E	73	VAL	2.3
1	F	136	VAL	2.3
1	B	148	GLN	2.3
1	B	223	LEU	2.3
1	B	231	PHE	2.3
1	F	27	LEU	2.3
1	B	232	GLU	2.3
1	F	87	PRO	2.3
1	D	148	GLN	2.3
1	B	250	PHE	2.3
1	F	167	ARG	2.2
1	B	239	VAL	2.2
1	D	161	LEU	2.2
1	C	66	ILE	2.2
1	F	51	ALA	2.2
1	B	226	GLU	2.2
1	F	232	GLU	2.2
1	B	147	ASN	2.2
1	E	91	TRP	2.2
1	E	115	ILE	2.2
1	F	53	ILE	2.2
1	F	248	ARG	2.2
1	B	249	LEU	2.2
1	E	56	LEU	2.2
1	B	171	VAL	2.2
1	E	137	ALA	2.2
1	F	192	PRO	2.1
1	F	86	VAL	2.1
1	F	180	SER	2.1
1	E	271	ILE	2.1
1	F	145	ILE	2.1
1	D	66	ILE	2.1
1	F	66	ILE	2.1
1	F	90	TRP	2.1
1	E	119	PHE	2.1
1	E	135	PHE	2.1
1	F	62	GLU	2.0
1	D	147	ASN	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	154	GLY	2.0
1	F	30	GLY	2.0
1	F	152	GLU	2.0
1	E	99	PRO	2.0
1	F	99	PRO	2.0
1	B	22	LEU	2.0
1	F	22	LEU	2.0
1	F	164	LEU	2.0
1	F	225	GLN	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

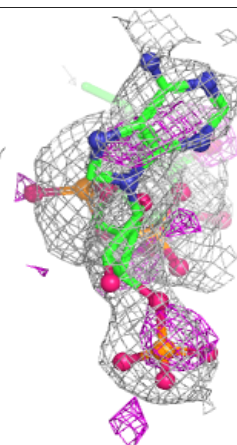
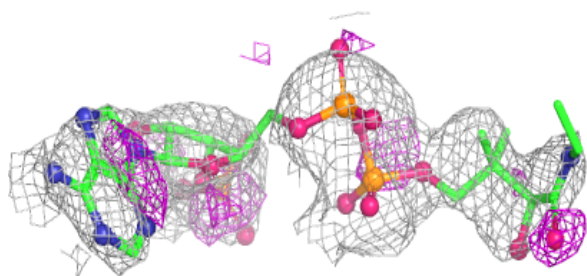
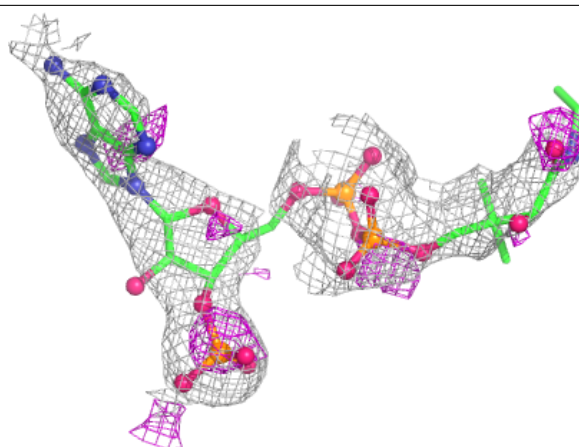
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	COA	B	302	42/48	0.77	0.13	59,65,73,74	0
2	COA	E	305	42/48	0.77	0.13	58,64,76,77	0
2	COA	D	304	42/48	0.86	0.12	41,50,72,74	0
2	COA	A	301	42/48	0.89	0.11	44,53,66,68	0
2	COA	C	303	42/48	0.92	0.09	43,51,67,68	0

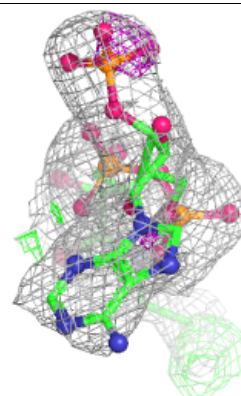
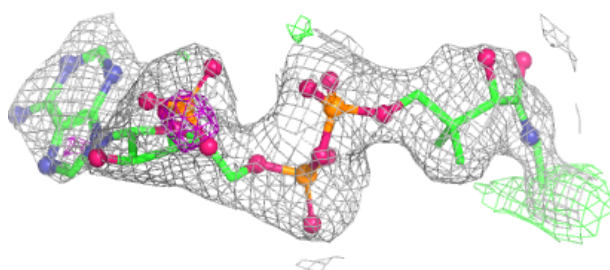
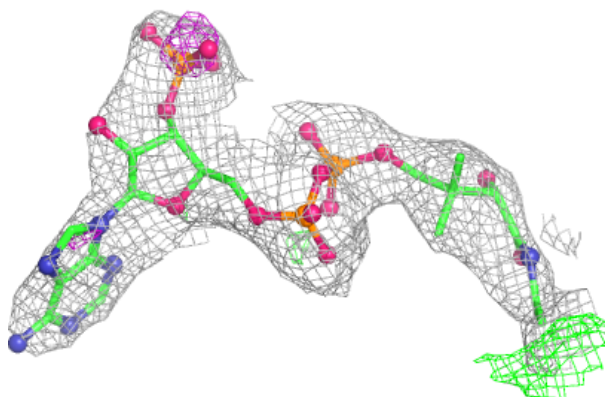
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around COA B 302:

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

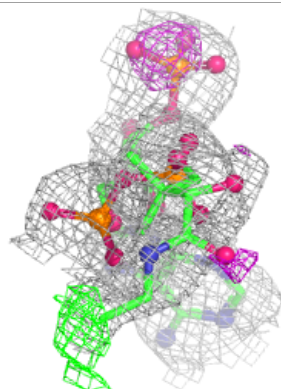
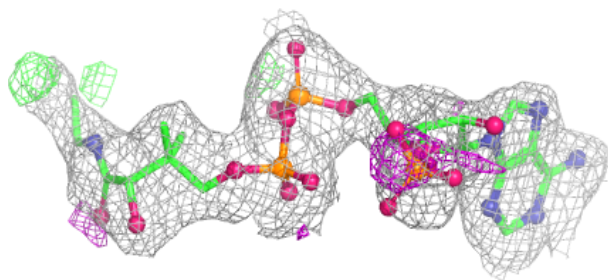
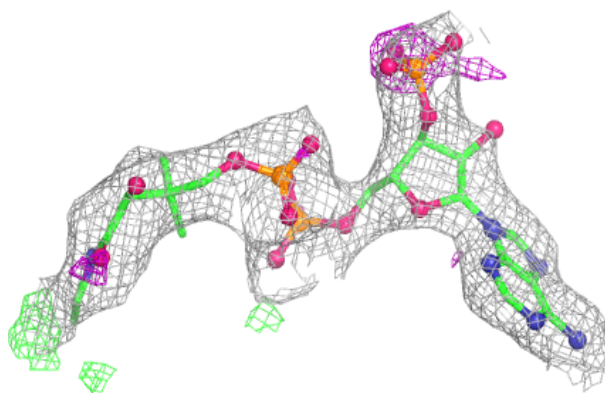
**Electron density around COA E 305:**

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

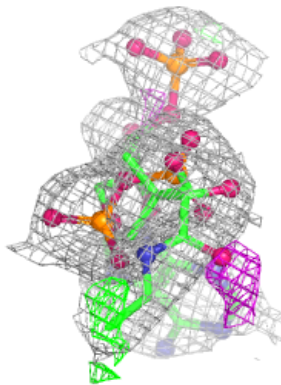
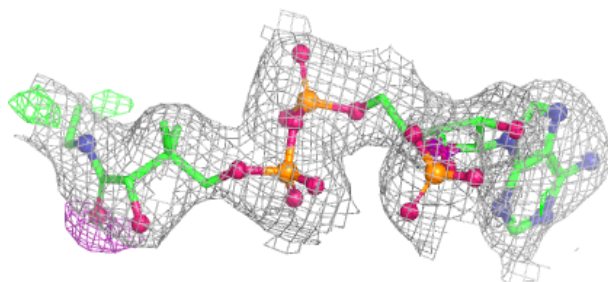
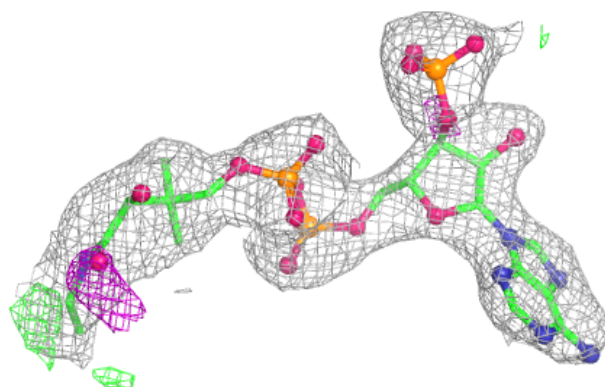


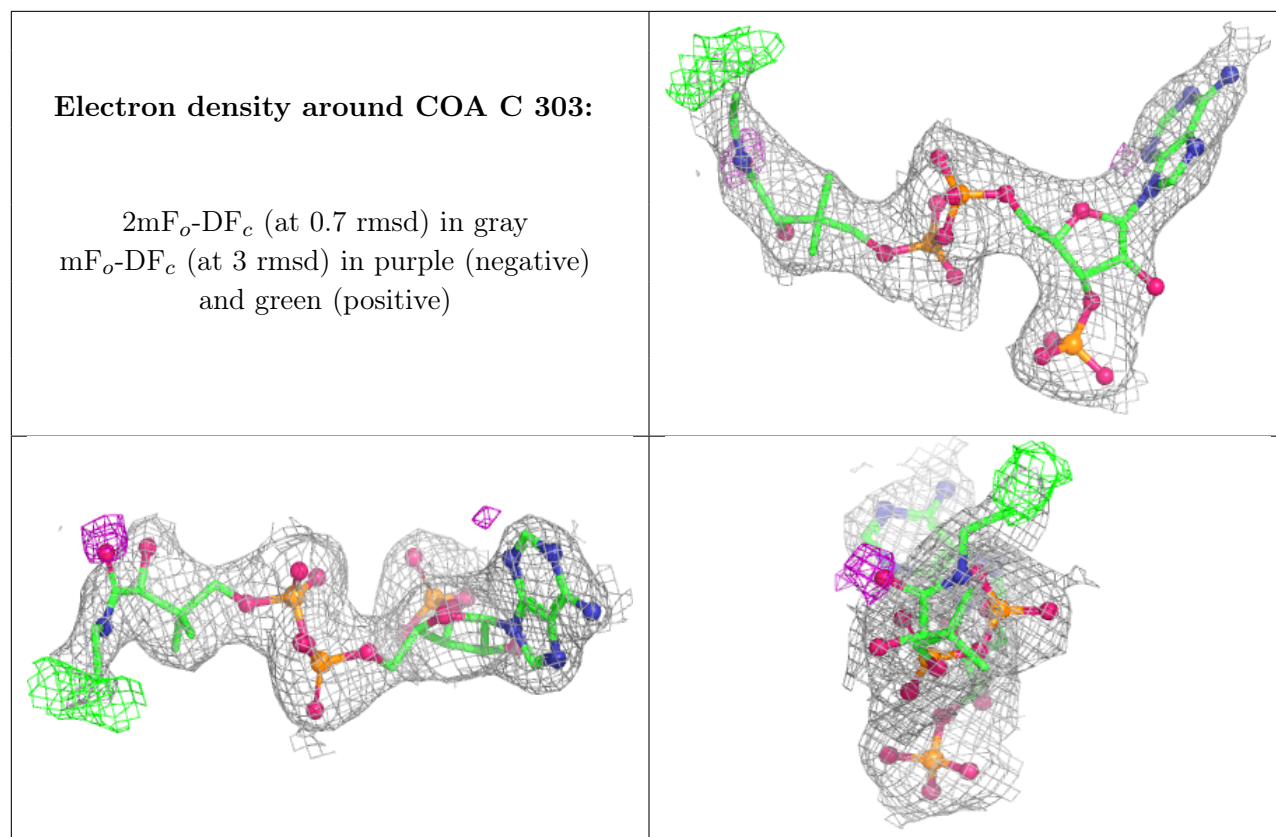
Electron density around COA D 304:

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

**Electron density around COA A 301:**

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





6.5 Other polymers [i](#)

There are no such residues in this entry.