



Full wwPDB EM Validation Report ⓘ

Aug 5, 2026 – 05:19 AM EDT

PDB ID : 9NPW / pdb_00009npw
EMDB ID : EMD-49634
Title : CCT G beta 5 R269E complex state 2
Authors : Mack, D.C.; Shen, P.S.
Deposited on : 2025-03-11
Resolution : 3.00 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp>

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:

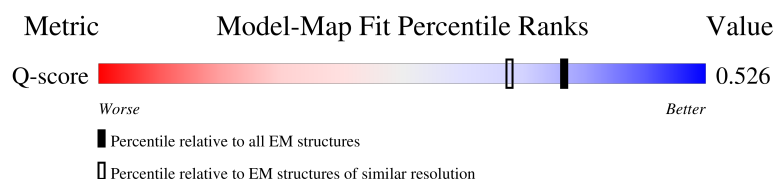
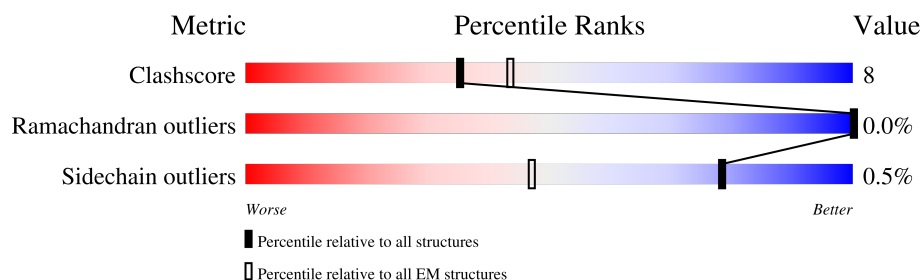
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 Å.

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



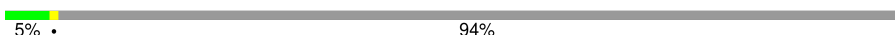
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14081 (2.50 - 3.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	556	
1	a	556	
2	B	535	
2	b	535	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	D	539	
3	d	539	
4	E	541	
4	e	541	
5	G	545	
5	g	545	
6	H	543	
6	h	543	
7	Q	548	
7	q	548	
8	Z	531	
8	z	531	
9	P	326	
10	N	441	

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
13	AF3	A	603	-	-	X	-
13	AF3	G	603	-	-	X	-
13	AF3	H	603	-	-	X	-
13	AF3	Q	603	-	-	X	-
13	AF3	Z	603	-	-	X	-
13	AF3	a	603	-	-	X	-
13	AF3	g	603	-	-	X	-
13	AF3	h	603	-	-	X	-
13	AF3	q	603	-	-	X	-
13	AF3	z	603	-	-	X	-

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 66098 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 T-complex protein 1 subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	536	Total	C	N	O	S	0	0
			4069	2548	711	787	23		
1	a	532	Total	C	N	O	S	0	0
			4041	2533	707	778	23		

- Molecule 2 is a protein called T-complex protein 1 subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	526	Total	C	N	O	S	0	0
			3952	2473	696	764	19		
2	b	525	Total	C	N	O	S	0	0
			3943	2467	694	763	19		

- Molecule 3 is a protein called T-complex protein 1 subunit delta.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	520	Total	C	N	O	S	0	0
			3923	2453	683	764	23		
3	d	520	Total	C	N	O	S	0	0
			3917	2450	680	764	23		

- Molecule 4 is a protein called T-complex protein 1 subunit epsilon.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	535	Total	C	N	O	S	1	0
			4132	2590	719	792	31		
4	e	540	Total	C	N	O	S	1	0
			4169	2610	724	804	31		

- Molecule 5 is a protein called T-complex protein 1 subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	526	Total	C	N	O	S	0	0
			4089	2548	726	785	30		
5	g	528	Total	C	N	O	S	0	0
			4102	2556	729	787	30		

- Molecule 6 is a protein called T-complex protein 1 subunit eta.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	H	528	Total	C	N	O	S	0	0
			4054	2561	699	769	25		
6	h	525	Total	C	N	O	S	0	0
			4032	2548	696	763	25		

- Molecule 7 is a protein called T-complex protein 1 subunit theta.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Q	538	Total	C	N	O	S	0	0
			4086	2579	696	784	27		
7	q	533	Total	C	N	O	S	0	0
			4053	2558	690	778	27		

- Molecule 8 is a protein called T-complex protein 1 subunit zeta.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Z	525	Total	C	N	O	S	0	0
			4022	2528	704	769	21		
8	z	527	Total	C	N	O	S	0	0
			4033	2534	706	772	21		

- Molecule 9 is a protein called Phosducin-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	P	98	Total	C	N	O	S	0	0
			739	467	118	147	7		

There are 25 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	302	ALA	-	expression tag	UNP Q13371
P	303	LEU	-	expression tag	UNP Q13371
P	304	GLU	-	expression tag	UNP Q13371
P	305	GLY	-	expression tag	UNP Q13371

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
P	306	PRO	-	expression tag	UNP Q13371
P	307	ARG	-	expression tag	UNP Q13371
P	308	PHE	-	expression tag	UNP Q13371
P	309	GLU	-	expression tag	UNP Q13371
P	310	GLN	-	expression tag	UNP Q13371
P	311	LYS	-	expression tag	UNP Q13371
P	312	LEU	-	expression tag	UNP Q13371
P	313	ILE	-	expression tag	UNP Q13371
P	314	SER	-	expression tag	UNP Q13371
P	315	GLU	-	expression tag	UNP Q13371
P	316	GLU	-	expression tag	UNP Q13371
P	317	ASP	-	expression tag	UNP Q13371
P	318	LEU	-	expression tag	UNP Q13371
P	319	ASN	-	expression tag	UNP Q13371
P	320	MET	-	expression tag	UNP Q13371
P	321	HIS	-	expression tag	UNP Q13371
P	322	HIS	-	expression tag	UNP Q13371
P	323	HIS	-	expression tag	UNP Q13371
P	324	HIS	-	expression tag	UNP Q13371
P	325	HIS	-	expression tag	UNP Q13371
P	326	HIS	-	expression tag	UNP Q13371

- Molecule 10 is a protein called Guanine nucleotide-binding protein subunit beta-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	N	26	Total	C	N	O	S	0	0
			211	131	35	42	3		

There are 47 discrepancies between the modelled and reference sequences:

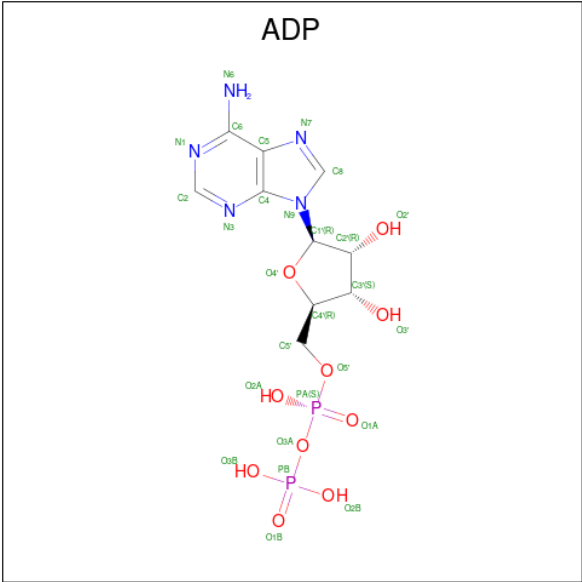
Chain	Residue	Modelled	Actual	Comment	Reference
N	-31	MET	-	initiating methionine	UNP O14775
N	-30	TRP	-	expression tag	UNP O14775
N	-29	SER	-	expression tag	UNP O14775
N	-28	HIS	-	expression tag	UNP O14775
N	-27	PRO	-	expression tag	UNP O14775
N	-26	GLN	-	expression tag	UNP O14775
N	-25	PHE	-	expression tag	UNP O14775
N	-24	GLU	-	expression tag	UNP O14775
N	-23	LYS	-	expression tag	UNP O14775
N	-22	GLY	-	expression tag	UNP O14775
N	-21	GLY	-	expression tag	UNP O14775

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
N	-20	GLY	-	expression tag	UNP O14775
N	-19	SER	-	expression tag	UNP O14775
N	-18	GLY	-	expression tag	UNP O14775
N	-17	GLY	-	expression tag	UNP O14775
N	-16	GLY	-	expression tag	UNP O14775
N	-15	SER	-	expression tag	UNP O14775
N	-14	GLY	-	expression tag	UNP O14775
N	-13	GLY	-	expression tag	UNP O14775
N	-12	SER	-	expression tag	UNP O14775
N	-11	SER	-	expression tag	UNP O14775
N	-10	ALA	-	expression tag	UNP O14775
N	-9	TRP	-	expression tag	UNP O14775
N	-8	SER	-	expression tag	UNP O14775
N	-7	HIS	-	expression tag	UNP O14775
N	-6	PRO	-	expression tag	UNP O14775
N	-5	GLN	-	expression tag	UNP O14775
N	-4	PHE	-	expression tag	UNP O14775
N	-3	GLU	-	expression tag	UNP O14775
N	-2	LYS	-	expression tag	UNP O14775
N	-1	ALA	-	expression tag	UNP O14775
N	0	ALA	-	expression tag	UNP O14775
N	269	GLU	ARG	engineered mutation	UNP O14775
N	396	GLY	-	expression tag	UNP O14775
N	397	GLY	-	expression tag	UNP O14775
N	398	GLU	-	expression tag	UNP O14775
N	399	ASP	-	expression tag	UNP O14775
N	400	GLN	-	expression tag	UNP O14775
N	401	VAL	-	expression tag	UNP O14775
N	402	ASP	-	expression tag	UNP O14775
N	403	PRO	-	expression tag	UNP O14775
N	404	ARG	-	expression tag	UNP O14775
N	405	LEU	-	expression tag	UNP O14775
N	406	ILE	-	expression tag	UNP O14775
N	407	ASP	-	expression tag	UNP O14775
N	408	GLY	-	expression tag	UNP O14775
N	409	LYS	-	expression tag	UNP O14775

- Molecule 11 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					AltConf
11	A	1	Total	C	N	O	P	0
			27	10	5	10	2	
11	B	1	Total	C	N	O	P	0
			27	10	5	10	2	
11	D	1	Total	C	N	O	P	0
			27	10	5	10	2	
11	E	1	Total	C	N	O	P	0
			27	10	5	10	2	
11	G	1	Total	C	N	O	P	0
			27	10	5	10	2	
11	H	1	Total	C	N	O	P	0
			27	10	5	10	2	
11	Q	1	Total	C	N	O	P	0
			27	10	5	10	2	
11	Z	1	Total	C	N	O	P	0
			27	10	5	10	2	
11	a	1	Total	C	N	O	P	0
			27	10	5	10	2	
11	b	1	Total	C	N	O	P	0
			27	10	5	10	2	
11	d	1	Total	C	N	O	P	0
			27	10	5	10	2	
11	e	1	Total	C	N	O	P	0
			27	10	5	10	2	
11	g	1	Total	C	N	O	P	0
			27	10	5	10	2	
11	h	1	Total	C	N	O	P	0
			27	10	5	10	2	

Continued on next page...

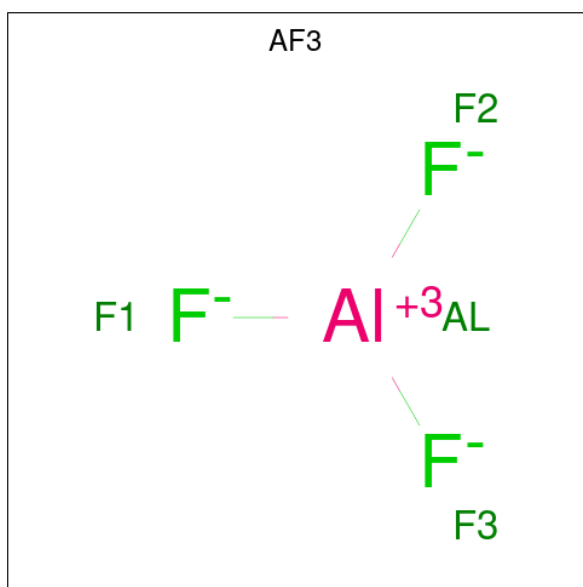
Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf
11	q	1	Total	C	N	O	P	0
			27	10	5	10	2	
11	z	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 12 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
12	A	1	Total	Mg	0
			1	1	
12	B	1	Total	Mg	0
			1	1	
12	D	1	Total	Mg	0
			1	1	
12	E	1	Total	Mg	0
			1	1	
12	G	1	Total	Mg	0
			1	1	
12	H	1	Total	Mg	0
			1	1	
12	Q	1	Total	Mg	0
			1	1	
12	Z	1	Total	Mg	0
			1	1	
12	a	1	Total	Mg	0
			1	1	
12	b	1	Total	Mg	0
			1	1	
12	d	1	Total	Mg	0
			1	1	
12	e	1	Total	Mg	0
			1	1	
12	g	1	Total	Mg	0
			1	1	
12	h	1	Total	Mg	0
			1	1	
12	q	1	Total	Mg	0
			1	1	
12	z	1	Total	Mg	0
			1	1	

- Molecule 13 is ALUMINUM FLUORIDE (CCD ID: AF3) (formula: AlF₃).



Mol	Chain	Residues	Atoms			AltConf
13	A	1	Total	Al	F	0
			4	1	3	
13	B	1	Total	Al	F	0
			4	1	3	
13	D	1	Total	Al	F	0
			4	1	3	
13	E	1	Total	Al	F	0
			4	1	3	
13	G	1	Total	Al	F	0
			4	1	3	
13	H	1	Total	Al	F	0
			4	1	3	
13	Q	1	Total	Al	F	0
			4	1	3	
13	Z	1	Total	Al	F	0
			4	1	3	
13	a	1	Total	Al	F	0
			4	1	3	
13	b	1	Total	Al	F	0
			4	1	3	
13	d	1	Total	Al	F	0
			4	1	3	
13	e	1	Total	Al	F	0
			4	1	3	
13	g	1	Total	Al	F	0
			4	1	3	
13	h	1	Total	Al	F	0
			4	1	3	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			AltConf
13	q	1	Total	Al	F	0
			4	1	3	
13	z	1	Total	Al	F	0
			4	1	3	

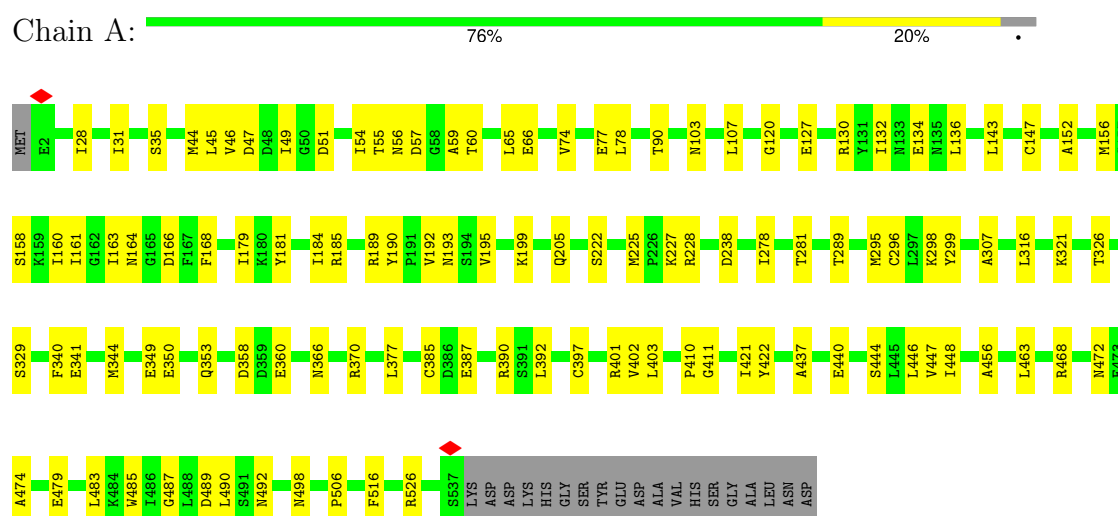
- Molecule 14 is water.

Mol	Chain	Residues	Atoms		AltConf
14	A	2	Total	O	0
			2	2	
14	B	2	Total	O	0
			2	2	
14	D	1	Total	O	0
			1	1	
14	E	1	Total	O	0
			1	1	
14	G	1	Total	O	0
			1	1	
14	H	1	Total	O	0
			1	1	
14	Q	1	Total	O	0
			1	1	
14	Z	1	Total	O	0
			1	1	
14	a	2	Total	O	0
			2	2	
14	b	1	Total	O	0
			1	1	
14	d	1	Total	O	0
			1	1	
14	e	1	Total	O	0
			1	1	
14	g	1	Total	O	0
			1	1	
14	h	1	Total	O	0
			1	1	
14	q	1	Total	O	0
			1	1	
14	z	1	Total	O	0
			1	1	

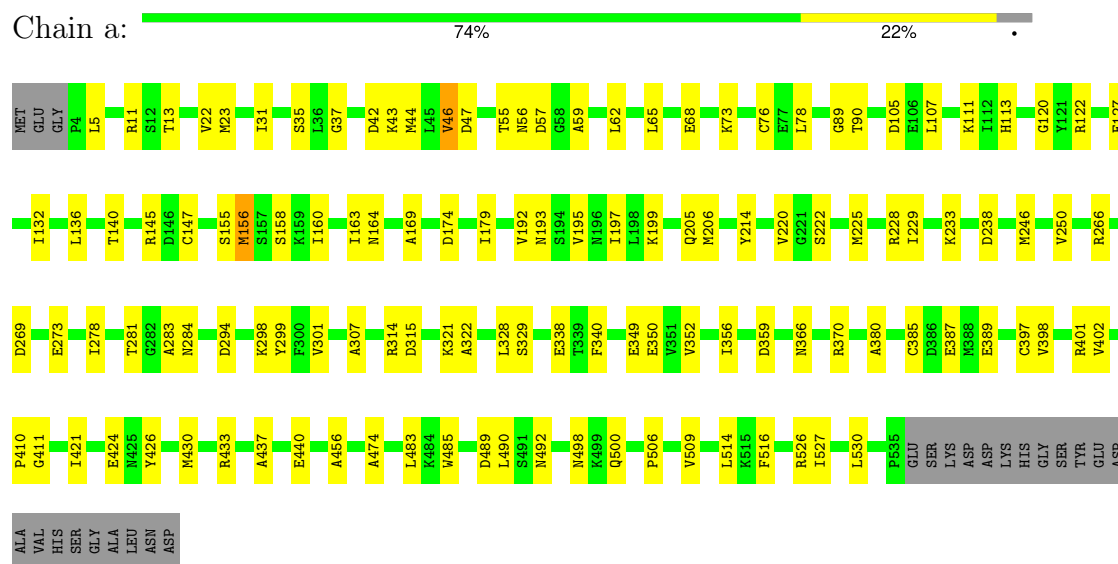
3 Residue-property plots

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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

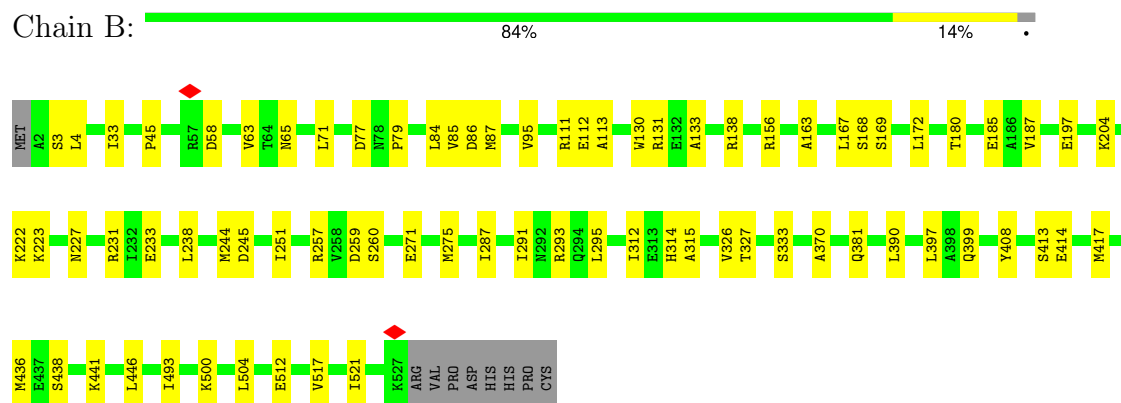
- Molecule 1: T-complex protein 1 subunit alpha



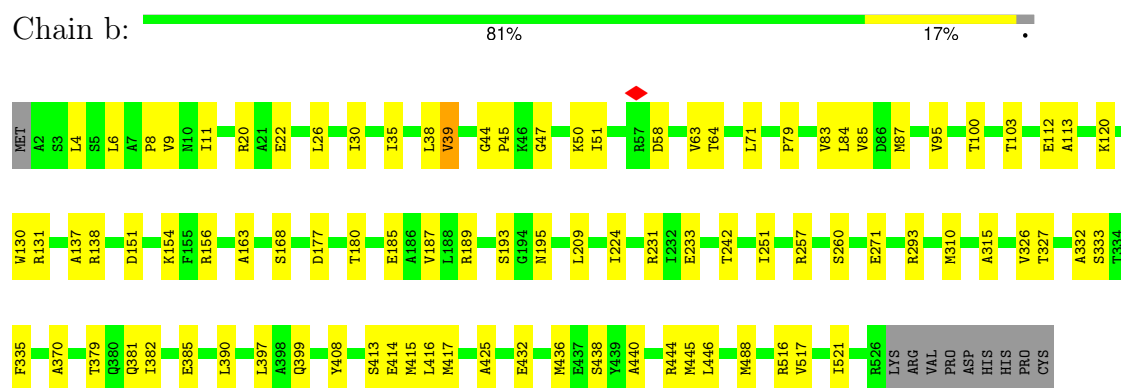
- Molecule 1: T-complex protein 1 subunit alpha



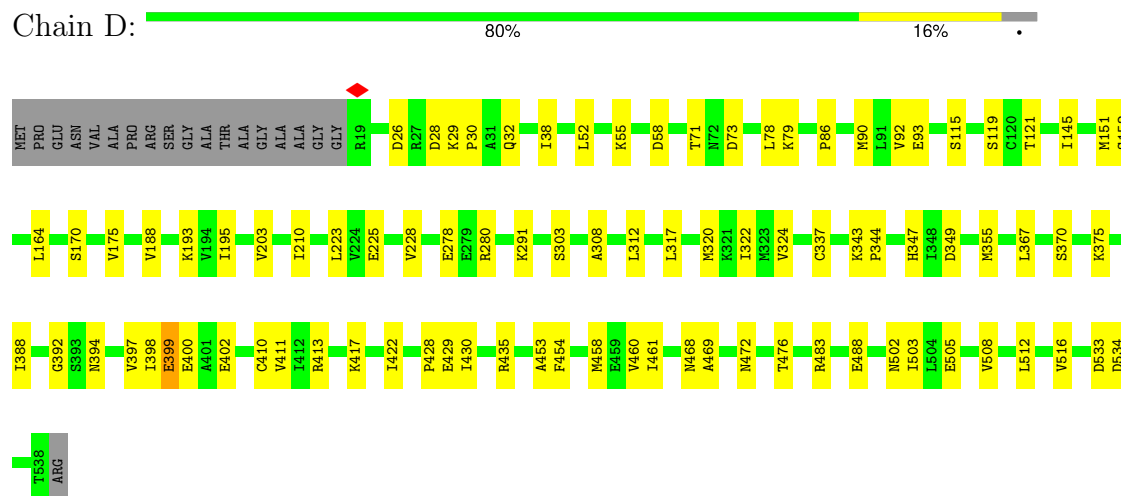
- Molecule 2: T-complex protein 1 subunit beta



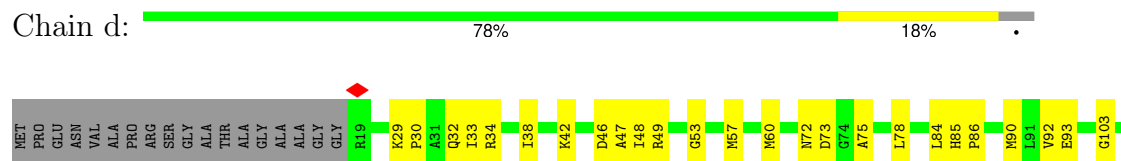
- Molecule 2: T-complex protein 1 subunit beta

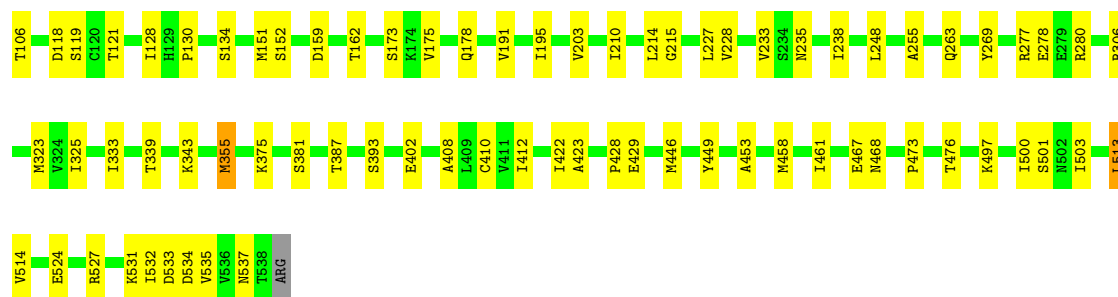


- Molecule 3: T-complex protein 1 subunit delta

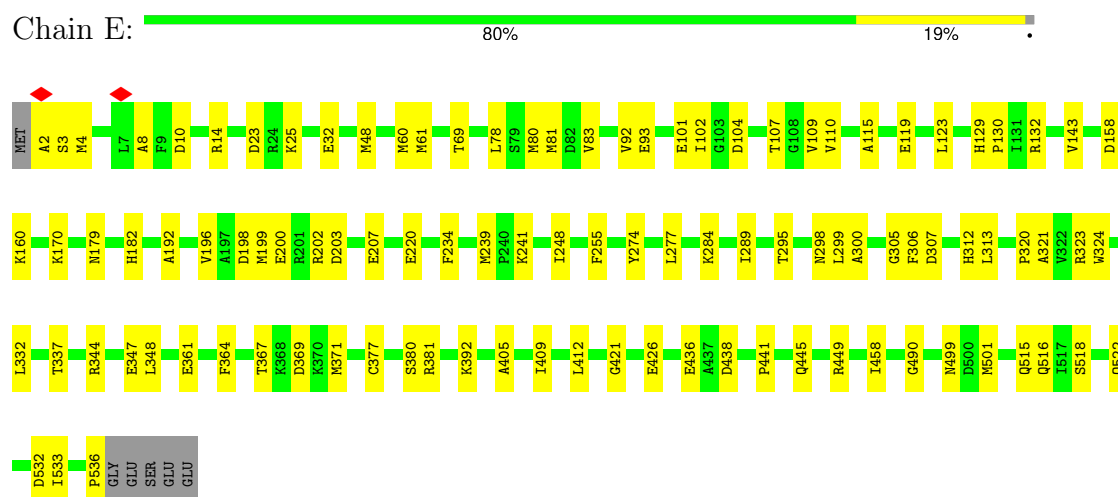


- Molecule 3: T-complex protein 1 subunit delta

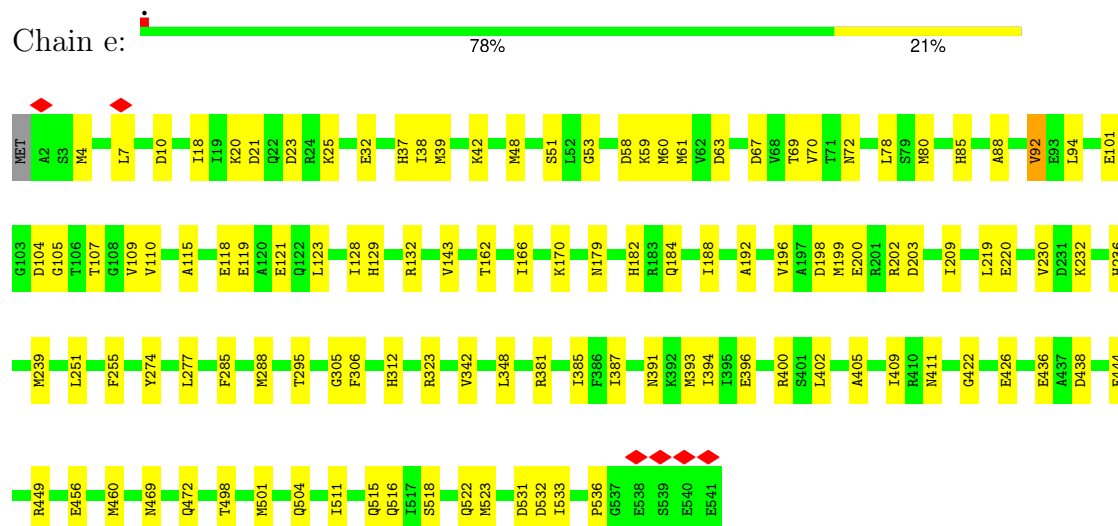




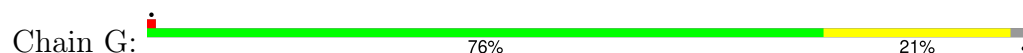
- Molecule 4: T-complex protein 1 subunit epsilon

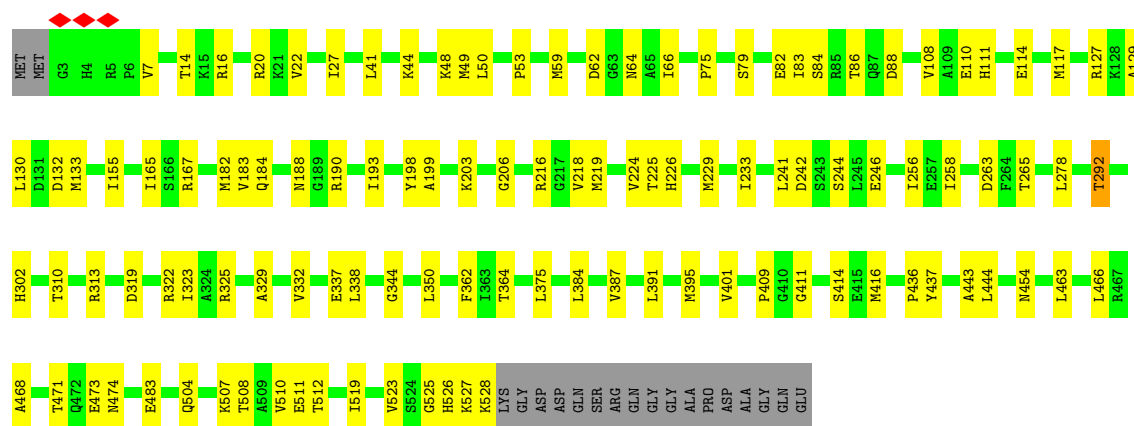


- Molecule 4: T-complex protein 1 subunit epsilon

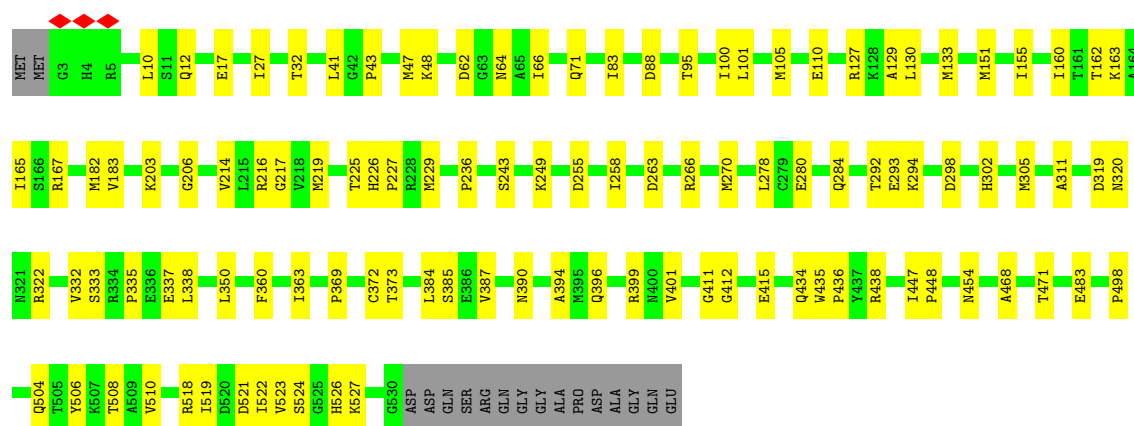
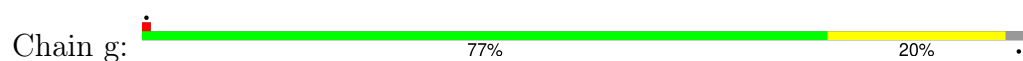


- Molecule 5: T-complex protein 1 subunit gamma

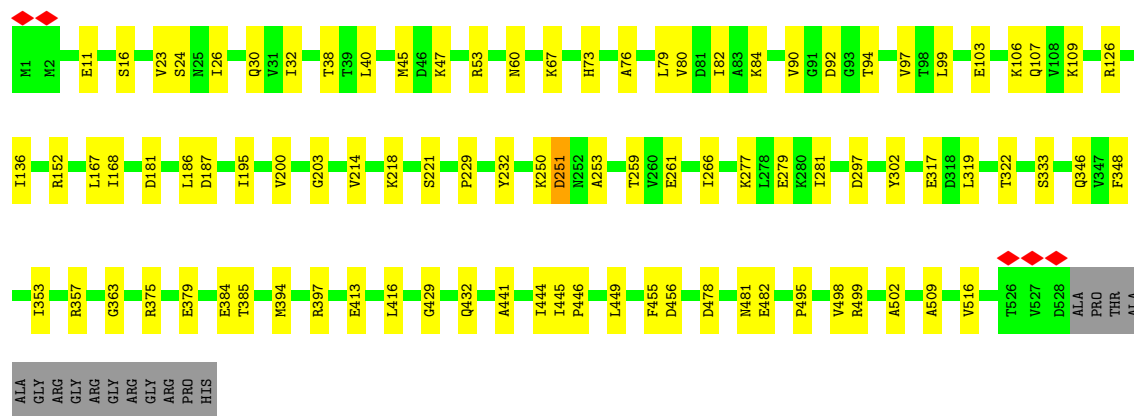
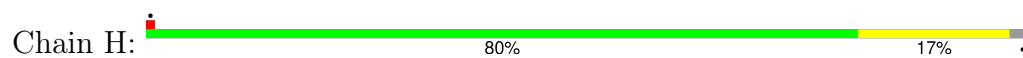




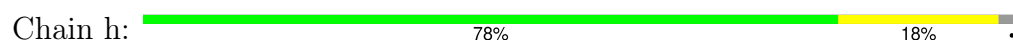
• Molecule 5: T-complex protein 1 subunit gamma

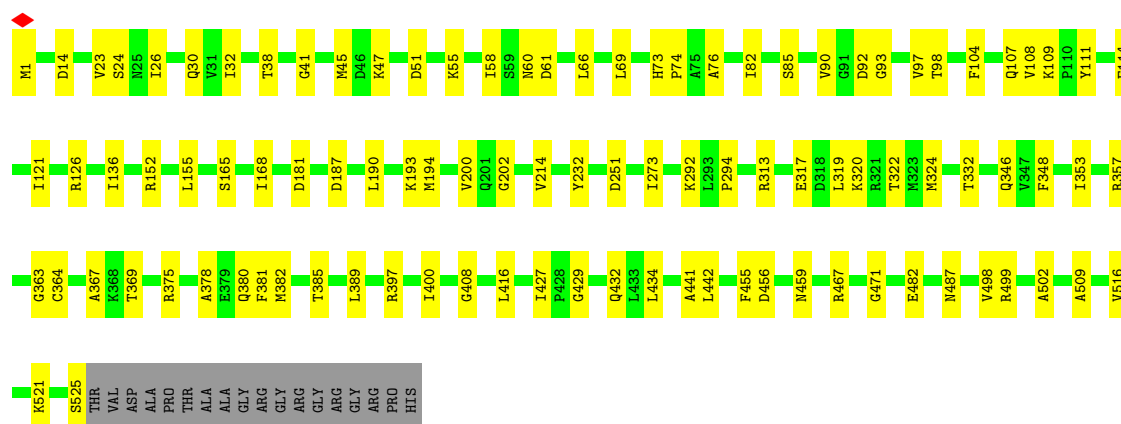


• Molecule 6: T-complex protein 1 subunit eta

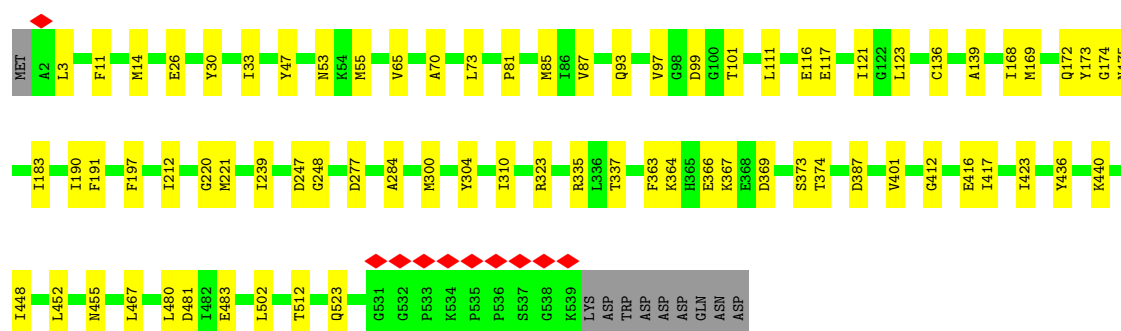
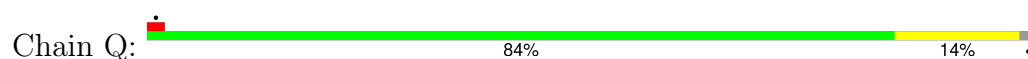


• Molecule 6: T-complex protein 1 subunit eta

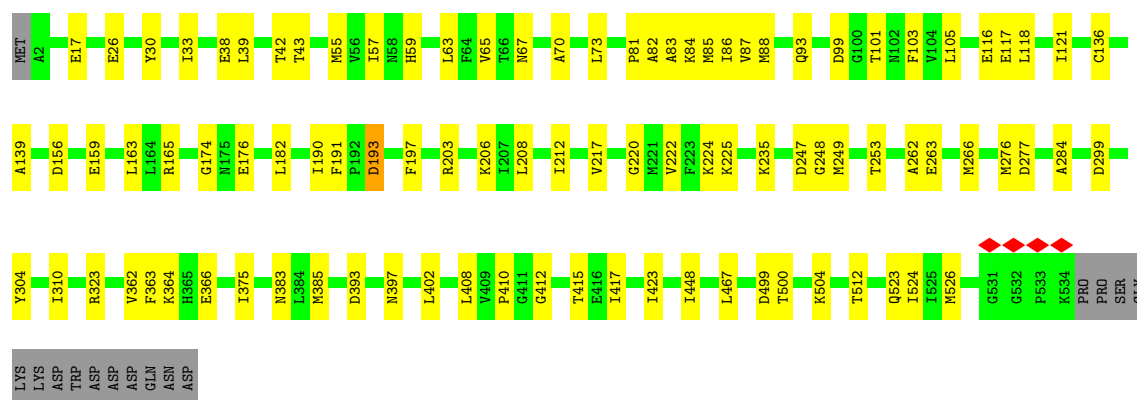
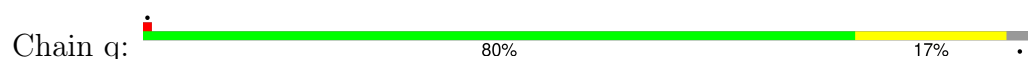




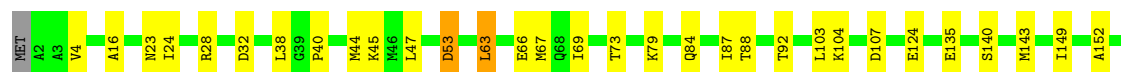
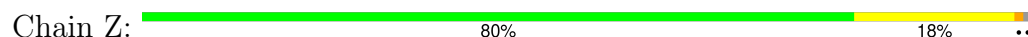
• Molecule 7: T-complex protein 1 subunit theta



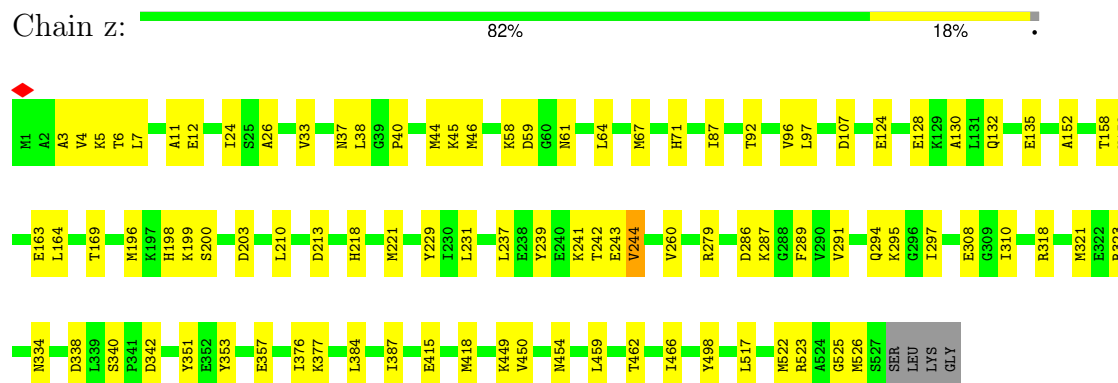
• Molecule 7: T-complex protein 1 subunit theta



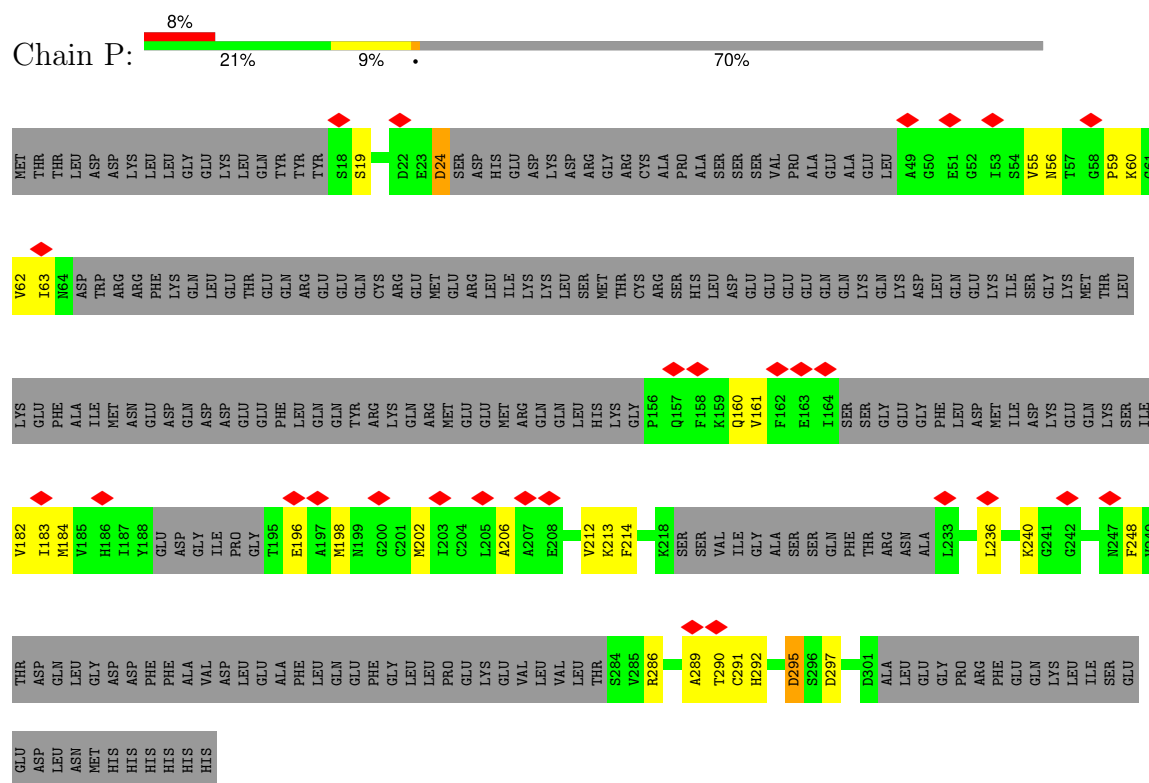
• Molecule 8: T-complex protein 1 subunit zeta



- Molecule 8: T-complex protein 1 subunit zeta



- Molecule 9: Phosducin-like protein



- Molecule 10: Guanine nucleotide-binding protein subunit beta-5



GLY	GLY	ALA	GLN	TRP	ALA	LYS	MET
GLU	ARG	PHE	ILE	VAL	LEU	SER	TRP
ASP	LEU	GLU	LEU	MET	GLY	SER	SER
GLN	LEU	THR	THR	ALA	GLN	GLN	HIS
VAL	PHE	HIS	ALA	ALA	CYS	LEU	PRO
ASP	ALA	GLU	SER	ALA	VAL	SER	GLN
PRO	GLY	SER	GLY	TYR	MET	TYR	PHE
ARG	TYR	ASP	ASP	ALA	GLY	CYS	GLU
LEU	ASN	ILE	GLY	PRO	THR	SER	LYS
ILE	ASP	ASN	THR	SER	ARG	THR	GLY
GLY	TYR	SER	CYS	GLY	ARG	CYS	GLY
ASP	THR	VAL	ALA	CYS	THR	ALA	GLY
THR	THR	VAL	ALA	CYS	THR	ALA	GLY
ILE	ASN	ARG	LEU	ALA	LEU	GLU	SER
ASN	TYR	TRP	TRP	ILE	LYS	ILE	GLY
VAL	VAL	TYR	ASP	ALA	LYS	MET	GLY
ASP	ASP	PRO	VAL	ALA	HIS	ALA	GLY
VAL	VAL	GLY	SER	GLY	ASN	GLU	GLY
LEU	LEU	D294	GLY	LEU	THR	LYS	GLY
LYS	LYS	A297	GLN	ASP	VAL	HIS	SER
GLY	GLY	SER	LEU	LYS	LEU	GLY	SER
SER	SER	GLY	GLN	CYS	MET	ASN	TRP
ARG	VAL	SER	SER	ASP	THR	GLU	SER
VAL	SER	ASP	PHE	VAL	ASP	THR	HIS
ILE	ILE	ASP	HIS	TYR	CYS	LEU	PRO
PHE	PHE	THR	HIS	ALA	LYS	ALA	GLN
GLY	GLY	THR	GLY	GLY	ASP	LEU	PHE
HIS	HIS	ARG	ALA	THR	LYS	LYS	GLY
THR	THR	ARG	ALA	PHE	ARG	LYS	LYS
LEU	LEU	VAL	LYS	ALA	THR	VAL	ALA
ARG	ARG	ASP	ALA	THR	VAL	GLU	LEU
VAL	VAL	PHE	THR	THR	THR	ASN	ARG
THR	THR	SER	ASP	ASN	PRO	GLU	VAL
ALA	GLY	LEU	ALA	MET	CYS	VAL	PHE
THR	THR	LEU	THR	ASP	THR	ASN	LYS
ARG	ARG	D313	LEU	ALA	GLN	LEU	THR
VAL	VAL	R314	ALA	ALA	ASP	GLY	PHE
SER	SER	F315	PRO	LYS	GLY	LYS	LEU
PRO	PRO	V316	SER	LYS	LYS	LEU	VAL
ASP	ASP	ALA	GLU	LYS	VAL	GLU	ASN
GLY	GLY	ILE	THR	SER	ILE	GLU	VAL
THR	THR	TYR	GLY	VAL	VAL	GLU	PHE
ALA	ALA	LYS	ASN	ALA	TRP	ARG	GLY
PHE	PHE	GLU	PHE	HIS	ASP	LYS	SER
SER	SER	SER	VAL	THR	PHE	LEU	ASP
ILE	ILE	ILE	SER	ASN	THR	HIS	LYS
GLY	GLY	PHE	GLY	TYR	THR	ASP	CYS
THR	THR	GLY	CYS	LEU	ASN	VAL	PHE
ASP	ASP	ALA	ASP	ALA	GLY	GLU	GLY
THR	THR	SER	LYS	SER	GLU	LEU	CYS
HIS	HIS	SER	LYS	THR	THR	LEU	GLN
ASP	ASP	VAL	LYS	THR	VAL	VAL	ALA
THR	THR	THR	ALA	PHE	THR	ALA	ARG
LEU	LEU	VAL	ALA	THR	THR	VAL	LEU
ARG	ARG	ASP	ALA	THR	THR	ALA	ARG
VAL	VAL	PHE	THR	ASN	MET	GLU	PRO
THR	THR	SER	SER	ASN	PRO	ARG	VAL
ALA	ALA	E266	THR	MET	CYS	VAL	PHE
GLY	GLY	MET	THR	THR	THR	VAL	LYS

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	94334	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	43.7	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.860	Depositor
Minimum map value	-0.322	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.042	Depositor
Recommended contour level	0.103	Depositor
Map size ($\text{\AA}$)	317.4, 317.4, 317.4	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.058, 1.058, 1.058	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ADP, MG, AF3

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	0.14	0/4109	0.30	0/5548
1	a	0.12	0/4081	0.29	0/5510
2	B	0.12	0/3995	0.27	0/5386
2	b	0.13	0/3986	0.29	0/5375
3	D	0.12	0/3955	0.29	0/5338
3	d	0.14	0/3949	0.32	1/5331 (0.0%)
4	E	0.13	0/4183	0.30	0/5635
4	e	0.13	0/4220	0.32	0/5684
5	G	0.13	0/4136	0.29	0/5579
5	g	0.12	0/4149	0.29	0/5595
6	H	0.13	0/4111	0.28	0/5550
6	h	0.12	0/4089	0.28	0/5519
7	Q	0.12	0/4147	0.27	0/5606
7	q	0.11	0/4112	0.28	0/5558
8	Z	0.12	0/4069	0.29	0/5486
8	z	0.12	0/4080	0.28	0/5501
9	P	0.18	0/745	0.48	0/996
10	N	0.13	0/212	0.37	0/282
All	All	0.13	0/66328	0.29	1/89479 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	d	514	VAL	N-CA-C	-5.79	106.03	111.48

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	4069	0	4224	75	0
1	a	4041	0	4205	94	0
2	B	3952	0	4070	55	0
2	b	3943	0	4057	72	0
3	D	3923	0	4131	56	0
3	d	3917	0	4120	74	0
4	E	4132	0	4246	80	0
4	e	4169	0	4272	86	0
5	G	4089	0	4224	80	0
5	g	4102	0	4240	86	0
6	H	4054	0	4160	64	0
6	h	4032	0	4140	73	0
7	Q	4086	0	4160	53	0
7	q	4053	0	4125	69	0
8	Z	4022	0	4161	69	0
8	z	4033	0	4171	65	0
9	P	739	0	723	32	0
10	N	211	0	190	5	0
11	A	27	0	12	2	0
11	B	27	0	12	2	0
11	D	27	0	12	0	0
11	E	27	0	12	0	0
11	G	27	0	12	2	0
11	H	27	0	12	2	0
11	Q	27	0	12	3	0
11	Z	27	0	12	1	0
11	a	27	0	12	4	0
11	b	27	0	12	5	0
11	d	27	0	12	1	0
11	e	27	0	12	3	0
11	g	27	0	12	4	0
11	h	27	0	12	3	0
11	q	27	0	12	2	0
11	z	27	0	12	2	0
12	A	1	0	0	0	0
12	B	1	0	0	0	0
12	D	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	E	1	0	0	0	0
12	G	1	0	0	0	0
12	H	1	0	0	0	0
12	Q	1	0	0	0	0
12	Z	1	0	0	0	0
12	a	1	0	0	0	0
12	b	1	0	0	0	0
12	d	1	0	0	0	0
12	e	1	0	0	0	0
12	g	1	0	0	0	0
12	h	1	0	0	0	0
12	q	1	0	0	0	0
12	z	1	0	0	0	0
13	A	4	0	0	2	0
13	B	4	0	0	0	0
13	D	4	0	0	1	0
13	E	4	0	0	0	0
13	G	4	0	0	2	0
13	H	4	0	0	2	0
13	Q	4	0	0	2	0
13	Z	4	0	0	3	0
13	a	4	0	0	2	0
13	b	4	0	0	1	0
13	d	4	0	0	1	0
13	e	4	0	0	1	0
13	g	4	0	0	4	0
13	h	4	0	0	3	0
13	q	4	0	0	2	0
13	z	4	0	0	3	0
14	A	2	0	0	0	0
14	B	2	0	0	0	0
14	D	1	0	0	0	0
14	E	1	0	0	0	0
14	G	1	0	0	0	0
14	H	1	0	0	0	0
14	Q	1	0	0	0	0
14	Z	1	0	0	0	0
14	a	2	0	0	0	0
14	b	1	0	0	0	0
14	d	1	0	0	0	0
14	e	1	0	0	0	0
14	g	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	h	1	0	0	0	0
14	q	1	0	0	0	0
14	z	1	0	0	0	0
All	All	66098	0	67811	1053	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 8.

All (1053) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:b:4:LEU:HD22	2:b:11:ILE:HD11	1.54	0.89
4:E:305:GLY:HA2	4:E:323:ARG:HB2	1.62	0.80
1:A:353:GLN:HE21	1:A:360:GLU:HB3	1.47	0.79
5:g:130:LEU:HA	5:g:133:MET:HE2	1.64	0.79
3:d:78:LEU:HB3	3:d:92:VAL:HG22	1.66	0.78
3:d:85:HIS:HA	9:P:60:LYS:NZ	2.00	0.77
7:Q:221:MET:HE1	7:Q:323:ARG:HB3	1.67	0.76
3:d:84:LEU:O	9:P:60:LYS:NZ	2.15	0.76
3:d:85:HIS:HA	9:P:60:LYS:HZ3	1.49	0.76
4:e:305:GLY:HA2	4:e:323:ARG:HB2	1.68	0.76
6:H:11:GLU:OE2	6:H:11:GLU:N	2.19	0.74
1:A:152:ALA:O	1:A:156:MET:HG2	1.87	0.74
3:D:151:MET:HE3	3:D:422:ILE:HD11	1.70	0.74
3:d:423:ALA:HB1	3:d:503:ILE:HD11	1.69	0.74
4:e:32:GLU:OE2	4:e:32:GLU:N	2.18	0.74
8:z:357:GLU:OE2	8:z:357:GLU:N	2.21	0.74
8:Z:67:MET:HB3	8:Z:69:ILE:HG12	1.70	0.74
1:a:68:GLU:OE2	1:a:68:GLU:N	2.21	0.73
1:a:228:ARG:HG3	1:a:352:VAL:HG22	1.69	0.73
3:D:30:PRO:HB3	3:D:533:ASP:HB2	1.70	0.73
4:E:199:MET:HE3	4:E:199:MET:HA	1.68	0.73
6:H:82:ILE:HG21	6:H:509:ALA:HB2	1.71	0.72
1:a:380:ALA:HB1	5:g:83:ILE:HD11	1.72	0.72
4:E:239:MET:HE3	4:E:320:PRO:HA	1.70	0.71
6:h:292:LYS:HG3	6:h:319:LEU:HD12	1.70	0.71
6:h:82:ILE:HG21	6:h:509:ALA:HB2	1.72	0.71
4:E:32:GLU:N	4:E:32:GLU:OE2	2.23	0.70
6:H:346:GLN:HB2	6:H:363:GLY:HA3	1.72	0.70
5:g:12:GLN:N	5:g:12:GLN:OE1	2.24	0.70
5:G:219:MET:HE1	5:G:375:LEU:HD13	1.71	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:502:ASN:HD22	3:D:505:GLU:HG2	1.56	0.70
1:A:60:THR:HG21	1:A:390:ARG:HD3	1.74	0.70
8:Z:189:PHE:O	8:Z:323:ARG:NH1	2.24	0.70
2:b:38:LEU:O	2:b:50:LYS:NZ	2.24	0.70
3:d:38:ILE:HG21	3:d:121:THR:HB	1.74	0.69
8:z:163:GLU:OE2	8:z:163:GLU:N	2.23	0.69
3:d:233:VAL:HG21	3:d:323:MET:HE2	1.75	0.69
3:d:429:GLU:OE2	3:d:429:GLU:N	2.24	0.69
2:b:11:ILE:HD12	2:b:11:ILE:O	1.93	0.68
8:z:242:THR:HG22	8:z:244:VAL:H	1.58	0.68
2:B:133:ALA:HB2	2:B:436:MET:HG3	1.76	0.68
1:A:474:ALA:HB2	1:A:483:LEU:HB2	1.75	0.68
8:z:525:GLY:O	9:P:160:GLN:NE2	2.25	0.68
6:H:67:LYS:HG2	6:H:84:LYS:HE2	1.75	0.68
3:D:343:LYS:HB2	3:D:355:MET:HG3	1.75	0.68
1:a:56:ASN:ND2	1:a:158:SER:O	2.26	0.68
1:a:145:ARG:NH2	1:a:174:ASP:OD1	2.27	0.68
5:g:27:ILE:HD13	5:g:110:GLU:HB2	1.74	0.68
3:D:429:GLU:N	3:D:429:GLU:OE2	2.28	0.67
5:G:233:ILE:HD12	5:G:350:LEU:HD23	1.75	0.67
5:G:302:HIS:HB2	8:Z:334:ASN:HB2	1.76	0.67
5:G:64:ASN:ND2	5:G:88:ASP:OD2	2.26	0.67
6:h:1:MET:SD	6:h:1:MET:N	2.65	0.67
5:g:64:ASN:ND2	5:g:88:ASP:OD2	2.27	0.67
5:g:219:MET:HB3	5:g:373:THR:HG21	1.77	0.67
2:b:379:THR:HB	2:b:382:ILE:HD13	1.76	0.66
2:B:112:GLU:HB3	2:B:438:SER:HB3	1.77	0.66
6:H:317:GLU:OE2	6:H:317:GLU:N	2.19	0.66
8:Z:358:GLU:OE1	8:Z:358:GLU:N	2.24	0.66
2:B:517:VAL:HG21	4:E:60:MET:HE2	1.77	0.66
3:d:227:LEU:HB3	3:d:339:THR:HG21	1.78	0.66
4:E:198:ASP:HB3	4:E:202:ARG:HB2	1.77	0.66
1:a:474:ALA:HB2	1:a:483:LEU:HB2	1.78	0.65
4:e:198:ASP:HB3	4:e:202:ARG:HB2	1.79	0.65
4:e:285:PHE:HA	4:e:288:MET:HE3	1.77	0.65
8:Z:242:THR:HG22	8:Z:244:VAL:H	1.62	0.65
2:b:11:ILE:HG22	4:e:85:HIS:HB2	1.79	0.65
5:G:155:ILE:HG21	5:G:401:VAL:HG21	1.79	0.65
2:b:44:GLY:H	11:b:601:ADP:H5'1	1.62	0.65
4:e:199:MET:HE2	4:e:199:MET:HA	1.77	0.65
4:e:236:HIS:HB3	4:e:239:MET:HG3	1.79	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:MET:HE3	5:G:75:PRO:HB2	1.79	0.65
6:h:521:LYS:HG2	7:q:57:ILE:HD12	1.79	0.65
8:z:128:GLU:OE2	8:z:132:GLN:NE2	2.30	0.65
2:b:156:ARG:NH2	2:b:185:GLU:OE2	2.30	0.65
6:h:294:PRO:HG3	6:h:313:ARG:HE	1.61	0.64
5:G:20:ARG:HH22	5:G:114:GLU:HA	1.61	0.64
8:Z:24:ILE:HD13	8:Z:107:ASP:HB2	1.80	0.64
4:E:255:PHE:HB2	4:E:306:PHE:HB3	1.79	0.64
6:H:45:MET:O	6:H:60:ASN:ND2	2.30	0.64
2:b:112:GLU:HB3	2:b:438:SER:HB3	1.78	0.64
2:B:381:GLN:NE2	3:D:93:GLU:OE2	2.30	0.64
3:d:48:ILE:HD12	3:d:48:ILE:O	1.98	0.64
4:e:60:MET:HG2	4:e:70:VAL:HG22	1.80	0.64
2:B:71:LEU:HB3	2:B:85:VAL:HG22	1.79	0.64
4:E:234:PHE:HB3	4:E:239:MET:HE2	1.78	0.64
7:Q:416:GLU:HG2	7:Q:448:ILE:HG13	1.79	0.64
1:a:225:MET:HE1	1:a:307:ALA:H	1.60	0.64
4:e:48:MET:HG3	4:e:107:THR:HG23	1.80	0.64
5:g:229:MET:HE3	5:g:311:ALA:H	1.63	0.64
1:A:179:ILE:HG21	1:A:195:VAL:HG22	1.80	0.63
5:g:32:THR:HG23	8:z:7:LEU:HD21	1.80	0.63
7:q:393:ASP:OD1	7:q:397:ASN:ND2	2.31	0.63
2:b:193:SER:OG	2:b:195:ASN:OD1	2.16	0.63
6:h:516:VAL:HG11	7:q:55:MET:HE3	1.79	0.63
7:q:93:GLN:NE2	7:q:99:ASP:O	2.32	0.63
4:e:78:LEU:HD13	4:e:92:VAL:HA	1.80	0.63
5:G:129:ALA:O	5:G:133:MET:HG3	1.99	0.63
4:E:532:ASP:HB2	6:H:47:LYS:HD2	1.81	0.63
9:P:24:ASP:OD1	9:P:24:ASP:N	2.32	0.62
1:A:353:GLN:O	5:G:190:ARG:NH1	2.32	0.62
1:A:56:ASN:ND2	1:A:158:SER:O	2.32	0.62
4:E:8:ALA:HA	1:a:23:MET:HE2	1.82	0.62
5:g:41:LEU:O	5:g:454:ASN:ND2	2.31	0.62
3:d:30:PRO:HB3	3:d:533:ASP:HB2	1.82	0.62
7:q:55:MET:HG2	7:q:63:LEU:HD11	1.81	0.62
5:G:48:LYS:HD2	5:G:66:ILE:HD13	1.82	0.62
5:G:132:ASP:OD2	5:G:437:TYR:OH	2.17	0.62
3:d:46:ASP:HA	3:d:49:ARG:HD3	1.82	0.62
4:E:515:GLN:HE22	6:H:203:GLY:H	1.45	0.62
1:a:199:LYS:HB2	9:P:286:ARG:HG3	1.82	0.62
1:A:143:LEU:HB2	1:A:147:CYS:HB2	1.82	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:59:ALA:HB2	1:a:90:THR:HG21	1.82	0.62
5:G:224:VAL:HB	5:G:229:MET:HE3	1.82	0.62
4:e:61:MET:HE3	4:e:61:MET:HA	1.82	0.62
7:q:73:LEU:HD11	7:q:105:LEU:HD22	1.80	0.62
7:q:84:LYS:O	7:q:88:MET:HG3	1.99	0.62
3:d:75:ALA:HB2	3:d:106:THR:HG21	1.82	0.61
4:e:426:GLU:OE2	4:e:426:GLU:N	2.27	0.61
6:H:251:ASP:OD1	6:H:251:ASP:N	2.33	0.61
8:Z:340:SER:OG	8:Z:342:ASP:OD1	2.16	0.61
2:B:244:MET:HA	2:B:275:MET:HE1	1.81	0.61
4:E:289:ILE:HG13	4:E:313:LEU:HB3	1.81	0.61
3:D:28:ASP:N	2:b:22:GLU:OE2	2.33	0.61
7:Q:47:TYR:O	7:Q:455:ASN:ND2	2.30	0.61
6:h:378:ALA:HB3	6:h:381:PHE:HB2	1.83	0.61
1:A:59:ALA:HB2	1:A:90:THR:HG21	1.83	0.61
6:h:346:GLN:HB2	6:h:363:GLY:HA3	1.82	0.61
1:A:326:THR:HB	1:A:344:MET:HB3	1.82	0.61
3:d:33:ILE:HD11	9:P:56:ASN:HD21	1.66	0.61
5:g:292:THR:HG22	5:g:294:LYS:H	1.65	0.61
2:b:50:LYS:HD3	3:d:534:ASP:HB3	1.82	0.61
3:D:367:LEU:O	3:D:370:SER:OG	2.19	0.60
7:Q:277:ASP:HB2	7:Q:304:TYR:CZ	2.36	0.60
5:G:206:GLY:HA3	8:Z:87:ILE:HG13	1.83	0.60
1:A:479:GLU:OE2	1:A:479:GLU:N	2.25	0.60
4:E:93:GLU:OE2	6:H:379:GLU:N	2.27	0.60
2:B:77:ASP:OD1	2:B:77:ASP:N	2.34	0.60
6:H:456:ASP:OD2	1:a:433:ARG:NH2	2.35	0.60
7:Q:173:TYR:OH	7:Q:483:GLU:OE2	2.18	0.60
1:A:526:ARG:NH2	3:D:58:ASP:OD1	2.33	0.60
9:P:184:MET:HE2	9:P:202:MET:HE1	1.84	0.60
4:E:367:THR:HG23	4:E:369:ASP:H	1.66	0.60
6:H:103:GLU:HG2	6:H:444:ILE:HB	1.83	0.60
2:B:33:ILE:HD11	2:B:111:ARG:HB2	1.84	0.59
2:b:163:ALA:HB3	2:b:180:THR:HG23	1.84	0.59
4:e:438:ASP:OD1	4:e:449:ARG:NH2	2.35	0.59
8:z:449:LYS:HD3	8:z:459:LEU:HD21	1.82	0.59
3:d:343:LYS:HB2	3:d:355:MET:HE3	1.84	0.59
4:e:422:GLY:HA3	4:e:501:MET:HE3	1.83	0.59
7:q:17:GLU:OE2	7:q:17:GLU:N	2.24	0.59
3:d:134:SER:HG	3:d:527:ARG:HE	1.50	0.59
7:q:193:ASP:N	7:q:193:ASP:OD1	2.33	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:7:VAL:HG12	4:e:7:LEU:HD23	1.84	0.59
3:d:103:GLY:HA3	3:d:410:CYS:HB3	1.83	0.59
8:z:210:LEU:HD11	8:z:323:ARG:HB3	1.84	0.59
5:G:409:PRO:O	5:G:414:SER:OG	2.21	0.59
2:B:197:GLU:OE1	2:B:197:GLU:N	2.30	0.59
3:D:228:VAL:HG22	3:D:375:LYS:HG2	1.84	0.59
7:q:39:LEU:HD23	7:q:105:LEU:HD11	1.84	0.59
7:q:262:ALA:O	7:q:266:MET:HG3	2.02	0.59
3:D:55:LYS:HG3	3:D:469:ALA:HA	1.84	0.58
5:g:64:ASN:HB2	5:g:95:THR:HG21	1.85	0.58
3:D:193:LYS:NZ	3:D:225:GLU:OE2	2.27	0.58
1:a:122:ARG:HG3	3:d:178:GLN:HG3	1.85	0.58
6:H:446:PRO:HA	6:H:449:LEU:HD12	1.85	0.58
7:Q:117:GLU:O	7:Q:121:ILE:HG23	2.04	0.58
6:h:251:ASP:OD1	6:h:251:ASP:N	2.35	0.58
7:q:38:GLU:O	7:q:42:THR:HG23	2.03	0.58
3:D:119:SER:HB3	3:D:453:ALA:HB1	1.85	0.58
8:Z:159:LYS:NZ	13:Z:603:AF3:F1	2.26	0.58
8:Z:445:LEU:HD22	8:Z:463:LEU:HD21	1.85	0.58
2:b:39:VAL:HG13	2:b:100:THR:HG23	1.86	0.58
4:e:51:SER:OG	4:e:59:LYS:NZ	2.30	0.58
8:z:4:VAL:HG11	8:z:522:MET:HE1	1.84	0.58
4:E:426:GLU:N	4:E:426:GLU:OE2	2.37	0.58
5:G:41:LEU:O	5:G:454:ASN:ND2	2.32	0.58
1:a:78:LEU:HD11	1:a:516:PHE:HB3	1.85	0.58
3:d:195:ILE:HG21	3:d:203:VAL:HG22	1.86	0.58
1:a:229:ILE:HD13	1:a:284:ASN:HB3	1.85	0.58
7:q:222:VAL:HG22	7:q:362:VAL:HG22	1.86	0.58
4:E:200:GLU:HG2	4:E:202:ARG:HG3	1.84	0.58
2:B:291:ILE:HG13	2:B:312:ILE:HB	1.86	0.58
6:H:516:VAL:HG11	7:Q:55:MET:SD	2.44	0.58
7:Q:172:GLN:NE2	7:Q:387:ASP:OD2	2.32	0.58
5:g:319:ASP:OD1	5:g:322:ARG:NH1	2.37	0.58
6:h:85:SER:HB2	7:q:208:LEU:HD22	1.84	0.58
1:A:103:ASN:ND2	1:A:444:SER:OG	2.31	0.57
8:z:198:HIS:CE1	8:z:199:LYS:HG2	2.38	0.57
8:z:526:MET:SD	8:z:526:MET:N	2.74	0.57
1:A:411:GLY:O	1:A:498:ASN:ND2	2.37	0.57
3:D:291:LYS:HD3	3:D:322:ILE:HD11	1.85	0.57
4:E:490:GLY:O	4:E:499:ASN:ND2	2.36	0.57
4:e:94:LEU:HD22	4:e:523:MET:HG2	1.86	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:h:525:SER:HB2	7:q:59:HIS:HB2	1.86	0.57
8:Z:103:LEU:HD21	8:Z:515:ILE:HG21	1.86	0.57
8:z:340:SER:OG	8:z:342:ASP:OD1	2.18	0.57
5:G:130:LEU:HB2	5:G:510:VAL:HG11	1.85	0.57
5:G:265:THR:HG21	8:Z:265:LYS:HB3	1.87	0.57
6:H:429:GLY:HA2	6:H:432:GLN:HB3	1.86	0.57
4:e:23:ASP:OD1	4:e:23:ASP:N	2.34	0.57
2:b:71:LEU:HB3	2:b:85:VAL:HG22	1.85	0.57
2:b:151:ASP:HB3	2:b:154:LYS:HB2	1.86	0.57
6:h:194:MET:O	6:h:369:THR:OG1	2.17	0.57
1:A:377:LEU:HD21	1:A:392:LEU:HD22	1.85	0.57
6:H:499:ARG:NH2	11:H:601:ADP:O3'	2.37	0.57
1:a:65:LEU:HD21	5:g:523:VAL:HG11	1.86	0.57
1:a:430:MET:HE2	1:a:430:MET:HA	1.86	0.57
5:g:130:LEU:HB2	5:g:510:VAL:HG11	1.86	0.57
3:d:34:ARG:NH1	3:d:130:PRO:HG3	2.19	0.57
3:D:195:ILE:HG21	3:D:203:VAL:HG22	1.85	0.57
1:a:160:ILE:HD12	5:g:518:ARG:HD3	1.86	0.57
2:b:51:ILE:HG12	2:b:63:VAL:HG22	1.87	0.57
3:d:458:MET:HE3	3:d:458:MET:HA	1.87	0.57
6:h:456:ASP:OD2	6:h:459:ASN:ND2	2.38	0.57
4:E:78:LEU:HD11	4:E:110:VAL:HG21	1.86	0.57
7:Q:55:MET:HG3	7:Q:65:VAL:HG22	1.87	0.57
8:Z:84:GLN:NE2	8:Z:88:THR:OG1	2.30	0.57
4:e:295:THR:HG21	4:e:348:LEU:HG	1.86	0.57
8:Z:135:GLU:OE2	8:Z:498:TYR:OH	2.19	0.56
4:E:48:MET:HG3	4:E:107:THR:HG23	1.86	0.56
7:Q:14:MET:HB3	8:Z:69:ILE:HD12	1.87	0.56
1:a:43:LYS:HD3	5:g:521:ASP:HB2	1.87	0.56
1:A:44:MET:SD	5:G:519:ILE:HD13	2.46	0.56
5:G:182:MET:HE1	5:G:216:ARG:HD2	1.87	0.56
4:e:198:ASP:OD2	4:e:202:ARG:NH1	2.35	0.56
6:h:32:ILE:HG13	6:h:76:ALA:HB1	1.87	0.56
3:D:394:ASN:OD1	3:D:397:VAL:N	2.30	0.56
6:h:90:VAL:HG12	6:h:92:ASP:H	1.69	0.56
8:z:279:ARG:NH1	8:z:308:GLU:OE2	2.37	0.56
2:B:79:PRO:HB2	4:E:60:MET:SD	2.46	0.56
7:Q:367:LYS:HE3	7:Q:369:ASP:HB3	1.88	0.56
4:e:53:GLY:H	11:e:601:ADP:H5'1	1.71	0.56
7:Q:190:ILE:HG22	7:Q:191:PHE:H	1.70	0.56
2:b:131:ARG:NH2	4:e:179:ASN:OD1	2.38	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:70:ALA:HB2	7:Q:101:THR:HG21	1.88	0.56
4:e:102:ILE:HG22	4:e:104:ASP:H	1.70	0.56
4:e:230:VAL:HG12	4:e:232:LYS:H	1.70	0.56
5:G:27:ILE:HD13	5:G:110:GLU:HB2	1.87	0.56
3:d:210:ILE:HG21	3:d:402:GLU:HG2	1.87	0.56
11:z:601:ADP:O2B	13:z:603:AF3:F1	2.13	0.56
3:d:57:MET:HE2	3:d:57:MET:HA	1.86	0.56
5:g:298:ASP:OD2	8:z:295:LYS:NZ	2.37	0.56
9:P:182:VAL:HG22	9:P:240:LYS:HD3	1.88	0.56
5:g:206:GLY:HA3	8:z:87:ILE:HG13	1.88	0.55
5:G:416:MET:HE3	5:G:416:MET:HA	1.88	0.55
5:G:468:ALA:O	5:G:471:THR:OG1	2.24	0.55
2:b:432:GLU:O	2:b:436:MET:HG3	2.06	0.55
1:A:205:GLN:OE1	5:G:127:ARG:NH2	2.39	0.55
4:E:426:GLU:HG2	4:E:458:ILE:HB	1.89	0.55
7:Q:93:GLN:NE2	7:Q:99:ASP:O	2.38	0.55
1:a:68:GLU:HA	1:a:73:LYS:HE2	1.88	0.55
3:d:476:THR:HG23	3:d:500:ILE:HD11	1.87	0.55
6:H:455:PHE:CE1	6:H:482:GLU:HG2	2.41	0.55
6:h:202:GLY:O	6:h:375:ARG:NH2	2.40	0.55
2:B:251:ILE:HG13	4:E:277:LEU:HD11	1.89	0.55
1:a:349:GLU:HB3	1:a:366:ASN:HB3	1.88	0.55
5:G:225:THR:O	8:Z:318:ARG:NH2	2.39	0.55
2:B:326:VAL:HG13	2:B:327:THR:HG23	1.89	0.55
7:q:277:ASP:HB2	7:q:304:TYR:CZ	2.41	0.55
11:g:601:ADP:O2B	13:g:603:AF3:F3	2.14	0.55
6:H:80:VAL:HG12	6:H:84:LYS:HE3	1.89	0.55
1:a:163:ILE:HB	5:g:127:ARG:HD2	1.88	0.55
4:e:37:HIS:NE2	4:e:533:ILE:HD11	2.22	0.55
4:E:364:PHE:HE2	4:E:371:MET:HG3	1.70	0.55
11:A:601:ADP:O2B	13:A:603:AF3:F3	2.16	0.54
6:H:200:VAL:HG11	6:H:353:ILE:HG22	1.89	0.54
7:q:81:PRO:O	7:q:85:MET:HG3	2.07	0.54
2:B:113:ALA:HB2	2:B:130:TRP:CH2	2.43	0.54
11:G:601:ADP:O1B	13:G:603:AF3:F1	2.16	0.54
2:b:209:LEU:N	3:d:524:GLU:OE2	2.31	0.54
7:q:55:MET:HG3	7:q:65:VAL:HG22	1.89	0.54
4:E:129:HIS:HB3	4:E:132:ARG:HG2	1.89	0.54
1:a:299:TYR:OH	5:g:337:GLU:OE2	2.23	0.54
2:b:379:THR:HG23	3:d:93:GLU:HB2	1.90	0.54
5:g:47:MET:HE3	5:g:47:MET:HA	1.88	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:132:ILE:HG12	1:a:136:LEU:HD12	1.90	0.54
7:q:412:GLY:N	11:q:601:ADP:O2'	2.34	0.54
4:E:295:THR:HG21	4:E:348:LEU:HG	1.89	0.54
1:a:225:MET:HG2	1:a:301:VAL:HG22	1.89	0.54
3:D:73:ASP:OD1	13:D:603:AF3:F3	2.15	0.54
2:b:26:LEU:O	2:b:30:ILE:HD13	2.08	0.54
5:G:473:GLU:HG2	5:G:474:ASN:H	1.73	0.54
8:Z:44:MET:SD	8:Z:386:GLN:NE2	2.81	0.54
2:b:58:ASP:OD1	2:b:58:ASP:N	2.39	0.54
5:g:155:ILE:HG21	5:g:401:VAL:HG21	1.89	0.54
1:A:54:ILE:HG12	5:G:519:ILE:HD11	1.88	0.54
8:Z:449:LYS:HB3	8:Z:459:LEU:HD23	1.90	0.54
1:a:266:ARG:HG3	3:d:269:TYR:HB2	1.90	0.54
4:e:115:ALA:O	4:e:119:GLU:HG2	2.08	0.54
5:g:17:GLU:N	5:g:17:GLU:OE2	2.41	0.54
8:z:40:PRO:HA	8:z:158:THR:HA	1.89	0.54
1:A:489:ASP:OD2	1:A:492:ASN:ND2	2.41	0.54
4:E:25:LYS:HG2	4:E:536:PRO:HA	1.90	0.53
6:H:168:ILE:HG21	6:H:385:THR:HG23	1.89	0.53
7:Q:523:GLN:HB2	8:Z:45:LYS:HG3	1.90	0.53
1:a:164:ASN:ND2	1:a:206:MET:SD	2.80	0.53
4:e:531:ASP:HB3	6:h:45:MET:HE3	1.89	0.53
5:g:182:MET:HE2	5:g:369:PRO:HG2	1.90	0.53
7:q:364:LYS:NZ	7:q:366:GLU:OE2	2.40	0.53
1:A:298:LYS:NZ	5:G:242:ASP:OD2	2.35	0.53
9:P:198:MET:O	9:P:202:MET:HB2	2.08	0.53
1:A:349:GLU:HB2	1:A:366:ASN:HB2	1.89	0.53
2:B:138:ARG:NH2	4:E:220:GLU:OE2	2.32	0.53
5:G:83:ILE:HD13	5:G:512:THR:HG21	1.89	0.53
11:a:601:ADP:O2B	13:a:603:AF3:F3	2.16	0.53
5:g:293:GLU:HG3	5:g:320:ASN:HD22	1.72	0.53
5:g:434:GLN:OE1	5:g:438:ARG:NH2	2.40	0.53
6:h:61:ASP:OD1	13:h:603:AF3:F2	2.17	0.53
8:z:152:ALA:HB3	8:z:169:THR:HG23	1.89	0.53
6:H:516:VAL:HG22	7:Q:53:ASN:HB2	1.91	0.53
2:b:326:VAL:HB	2:b:370:ALA:HB3	1.91	0.53
8:z:61:ASN:HB2	8:z:92:THR:HG21	1.91	0.53
3:D:170:SER:HB2	3:D:411:VAL:HG21	1.89	0.53
5:G:504:GLN:NE2	5:G:508:THR:OG1	2.42	0.53
3:d:72:ASN:ND2	3:d:173:SER:O	2.41	0.53
5:g:182:MET:HE1	5:g:216:ARG:HD2	1.90	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:26:ASP:OD1	2:b:120:LYS:NZ	2.38	0.53
4:E:248:ILE:HD12	4:E:337:THR:HG21	1.90	0.53
2:b:168:SER:OG	11:b:601:ADP:N7	2.38	0.53
2:b:408:TYR:O	2:b:413:SER:OG	2.23	0.53
5:g:468:ALA:O	5:g:471:THR:OG1	2.27	0.53
4:E:198:ASP:OD2	4:E:202:ARG:NH1	2.40	0.53
6:h:168:ILE:HG21	6:h:385:THR:HG23	1.90	0.53
6:H:214:VAL:HG11	6:H:322:THR:HA	1.91	0.53
7:Q:412:GLY:N	11:Q:601:ADP:O2'	2.36	0.53
2:b:326:VAL:HG13	2:b:327:THR:HG23	1.89	0.53
3:d:42:LYS:HD3	3:d:118:ASP:HB2	1.91	0.53
9:P:290:THR:H	9:P:292:HIS:CE1	2.26	0.53
11:Z:601:ADP:O1B	13:Z:603:AF3:F1	2.17	0.53
11:g:601:ADP:O2B	13:g:603:AF3:F1	2.17	0.53
7:q:43:THR:HG21	7:q:105:LEU:HD23	1.91	0.53
1:A:227:LYS:HD3	1:A:353:GLN:HG2	1.91	0.52
3:D:503:ILE:HG13	3:D:508:VAL:HB	1.90	0.52
7:Q:175:ASN:HD21	7:Q:212:ILE:HD11	1.73	0.52
8:Z:28:ARG:HD3	8:Z:104:LYS:HB2	1.91	0.52
1:a:37:GLY:H	11:a:601:ADP:H5'1	1.74	0.52
1:A:225:MET:HE1	1:A:307:ALA:HB3	1.91	0.52
6:h:378:ALA:O	6:h:382:MET:HE2	2.09	0.52
7:q:190:ILE:HG22	7:q:191:PHE:H	1.74	0.52
11:z:601:ADP:O2B	13:z:603:AF3:F3	2.17	0.52
7:Q:417:ILE:HG13	7:Q:467:LEU:HD13	1.91	0.52
7:q:249:MET:HG3	8:z:260:VAL:HG11	1.91	0.52
3:D:78:LEU:HB3	3:D:92:VAL:HG22	1.91	0.52
4:E:78:LEU:HB3	4:E:92:VAL:HG22	1.89	0.52
6:H:478:ASP:OD2	6:H:481:ASN:ND2	2.36	0.52
7:Q:220:GLY:O	7:Q:374:THR:OG1	2.24	0.52
1:a:402:VAL:HG23	1:a:506:PRO:HG3	1.92	0.52
2:b:414:GLU:HG2	2:b:446:LEU:HD23	1.90	0.52
4:e:391:ASN:OD1	4:e:394:ILE:HG22	2.09	0.52
3:d:86:PRO:CD	9:P:60:LYS:HZ3	2.23	0.52
6:h:200:VAL:HG11	6:h:353:ILE:HG22	1.91	0.52
6:H:97:VAL:HG12	6:H:502:ALA:HA	1.91	0.52
6:h:97:VAL:HG12	6:h:502:ALA:HA	1.91	0.52
1:A:164:ASN:HB3	1:A:168:PHE:CD2	2.45	0.52
1:A:192:VAL:HG12	1:A:193:ASN:H	1.75	0.52
8:Z:455:SER:OG	8:Z:481:LEU:O	2.26	0.52
4:e:109:VAL:HG13	4:e:516:GLN:HG2	1.90	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:411:ASN:HB3	4:e:511:ILE:HD11	1.91	0.52
4:E:143:VAL:HG21	4:E:436:GLU:HG2	1.91	0.52
5:G:244:SER:HB3	5:G:246:GLU:HG2	1.92	0.52
6:H:413:GLU:OE2	6:H:445:ILE:HB	2.10	0.52
1:A:222:SER:H	1:A:225:MET:HE3	1.74	0.51
1:A:321:LYS:HE2	1:A:370:ARG:HH12	1.75	0.51
1:A:526:ARG:HG3	3:D:175:VAL:HG23	1.92	0.51
3:D:223:LEU:HD12	3:D:388:ILE:HG12	1.91	0.51
4:e:200:GLU:HG2	4:e:202:ARG:HG3	1.93	0.51
4:E:23:ASP:OD1	4:E:23:ASP:N	2.34	0.51
6:H:167:LEU:HD22	6:H:384:GLU:HG3	1.92	0.51
4:e:498:THR:O	4:e:504:GLN:NE2	2.43	0.51
1:A:278:ILE:O	1:A:281:THR:HG22	2.10	0.51
6:H:152:ARG:NH2	6:H:181:ASP:OD1	2.43	0.51
4:e:129:HIS:HB3	4:e:132:ARG:HG2	1.92	0.51
8:Z:216:ALA:HB1	8:Z:221:MET:HE2	1.92	0.51
3:d:228:VAL:HG22	3:d:387:THR:HG21	1.92	0.51
9:P:202:MET:HE3	9:P:214:PHE:HB3	1.92	0.51
2:B:45:PRO:HG3	11:B:601:ADP:C5	2.44	0.51
5:G:167:ARG:NH2	8:Z:124:GLU:OE1	2.43	0.51
2:b:231:ARG:NH1	2:b:233:GLU:OE2	2.37	0.51
1:A:456:ALA:HB2	1:A:490:LEU:HD12	1.91	0.51
7:Q:97:VAL:HG13	7:Q:401:VAL:HG21	1.91	0.51
5:g:236:PRO:HG3	5:g:350:LEU:HB2	1.93	0.51
3:D:483:ARG:NE	3:D:488:GLU:OE2	2.37	0.51
6:H:32:ILE:HG13	6:H:76:ALA:HB1	1.93	0.51
1:a:197:ILE:HG21	1:a:389:GLU:HG3	1.92	0.51
3:D:29:LYS:NZ	3:D:534:ASP:OD1	2.44	0.50
11:Q:601:ADP:O1B	13:Q:603:AF3:F2	2.18	0.50
1:a:338:GLU:OE1	3:d:280:ARG:NH1	2.44	0.50
3:d:152:SER:HA	3:d:422:ILE:HG22	1.93	0.50
6:h:155:LEU:HD11	6:h:400:ILE:HD11	1.93	0.50
8:z:229:TYR:HE2	8:z:287:LYS:HD3	1.76	0.50
5:G:22:VAL:HA	6:h:1:MET:HE1	1.92	0.50
8:Z:213:ASP:OD1	8:Z:213:ASP:N	2.41	0.50
3:d:86:PRO:HD2	9:P:60:LYS:HZ3	1.76	0.50
2:B:3:SER:N	3:d:32:GLN:OE1	2.43	0.50
3:d:118:ASP:O	3:d:121:THR:HG22	2.11	0.50
4:e:285:PHE:HA	4:e:288:MET:CE	2.40	0.50
6:h:429:GLY:HA2	6:h:432:GLN:HB3	1.94	0.50
5:G:241:LEU:HB2	5:G:292:THR:HB	1.93	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:33:ILE:HG21	7:Q:116:GLU:HB2	1.93	0.50
7:Q:123:LEU:HD11	7:Q:436:TYR:HB2	1.93	0.50
8:Z:40:PRO:HA	8:Z:158:THR:HA	1.94	0.50
3:d:228:VAL:HG12	3:d:375:LYS:HG2	1.92	0.50
6:h:136:ILE:HD11	6:h:416:LEU:HD11	1.94	0.50
7:q:136:CYS:HB2	7:q:512:THR:HG21	1.93	0.50
8:z:5:LYS:NZ	8:z:11:ALA:O	2.44	0.50
8:z:164:LEU:HD21	8:z:387:ILE:HG12	1.94	0.50
1:A:199:LYS:HB3	1:A:385:CYS:HB3	1.93	0.50
5:G:411:GLY:N	11:G:601:ADP:O2'	2.40	0.50
4:E:239:MET:HE1	4:E:321:ALA:H	1.76	0.50
1:a:47:ASP:OD1	5:g:526:HIS:NE2	2.45	0.50
4:e:88:ALA:O	4:e:92:VAL:HG12	2.12	0.50
5:g:266:ARG:O	5:g:270:MET:HG3	2.11	0.50
4:E:239:MET:CE	4:E:321:ALA:H	2.25	0.50
3:D:210:ILE:HG21	3:D:402:GLU:HG2	1.93	0.50
5:G:362:PHE:HB3	5:G:364:THR:HG23	1.93	0.50
1:a:500:GLN:O	1:a:500:GLN:NE2	2.41	0.50
4:e:78:LEU:HB3	4:e:92:VAL:HG23	1.93	0.50
7:q:70:ALA:HB2	7:q:101:THR:HG21	1.93	0.50
2:B:326:VAL:HB	2:B:370:ALA:HB3	1.94	0.50
3:d:429:GLU:HG2	3:d:461:ILE:HB	1.93	0.50
5:g:411:GLY:N	11:g:601:ADP:O2'	2.34	0.50
6:H:187:ASP:OD1	6:H:187:ASP:N	2.43	0.49
8:Z:415:GLU:CD	8:Z:415:GLU:H	2.19	0.49
3:D:145:ILE:HD12	3:D:516:VAL:HG13	1.93	0.49
6:h:273:ILE:HD11	7:q:266:MET:HA	1.95	0.49
8:z:135:GLU:OE1	8:z:498:TYR:OH	2.16	0.49
1:A:107:LEU:HG	1:A:440:GLU:HG3	1.94	0.49
3:D:392:GLY:N	3:D:398:ILE:HD11	2.26	0.49
7:Q:73:LEU:HD13	7:Q:87:VAL:HG22	1.95	0.49
8:Z:155:SER:O	8:Z:158:THR:HG22	2.11	0.49
2:b:413:SER:O	2:b:417:MET:HG3	2.12	0.49
2:B:408:TYR:O	2:B:413:SER:OG	2.31	0.49
3:D:86:PRO:O	3:D:90:MET:HG3	2.12	0.49
5:G:218:VAL:HG21	5:G:323:ILE:HG12	1.94	0.49
5:g:219:MET:HE2	5:g:360:PHE:HB3	1.94	0.49
7:Q:14:MET:HG2	8:Z:69:ILE:HG23	1.94	0.49
2:b:251:ILE:HG13	4:e:277:LEU:HD11	1.93	0.49
6:h:467:ARG:NH1	6:h:471:GLY:O	2.45	0.49
7:q:217:VAL:HG22	7:q:375:ILE:HG12	1.94	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:q:417:ILE:HG13	7:q:467:LEU:HD13	1.93	0.49
4:E:241:LYS:HD2	4:E:361:GLU:OE1	2.13	0.49
8:Z:140:SER:HA	8:Z:406:CYS:HA	1.95	0.49
1:a:356:ILE:N	1:a:359:ASP:O	2.37	0.49
5:g:163:LYS:NZ	13:g:603:AF3:F1	2.32	0.49
5:g:203:LYS:HB2	5:g:384:LEU:HD13	1.95	0.49
6:h:107:GLN:HG3	6:h:441:ALA:HB2	1.94	0.49
2:b:257:ARG:HD3	3:d:263:GLN:HE21	1.78	0.49
5:g:167:ARG:NH1	8:z:124:GLU:HG3	2.28	0.49
5:g:350:LEU:HD23	5:g:363:ILE:HG12	1.95	0.49
5:g:415:GLU:OE1	5:g:506:TYR:OH	2.16	0.49
8:z:3:ALA:O	8:z:6:THR:OG1	2.23	0.49
2:B:163:ALA:HB3	2:B:180:THR:HG23	1.93	0.49
4:e:18:ILE:HA	6:h:73:HIS:HB2	1.93	0.49
6:h:152:ARG:NH2	6:h:181:ASP:OD1	2.26	0.49
7:q:33:ILE:HD13	7:q:116:GLU:HB2	1.94	0.49
7:Q:3:LEU:HD13	9:P:196:GLU:HG3	1.95	0.49
2:b:379:THR:HG22	2:b:381:GLN:H	1.78	0.49
7:q:410:PRO:O	7:q:415:THR:OG1	2.25	0.49
8:z:24:ILE:HD13	8:z:107:ASP:HB2	1.93	0.49
11:H:601:ADP:O2B	13:H:603:AF3:F1	2.20	0.49
8:Z:172:VAL:HG13	8:Z:395:LEU:HD23	1.94	0.49
2:b:95:VAL:HG12	2:b:399:GLN:HG3	1.95	0.49
3:d:428:PRO:HG2	3:d:429:GLU:OE2	2.13	0.49
8:z:213:ASP:OD1	8:z:213:ASP:N	2.46	0.49
1:A:163:ILE:HB	5:G:127:ARG:HH11	1.77	0.48
1:A:164:ASN:HB3	1:A:168:PHE:HD2	1.78	0.48
4:E:170:LYS:O	4:E:182:HIS:NE2	2.42	0.48
5:G:53:PRO:HG3	8:Z:525:GLY:HA3	1.94	0.48
5:G:225:THR:HG22	5:G:313:ARG:HB2	1.95	0.48
8:Z:200:SER:OG	8:Z:203:ASP:OD2	2.30	0.48
5:g:243:SER:OG	5:g:333:SER:O	2.24	0.48
7:q:524:ILE:HG23	8:z:46:MET:HG2	1.95	0.48
1:A:295:MET:HG3	1:A:296:CYS:N	2.28	0.48
3:D:38:ILE:HG21	3:D:121:THR:OG1	2.13	0.48
4:E:438:ASP:OD1	4:E:449:ARG:NH2	2.46	0.48
6:H:259:THR:HG22	6:H:261:GLU:H	1.78	0.48
1:a:225:MET:CE	1:a:307:ALA:H	2.26	0.48
2:b:113:ALA:HB2	2:b:130:TRP:CH2	2.48	0.48
3:d:119:SER:HB2	3:d:453:ALA:HB1	1.95	0.48
4:e:105:GLY:HA2	11:e:601:ADP:O2B	2.13	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:z:12:GLU:OE2	8:z:523:ARG:NH1	2.43	0.48
5:G:473:GLU:HG2	5:G:474:ASN:N	2.28	0.48
6:H:250:LYS:HB2	6:H:253:ALA:HB2	1.95	0.48
7:Q:191:PHE:HB2	7:Q:197:PHE:HD1	1.78	0.48
8:Z:399:LYS:NZ	8:Z:403:ASP:OD2	2.46	0.48
2:b:84:LEU:HA	2:b:87:MET:HE2	1.95	0.48
6:h:111:TYR:HA	6:h:114:GLU:HG2	1.94	0.48
6:h:126:ARG:NH1	7:q:174:GLY:HA3	2.28	0.48
6:h:317:GLU:OE2	6:h:317:GLU:N	2.31	0.48
1:A:181:TYR:HH	1:A:189:ARG:HH22	1.61	0.48
2:B:414:GLU:OE2	2:B:500:LYS:NZ	2.42	0.48
5:G:44:LYS:HD2	5:G:483:GLU:HA	1.94	0.48
4:e:518:SER:O	4:e:522:GLN:HG2	2.14	0.48
5:g:71:GLN:HE22	9:P:160:GLN:HB2	1.78	0.48
6:h:194:MET:HE2	6:h:194:MET:HA	1.96	0.48
1:A:446:LEU:HD11	1:A:468:ARG:HD2	1.94	0.48
3:D:399:GLU:OE1	3:D:399:GLU:N	2.47	0.48
4:e:4:MET:HG3	4:e:25:LYS:O	2.13	0.48
2:B:227:ASN:HD21	3:D:343:LYS:HD3	1.77	0.48
7:Q:81:PRO:O	7:Q:85:MET:HG3	2.14	0.48
1:a:349:GLU:OE1	1:a:366:ASN:ND2	2.38	0.48
6:h:23:VAL:HG13	6:h:109:LYS:HE3	1.95	0.48
1:A:130:ARG:NH1	1:A:134:GLU:OE1	2.47	0.48
1:A:421:ILE:HD12	1:A:472:ASN:HB2	1.96	0.48
6:H:126:ARG:NH1	7:Q:174:GLY:HA3	2.28	0.48
1:a:44:MET:HE3	5:g:519:ILE:HG21	1.95	0.48
1:a:294:ASP:O	1:a:298:LYS:HG2	2.13	0.48
4:E:102:ILE:HG22	4:E:104:ASP:H	1.78	0.48
5:G:198:TYR:CE1	5:G:325:ARG:HG3	2.48	0.48
7:Q:136:CYS:HB2	7:Q:512:THR:HG21	1.95	0.48
8:Z:289:PHE:HB3	8:Z:310:ILE:HG12	1.95	0.48
2:b:79:PRO:HB2	4:e:60:MET:HE1	1.96	0.48
8:z:40:PRO:HD3	8:z:158:THR:HG22	1.96	0.48
9:P:295:ASP:OD1	9:P:295:ASP:N	2.46	0.48
4:E:81:MET:HG2	4:E:83:VAL:HG13	1.94	0.48
6:h:60:ASN:ND2	6:h:165:SER:O	2.47	0.48
9:P:183:ILE:HG12	9:P:213:LYS:HB2	1.95	0.48
4:E:518:SER:O	4:E:522:GLN:HG2	2.13	0.48
6:H:136:ILE:HD11	6:H:416:LEU:HD11	1.96	0.48
8:Z:152:ALA:HB3	8:Z:169:THR:HG23	1.95	0.48
5:g:151:MET:HE2	5:g:151:MET:HA	1.96	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:z:449:LYS:HB3	8:z:459:LEU:HD11	1.96	0.48
1:A:57:ASP:OD1	13:A:603:AF3:F2	2.22	0.47
4:E:158:ASP:OD2	4:E:160:LYS:NZ	2.39	0.47
1:a:421:ILE:O	1:a:424:GLU:HG3	2.13	0.47
2:b:413:SER:O	2:b:416:LEU:HG	2.14	0.47
7:q:33:ILE:HG21	7:q:116:GLU:HB2	1.96	0.47
1:A:74:VAL:O	1:A:77:GLU:HG3	2.14	0.47
2:B:156:ARG:NH2	2:B:185:GLU:OE2	2.37	0.47
2:B:293:ARG:HA	2:B:315:ALA:O	2.14	0.47
3:D:428:PRO:HG2	3:D:429:GLU:OE2	2.14	0.47
5:G:82:GLU:O	5:G:86:THR:HG23	2.14	0.47
6:H:90:VAL:HG12	6:H:92:ASP:H	1.79	0.47
5:g:225:THR:O	8:z:318:ARG:NH2	2.47	0.47
6:h:408:GLY:O	6:h:487:ASN:ND2	2.34	0.47
7:q:82:ALA:O	7:q:86:ILE:HG12	2.14	0.47
3:D:32:GLN:HB3	2:b:6:LEU:HD23	1.96	0.47
2:b:293:ARG:HA	2:b:315:ALA:O	2.13	0.47
5:G:165:ILE:HD12	5:G:387:VAL:HG13	1.96	0.47
2:b:8:PRO:HD2	2:b:9:VAL:H	1.79	0.47
1:A:181:TYR:OH	1:A:189:ARG:NH2	2.47	0.47
4:E:255:PHE:HB2	4:E:306:PHE:CB	2.44	0.47
4:e:162:THR:O	4:e:166:ILE:HG12	2.14	0.47
6:H:279:GLU:OE1	6:H:302:TYR:OH	2.32	0.47
2:b:187:VAL:HG21	2:b:397:LEU:HB2	1.96	0.47
7:q:63:LEU:HD23	7:q:383:ASN:HD21	1.80	0.47
8:z:462:THR:O	8:z:466:ILE:HG12	2.14	0.47
4:E:192:ALA:O	4:E:196:VAL:HG22	2.15	0.47
1:a:62:LEU:HB3	1:a:76:CYS:SG	2.55	0.47
2:b:415:MET:HE1	2:b:444:ARG:HE	1.78	0.47
3:d:29:LYS:NZ	9:P:56:ASN:HD22	2.12	0.47
3:d:446:MET:HA	3:d:449:TYR:HD1	1.80	0.47
3:d:497:LYS:HE2	3:d:501:SER:HB3	1.96	0.47
6:h:190:LEU:O	6:h:397:ARG:NE	2.48	0.47
6:h:320:LYS:O	6:h:324:MET:HG2	2.15	0.47
7:q:73:LEU:HD13	7:q:87:VAL:HG22	1.97	0.47
11:q:601:ADP:O2B	13:q:603:AF3:F2	2.22	0.47
8:z:44:MET:HE2	8:z:44:MET:HB2	1.75	0.47
5:G:79:SER:O	5:G:83:ILE:HG23	2.15	0.47
6:H:107:GLN:HG3	6:H:441:ALA:HB2	1.96	0.47
6:h:499:ARG:HA	6:h:499:ARG:HD3	1.77	0.47
8:z:59:ASP:OD2	13:z:603:AF3:F2	2.23	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:N:310:LEU:HD22	10:N:310:LEU:H	1.79	0.47
2:B:84:LEU:HA	2:B:87:MET:HE2	1.97	0.47
4:e:385:ILE:HG21	4:e:402:LEU:HD13	1.96	0.47
5:g:83:ILE:HD12	5:g:508:THR:HG22	1.97	0.47
11:h:601:ADP:O3B	13:h:603:AF3:F3	2.23	0.47
7:q:139:ALA:HB2	7:q:423:ILE:HD11	1.96	0.47
8:z:97:LEU:HD13	8:z:450:VAL:HG21	1.96	0.47
8:z:338:ASP:N	8:z:338:ASP:OD1	2.43	0.47
3:d:535:VAL:HB	9:P:56:ASN:OD1	2.15	0.47
5:g:165:ILE:HD12	5:g:387:VAL:HG13	1.97	0.47
6:h:38:THR:OG1	6:h:47:LYS:NZ	2.45	0.47
6:h:193:LYS:HE3	6:h:194:MET:HE3	1.97	0.47
7:q:402:LEU:HD21	7:q:408:LEU:HD21	1.96	0.47
9:P:202:MET:HE3	9:P:214:PHE:CD1	2.50	0.47
2:B:414:GLU:HG2	2:B:446:LEU:HD23	1.96	0.46
3:D:454:PHE:O	3:D:458:MET:HG2	2.15	0.46
1:a:120:GLY:HA3	1:a:437:ALA:HB3	1.97	0.46
5:g:415:GLU:HG2	5:g:447:ILE:HB	1.97	0.46
1:A:228:ARG:O	5:G:188:ASN:ND2	2.41	0.46
5:G:20:ARG:HH11	5:G:20:ARG:HG3	1.80	0.46
6:H:40:LEU:HD13	6:H:99:LEU:HD12	1.97	0.46
4:e:38:ILE:HG21	4:e:121:GLU:HB2	1.97	0.46
5:g:411:GLY:H	11:g:601:ADP:HO2'	1.59	0.46
7:q:39:LEU:HD13	7:q:83:ALA:HB1	1.97	0.46
2:B:231:ARG:NH1	2:B:233:GLU:OE2	2.41	0.46
5:G:117:MET:HE1	5:G:436:PRO:HG3	1.97	0.46
6:H:218:LYS:HE3	6:H:221:SER:HB2	1.96	0.46
8:z:415:GLU:CD	8:z:415:GLU:H	2.22	0.46
1:A:78:LEU:HD11	1:A:516:PHE:HB3	1.98	0.46
2:B:65:ASN:ND2	2:B:169:SER:O	2.48	0.46
6:H:333:SER:HB3	7:Q:300:MET:HE1	1.97	0.46
1:a:107:LEU:HG	1:a:440:GLU:HG3	1.96	0.46
2:b:44:GLY:N	11:b:601:ADP:H5'1	2.31	0.46
4:e:42:LYS:HD2	4:e:118:GLU:HG3	1.96	0.46
5:g:447:ILE:HB	5:g:448:PRO:HD3	1.97	0.46
6:h:121:ILE:HA	6:h:434:LEU:HD13	1.98	0.46
10:N:309:ASP:O	10:N:313:ASP:N	2.48	0.46
8:Z:92:THR:N	13:Z:603:AF3:F3	2.37	0.46
1:a:214:TYR:OH	1:a:315:ASP:OD1	2.24	0.46
3:d:191:VAL:HG21	3:d:412:ILE:HB	1.98	0.46
1:A:463:LEU:HD23	1:A:463:LEU:HA	1.84	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:381:GLN:HE22	3:D:93:GLU:CD	2.23	0.46
4:E:101:GLU:OE1	6:H:375:ARG:NH2	2.44	0.46
5:G:184:GLN:HG3	5:G:193:ILE:HG12	1.98	0.46
2:b:332:ALA:HA	4:e:312:HIS:CD2	2.50	0.46
5:g:130:LEU:HA	5:g:133:MET:CE	2.39	0.46
7:q:182:LEU:HD22	7:q:217:VAL:HG23	1.96	0.46
1:A:238:ASP:HB3	1:A:329:SER:HA	1.97	0.46
2:B:168:SER:OG	11:B:601:ADP:N7	2.38	0.46
3:D:429:GLU:HG2	3:D:461:ILE:HB	1.97	0.46
4:E:515:GLN:HE22	6:H:203:GLY:N	2.12	0.46
7:Q:139:ALA:HB2	7:Q:423:ILE:HD11	1.97	0.46
7:Q:175:ASN:ND2	7:Q:212:ILE:HD11	2.31	0.46
1:a:57:ASP:OD1	13:a:603:AF3:F2	2.24	0.46
3:d:86:PRO:O	3:d:90:MET:HG3	2.16	0.46
5:g:47:MET:HB2	8:z:517:LEU:C	2.41	0.46
8:z:218:HIS:HB3	8:z:221:MET:HG2	1.97	0.46
4:E:377:CYS:HB2	4:E:380:SER:HB2	1.98	0.46
5:G:111:HIS:CD2	5:G:111:HIS:C	2.93	0.46
7:Q:284:ALA:HB2	7:Q:310:ILE:HD11	1.98	0.46
8:Z:461:GLU:OE1	8:Z:461:GLU:N	2.46	0.46
7:q:284:ALA:HB2	7:q:310:ILE:HD11	1.98	0.46
1:A:281:THR:HG21	1:A:340:PHE:CE1	2.50	0.46
3:D:26:ASP:OD1	3:D:26:ASP:N	2.47	0.46
4:E:14:ARG:NH2	6:H:16:SER:OG	2.48	0.46
4:E:196:VAL:HG12	4:E:381:ARG:O	2.16	0.46
5:G:507:LYS:O	5:G:511:GLU:HG2	2.15	0.46
1:a:179:ILE:HD13	1:a:195:VAL:HG23	1.97	0.46
2:b:271:GLU:HG2	4:e:274:TYR:CZ	2.51	0.46
4:e:4:MET:HA	4:e:25:LYS:O	2.16	0.46
3:D:152:SER:HB3	3:D:512:LEU:HD13	1.98	0.46
5:G:258:ILE:HG23	5:G:263:ASP:HB2	1.98	0.46
1:a:163:ILE:HB	5:g:127:ARG:HH11	1.81	0.46
2:b:45:PRO:HG3	11:b:601:ADP:C5	2.51	0.46
11:b:601:ADP:PB	13:b:603:AF3:F1	2.64	0.46
4:e:255:PHE:HB2	4:e:306:PHE:CB	2.46	0.46
6:h:319:LEU:HA	6:h:319:LEU:HD23	1.80	0.46
8:Z:227:ASP:OD1	8:Z:346:HIS:NE2	2.49	0.45
1:a:89:GLY:N	11:a:601:ADP:O3B	2.49	0.45
4:e:192:ALA:O	4:e:196:VAL:HG22	2.16	0.45
5:g:27:ILE:HG21	5:g:110:GLU:HB2	1.98	0.45
4:E:515:GLN:NE2	6:H:203:GLY:H	2.14	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:62:ASP:OD1	13:G:603:AF3:F3	2.23	0.45
1:a:266:ARG:NH1	1:a:273:GLU:OE2	2.49	0.45
1:a:527:ILE:HG21	3:d:60:MET:HE2	1.97	0.45
3:d:537:ASN:ND2	9:P:56:ASN:O	2.44	0.45
7:q:117:GLU:O	7:q:121:ILE:HG23	2.15	0.45
9:P:161:VAL:HG11	9:P:202:MET:HG2	1.98	0.45
5:G:332:VAL:HG21	5:G:338:LEU:HD13	1.98	0.45
6:H:23:VAL:HG13	6:H:109:LYS:HE3	1.97	0.45
5:g:217:GLY:HA3	5:g:363:ILE:O	2.16	0.45
6:h:26:ILE:O	6:h:30:GLN:HG2	2.15	0.45
1:A:47:ASP:HB2	1:A:51:ASP:HB2	1.99	0.45
2:B:417:MET:HE3	2:B:504:LEU:HD22	1.98	0.45
3:D:317:LEU:HD13	3:D:324:VAL:HG21	1.98	0.45
4:e:20:LYS:HG3	4:e:21:ASP:OD2	2.17	0.45
8:z:130:ALA:HB1	8:z:418:MET:SD	2.55	0.45
8:z:196:MET:HE2	8:z:377:LYS:HE2	1.97	0.45
4:E:69:THR:HB	4:E:80:MET:HE1	1.98	0.45
4:E:298:ASN:O	4:E:320:PRO:HD2	2.17	0.45
6:H:73:HIS:HB3	6:H:76:ALA:HB3	1.98	0.45
1:a:113:HIS:NE2	3:d:468:ASN:O	2.46	0.45
2:b:20:ARG:HD2	2:b:20:ARG:HA	1.72	0.45
5:g:302:HIS:HB2	8:z:334:ASN:HB2	1.98	0.45
3:D:303:SER:HB3	3:D:308:ALA:HB2	1.97	0.45
1:a:281:THR:HG21	1:a:340:PHE:CD1	2.52	0.45
5:g:101:LEU:O	5:g:105:MET:HG3	2.16	0.45
5:g:182:MET:SD	5:g:372:CYS:HB3	2.56	0.45
6:h:41:GLY:H	11:h:601:ADP:H5'1	1.82	0.45
4:E:2:ALA:N	1:a:11:ARG:O	2.50	0.45
4:E:441:PRO:O	4:E:445:GLN:HG3	2.17	0.45
5:G:14:THR:HA	5:G:525:GLY:HA3	1.99	0.45
5:G:391:LEU:O	5:G:395:MET:HG3	2.16	0.45
6:H:394:MET:SD	6:H:397:ARG:NH1	2.90	0.45
1:a:526:ARG:HD3	3:d:175:VAL:HG23	1.99	0.45
2:b:224:ILE:HD13	2:b:310:MET:HE2	1.98	0.45
3:d:73:ASP:OD1	13:d:603:AF3:F2	2.25	0.45
2:B:167:LEU:HD22	2:B:172:LEU:HD12	1.99	0.45
3:D:337:CYS:SG	3:D:344:PRO:HD3	2.56	0.45
3:D:472:ASN:O	3:D:476:THR:OG1	2.21	0.45
8:Z:522:MET:HB2	8:Z:522:MET:HE2	1.76	0.45
2:b:137:ALA:HB1	2:b:417:MET:HB3	1.99	0.45
5:g:43:PRO:HA	5:g:162:THR:HA	1.99	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:333:SER:H	4:E:312:HIS:CG	2.35	0.45
3:D:413:ARG:HD2	3:D:417:LYS:HE2	1.98	0.45
8:Z:4:VAL:HG21	8:Z:522:MET:SD	2.56	0.45
1:a:246:MET:HB3	1:a:250:VAL:HB	1.99	0.45
1:a:527:ILE:HD13	3:d:60:MET:HE2	1.99	0.45
4:e:58:ASP:OD1	4:e:72:ASN:HB2	2.16	0.45
4:e:69:THR:HG21	4:e:80:MET:HE1	1.98	0.45
4:e:143:VAL:HG21	4:e:436:GLU:HG2	1.97	0.45
5:g:435:TRP:HB2	5:g:436:PRO:HD3	1.99	0.45
7:q:253:THR:HG22	8:z:241:LYS:HG3	1.99	0.45
1:A:35:SER:HB3	1:A:56:ASN:OD1	2.16	0.45
2:B:187:VAL:HG21	2:B:397:LEU:HB2	1.98	0.45
2:B:238:LEU:HB2	2:B:287:ILE:HG21	1.99	0.45
2:B:271:GLU:HG2	4:E:274:TYR:CZ	2.51	0.45
4:E:3:SER:OG	4:E:4:MET:N	2.50	0.45
5:G:463:LEU:HD12	5:G:463:LEU:HA	1.85	0.45
1:a:199:LYS:HB3	1:a:385:CYS:HB3	1.98	0.45
4:e:469:ASN:ND2	4:e:472:GLN:OE1	2.50	0.45
5:g:396:GLN:OE1	5:g:399:ARG:NH2	2.49	0.45
8:z:200:SER:OG	8:z:203:ASP:OD2	2.34	0.45
1:A:120:GLY:HA3	1:A:437:ALA:HB3	1.99	0.44
7:Q:168:ILE:HD13	7:Q:183:ILE:HD12	1.98	0.44
7:Q:247:ASP:OD1	7:Q:248:GLY:N	2.49	0.44
1:a:37:GLY:N	11:a:601:ADP:H5'1	2.32	0.44
5:g:401:VAL:HG23	5:g:498:PRO:HG3	1.98	0.44
6:h:51:ASP:OD1	6:h:55:LYS:N	2.49	0.44
8:z:294:GLN:HB2	8:z:321:MET:SD	2.57	0.44
2:B:521:ILE:HB	4:E:61:MET:HE3	1.98	0.44
5:G:49:MET:HE2	5:G:59:MET:HE2	1.99	0.44
8:Z:236:SER:O	8:Z:270:ARG:NH2	2.50	0.44
1:a:192:VAL:HG12	1:a:193:ASN:H	1.82	0.44
5:g:280:GLU:OE2	5:g:284:GLN:NE2	2.39	0.44
6:h:74:PRO:HB2	7:q:55:MET:SD	2.57	0.44
7:q:203:ARG:HD3	7:q:323:ARG:HD3	1.98	0.44
1:A:158:SER:OG	11:A:601:ADP:O1A	2.30	0.44
4:E:10:ASP:OD2	6:H:24:SER:OG	2.32	0.44
6:h:382:MET:HE3	6:h:382:MET:HB2	1.92	0.44
8:z:289:PHE:HB3	8:z:310:ILE:HG12	2.00	0.44
5:G:416:MET:HG3	5:G:466:LEU:HG	1.98	0.44
8:Z:466:ILE:HD13	8:Z:479:VAL:HG22	1.99	0.44
2:B:58:ASP:OD1	2:B:58:ASP:N	2.44	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:101:GLU:HG2	4:E:515:GLN:CD	2.43	0.44
5:G:203:LYS:HB3	5:G:384:LEU:HD13	2.00	0.44
6:H:53:ARG:HG2	6:H:53:ARG:HH11	1.82	0.44
1:a:411:GLY:O	1:a:498:ASN:ND2	2.38	0.44
2:b:177:ASP:OD1	2:b:177:ASP:N	2.50	0.44
3:d:277:ARG:O	3:d:280:ARG:HG2	2.17	0.44
7:q:191:PHE:HB2	7:q:197:PHE:HD1	1.82	0.44
7:q:499:ASP:OD2	7:q:504:LYS:NZ	2.50	0.44
1:a:155:SER:HB2	1:a:398:VAL:HG21	1.99	0.44
2:b:47:GLY:O	3:d:531:LYS:NZ	2.48	0.44
5:g:483:GLU:N	5:g:483:GLU:OE1	2.51	0.44
6:h:58:ILE:HD12	6:h:380:GLN:HG3	2.00	0.44
7:q:206:LYS:O	7:q:224:LYS:NZ	2.48	0.44
8:z:38:LEU:O	8:z:454:ASN:ND2	2.48	0.44
2:b:517:VAL:HG21	4:e:60:MET:HG3	1.99	0.44
3:d:381:SER:O	3:d:381:SER:OG	2.30	0.44
4:e:532:ASP:HB3	6:h:47:LYS:HD3	1.98	0.44
5:g:160:ILE:HG21	5:g:394:ALA:HB2	1.99	0.44
5:g:412:GLY:HA3	5:g:448:PRO:HG3	2.00	0.44
7:q:247:ASP:OD1	7:q:248:GLY:N	2.50	0.44
8:z:237:LEU:HB2	8:z:297:ILE:HG12	2.00	0.44
1:A:66:GLU:OE2	5:G:527:LYS:HG2	2.18	0.44
3:D:115:SER:OG	3:D:460:VAL:HG11	2.18	0.44
4:E:307:ASP:HB3	10:N:311:ARG:HD2	2.00	0.44
8:Z:47:LEU:HD13	8:Z:66:GLU:HB2	1.99	0.44
8:z:58:LYS:HB3	8:z:58:LYS:HE2	1.78	0.44
3:D:52:LEU:O	3:D:468:ASN:ND2	2.45	0.44
7:Q:452:LEU:HB3	7:Q:480:LEU:HD23	2.00	0.44
8:Z:47:LEU:HD11	8:Z:63:LEU:HD22	1.98	0.44
5:g:527:LYS:HB3	5:g:527:LYS:HE3	1.77	0.44
7:q:220:GLY:HA3	7:q:363:PHE:O	2.18	0.44
1:A:31:ILE:HG21	1:A:65:LEU:HD11	2.00	0.43
1:A:132:ILE:HG12	1:A:136:LEU:HD12	2.00	0.43
4:E:115:ALA:O	4:E:119:GLU:HG2	2.17	0.43
5:G:20:ARG:HG3	5:G:20:ARG:NH1	2.33	0.43
2:b:516:ARG:NE	4:e:58:ASP:OD2	2.33	0.43
7:q:408:LEU:HD23	7:q:500:THR:HA	1.98	0.43
8:z:87:ILE:HD13	8:z:87:ILE:HA	1.88	0.43
1:A:45:LEU:HD23	5:G:526:HIS:CE1	2.53	0.43
2:B:295:LEU:HD23	2:B:314:HIS:HB2	2.00	0.43
3:D:291:LYS:HG2	3:D:320:MET:HE2	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:506:PRO:HB2	1:a:509:VAL:HG23	2.00	0.43
2:b:242:THR:HG21	2:b:335:PHE:CE2	2.53	0.43
2:b:488:MET:HE2	2:b:488:MET:HA	2.00	0.43
5:g:48:LYS:HD2	5:g:66:ILE:HD13	2.00	0.43
5:g:62:ASP:OD2	13:g:603:AF3:F2	2.26	0.43
5:g:504:GLN:O	5:g:508:THR:OG1	2.27	0.43
8:z:286:ASP:OD1	8:z:287:LYS:N	2.49	0.43
1:A:397:CYS:O	1:A:401:ARG:HG2	2.18	0.43
2:B:259:ASP:OD1	2:B:259:ASP:N	2.50	0.43
8:Z:179:ILE:HD13	8:Z:191:ILE:CD1	2.49	0.43
1:a:397:CYS:O	1:a:401:ARG:HG2	2.18	0.43
2:b:51:ILE:HD11	3:d:532:ILE:HD13	2.00	0.43
3:d:53:GLY:H	11:d:601:ADP:H5'2	1.83	0.43
3:d:235:ASN:HD21	3:d:238:ILE:HD12	1.83	0.43
4:e:170:LYS:O	4:e:182:HIS:NE2	2.50	0.43
4:e:251:LEU:HD23	4:e:342:VAL:HB	2.00	0.43
6:h:194:MET:SD	6:h:324:MET:HG3	2.58	0.43
1:A:163:ILE:HB	5:G:127:ARG:HD2	2.01	0.43
5:G:444:LEU:HA	5:G:444:LEU:HD23	1.89	0.43
8:Z:44:MET:HE2	8:Z:44:MET:HB2	1.79	0.43
1:a:140:THR:HB	1:a:147:CYS:SG	2.59	0.43
5:g:332:VAL:HG21	5:g:338:LEU:HD23	2.00	0.43
7:q:156:ASP:HB3	7:q:159:GLU:HB2	1.99	0.43
1:A:127:GLU:HG3	1:A:422:TYR:HE2	1.83	0.43
5:G:83:ILE:HG13	5:G:84:SER:N	2.34	0.43
2:b:440:ALA:O	2:b:444:ARG:HD3	2.19	0.43
7:q:523:GLN:HB2	8:z:45:LYS:HD3	1.99	0.43
8:z:199:LYS:HD3	8:z:199:LYS:HA	1.77	0.43
2:B:131:ARG:NH2	4:E:179:ASN:OD1	2.48	0.43
7:Q:11:PHE:HE1	8:Z:69:ILE:HD11	1.84	0.43
7:Q:191:PHE:HB2	7:Q:197:PHE:CD1	2.53	0.43
2:b:521:ILE:HB	4:e:61:MET:HE1	2.01	0.43
4:e:39:MET:HE3	4:e:39:MET:HB2	1.80	0.43
6:h:90:VAL:HG11	6:h:498:VAL:HG13	2.00	0.43
1:A:447:VAL:HG13	1:A:448:ILE:HD12	2.01	0.43
3:D:79:LYS:HE3	3:D:79:LYS:HB3	1.57	0.43
5:G:16:ARG:HG3	5:G:523:VAL:HG22	2.01	0.43
7:Q:26:GLU:N	7:Q:26:GLU:OE2	2.52	0.43
8:Z:192:GLU:OE1	8:Z:323:ARG:NH2	2.52	0.43
3:d:159:ASP:OD2	3:d:162:THR:OG1	2.31	0.43
6:h:442:LEU:HD23	6:h:442:LEU:HA	1.86	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:q:253:THR:HG23	8:z:239:TYR:OH	2.18	0.43
8:z:522:MET:HE3	8:z:522:MET:HB3	1.67	0.43
5:G:329:ALA:HB2	5:G:344:GLY:HA3	1.99	0.43
8:Z:264:ARG:NH1	8:Z:298:ASP:OD2	2.51	0.43
1:a:55:THR:HA	1:a:387:GLU:OE1	2.19	0.43
1:a:205:GLN:OE1	5:g:127:ARG:NH2	2.52	0.43
2:b:79:PRO:O	2:b:83:VAL:HG23	2.19	0.43
3:d:467:GLU:HG2	3:d:473:PRO:HG3	2.00	0.43
9:P:55:VAL:HG22	9:P:59:PRO:HD3	2.00	0.43
1:A:299:TYR:OH	5:G:337:GLU:OE2	2.24	0.43
3:D:410:CYS:SG	3:D:413:ARG:NH2	2.91	0.43
4:E:300:ALA:O	4:E:321:ALA:HA	2.19	0.43
4:E:344:ARG:HG3	4:E:347:GLU:HG3	2.00	0.43
4:E:421:GLY:O	4:E:501:MET:HG3	2.19	0.43
8:Z:497:ASN:O	8:Z:501:LYS:HG2	2.17	0.43
1:a:238:ASP:HB3	1:a:329:SER:HA	2.01	0.43
1:a:278:ILE:O	1:a:281:THR:HG22	2.19	0.43
3:d:128:ILE:HD13	3:d:446:MET:HB3	2.00	0.43
2:B:260:SER:HB2	3:D:278:GLU:OE1	2.18	0.43
3:D:347:HIS:ND1	3:D:349:ASP:HB2	2.34	0.43
1:a:111:LYS:HD3	1:a:111:LYS:HA	1.76	0.43
2:b:333:SER:H	4:e:312:HIS:CG	2.37	0.43
3:d:151:MET:HE2	3:d:151:MET:HB2	1.91	0.43
6:h:73:HIS:HB3	6:h:76:ALA:HB3	2.01	0.43
6:h:214:VAL:HG11	6:h:322:THR:HG23	2.00	0.43
6:h:385:THR:O	6:h:389:LEU:HD23	2.19	0.43
7:q:526:MET:HE3	7:q:526:MET:HB3	1.96	0.43
2:B:131:ARG:NH2	2:B:512:GLU:OE2	2.43	0.42
8:Z:487:MET:HE2	8:Z:492:VAL:HG21	2.01	0.42
1:a:5:LEU:HD21	3:d:47:ALA:HB2	2.01	0.42
3:d:214:LEU:HD23	3:d:215:GLY:H	1.84	0.42
6:h:92:ASP:OD1	13:h:603:AF3:F1	2.27	0.42
6:H:53:ARG:HG2	6:H:53:ARG:NH1	2.33	0.42
8:Z:429:VAL:HG21	8:Z:437:VAL:HG21	2.00	0.42
3:d:408:ALA:O	3:d:412:ILE:HG12	2.19	0.42
3:d:446:MET:HE3	3:d:446:MET:HB2	1.87	0.42
7:q:191:PHE:HB2	7:q:197:PHE:CD1	2.54	0.42
9:P:212:VAL:HB	9:P:214:PHE:CE2	2.54	0.42
1:A:341:GLU:HG2	1:A:344:MET:HE2	2.01	0.42
2:B:257:ARG:HA	2:B:257:ARG:HD3	1.74	0.42
7:Q:440:LYS:HA	7:Q:440:LYS:HD3	1.80	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:530:LEU:HG	3:d:60:MET:HG2	2.01	0.42
4:e:196:VAL:HG12	4:e:381:ARG:O	2.19	0.42
4:e:203:ASP:OD2	6:h:357:ARG:NH2	2.39	0.42
6:h:332:THR:HG21	7:q:299:ASP:HB3	2.01	0.42
7:q:118:LEU:HA	7:q:121:ILE:HG12	2.01	0.42
9:P:236:LEU:HB3	9:P:248:PHE:HB2	2.01	0.42
1:A:49:ILE:HD11	5:G:528:LYS:HD2	2.02	0.42
4:E:364:PHE:CE2	4:E:371:MET:HG3	2.52	0.42
7:Q:169:MET:SD	11:Q:601:ADP:N6	2.83	0.42
4:e:405:ALA:O	4:e:409:ILE:HG12	2.19	0.42
5:g:226:HIS:CG	5:g:227:PRO:HD2	2.55	0.42
5:g:226:HIS:CG	5:g:305:MET:HE1	2.55	0.42
5:g:266:ARG:HA	5:g:266:ARG:HD2	1.78	0.42
6:h:427:ILE:HD11	6:h:432:GLN:HA	2.01	0.42
8:z:231:LEU:HD23	8:z:291:VAL:HG22	2.01	0.42
10:N:314:ARG:HE	10:N:314:ARG:HB3	1.57	0.42
3:D:430:ILE:HD12	3:D:430:ILE:HA	1.85	0.42
4:E:324:TRP:NE1	10:N:309:ASP:OD2	2.52	0.42
6:H:319:LEU:HD23	6:H:319:LEU:HA	1.92	0.42
1:a:35:SER:HB3	1:a:56:ASN:OD1	2.19	0.42
2:b:138:ARG:NH2	4:e:220:GLU:OE2	2.33	0.42
2:b:390:LEU:HD12	2:b:390:LEU:HA	1.81	0.42
3:d:248:LEU:HD21	3:d:333:ILE:HG23	2.01	0.42
4:e:396:GLU:O	4:e:400:ARG:HG2	2.18	0.42
5:g:129:ALA:O	5:g:133:MET:HG3	2.19	0.42
5:g:258:ILE:HG23	5:g:263:ASP:HB2	2.00	0.42
1:A:289:THR:HG23	1:A:316:LEU:HD22	2.01	0.42
2:B:63:VAL:HG12	2:B:381:GLN:HB3	2.00	0.42
4:E:123:LEU:HD23	4:E:123:LEU:HA	1.84	0.42
5:G:20:ARG:NH2	5:G:114:GLU:HA	2.33	0.42
1:a:31:ILE:HD11	5:g:10:LEU:HD11	2.02	0.42
1:a:44:MET:HE2	5:g:519:ILE:HD13	2.01	0.42
1:a:220:VAL:HB	1:a:225:MET:HE2	2.02	0.42
3:d:255:ALA:O	3:d:306:ARG:NH2	2.53	0.42
4:e:444:GLU:OE1	4:e:444:GLU:N	2.48	0.42
9:P:292:HIS:HB2	9:P:295:ASP:OD1	2.19	0.42
1:A:410:PRO:HG3	1:A:485:TRP:HE3	1.85	0.42
5:G:256:ILE:HD11	8:Z:244:VAL:HB	2.01	0.42
6:h:69:LEU:HD23	6:h:69:LEU:HA	1.91	0.42
7:q:165:ARG:HG3	7:q:176:GLU:HG3	2.02	0.42
1:A:222:SER:N	1:A:225:MET:HE3	2.35	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:26:GLU:HA	7:Q:30:TYR:CD2	2.55	0.42
2:b:35:ILE:HD13	2:b:35:ILE:HA	1.95	0.42
6:h:455:PHE:CZ	6:h:482:GLU:HA	2.55	0.42
7:Q:239:ILE:HD12	7:Q:239:ILE:H	1.85	0.42
8:Z:465:LYS:HB2	8:Z:465:LYS:HE3	1.80	0.42
2:b:415:MET:HE3	2:b:415:MET:HA	2.02	0.42
4:e:184:GLN:O	4:e:188:ILE:HG23	2.20	0.42
11:e:601:ADP:O3B	13:e:603:AF3:F3	2.27	0.42
6:h:187:ASP:OD1	6:h:187:ASP:N	2.44	0.42
6:h:232:TYR:HD1	6:h:348:PHE:HD2	1.68	0.42
9:P:60:LYS:O	9:P:63:ILE:HG22	2.19	0.42
2:B:95:VAL:HG12	2:B:399:GLN:HG3	2.02	0.42
6:H:79:LEU:HA	6:H:82:ILE:HG12	2.01	0.42
6:H:297:ASP:OD1	6:H:297:ASP:N	2.52	0.42
7:Q:502:LEU:HD23	7:Q:502:LEU:HA	1.89	0.42
8:Z:239:TYR:CD1	8:Z:239:TYR:C	2.98	0.42
4:e:10:ASP:OD2	6:h:24:SER:OG	2.30	0.42
4:e:25:LYS:HG2	4:e:536:PRO:HA	2.02	0.42
7:q:67:ASN:OD1	7:q:67:ASN:N	2.45	0.42
2:B:86:ASP:OD2	4:E:392:LYS:HG2	2.20	0.41
2:B:441:LYS:HE3	2:B:441:LYS:HB2	1.82	0.41
3:D:71:THR:HA	3:D:400:GLU:OE1	2.19	0.41
3:D:280:ARG:HG2	3:D:312:LEU:HD21	2.01	0.41
1:a:127:GLU:HG3	1:a:426:TYR:CZ	2.55	0.41
1:a:322:ALA:HA	1:a:370:ARG:HB3	2.00	0.41
4:e:123:LEU:HD22	4:e:128:ILE:HD12	2.02	0.41
5:g:278:LEU:HD22	5:g:335:PRO:HG2	2.01	0.41
6:h:104:PHE:O	6:h:108:VAL:HG22	2.20	0.41
4:E:78:LEU:HD13	4:E:92:VAL:HA	2.02	0.41
7:Q:364:LYS:NZ	7:Q:366:GLU:OE2	2.53	0.41
8:Z:221:MET:CE	8:Z:312:ALA:H	2.34	0.41
1:a:107:LEU:HD23	1:a:107:LEU:HA	1.87	0.41
1:a:266:ARG:HA	1:a:269:ASP:HB2	2.02	0.41
2:b:260:SER:HB2	3:d:278:GLU:OE1	2.19	0.41
4:e:78:LEU:HD11	4:e:110:VAL:HG21	2.02	0.41
5:g:384:LEU:HD23	5:g:384:LEU:HA	1.87	0.41
6:h:214:VAL:HG11	6:h:322:THR:HA	2.02	0.41
6:h:364:CYS:HB2	6:h:367:ALA:HB2	2.02	0.41
5:G:319:ASP:OD1	5:G:322:ARG:NH2	2.45	0.41
8:Z:149:ILE:HD13	8:Z:169:THR:HG22	2.02	0.41
1:a:314:ARG:NH1	1:a:315:ASP:OD1	2.53	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:b:83:VAL:HG22	4:e:393:MET:HE2	2.01	0.41
4:e:196:VAL:O	4:e:196:VAL:HG23	2.20	0.41
2:B:87:MET:HE2	2:B:87:MET:HB3	1.94	0.41
4:E:532:ASP:O	4:E:533:ILE:HD13	2.21	0.41
1:a:42:ASP:CG	5:g:518:ARG:HE	2.29	0.41
1:a:228:ARG:NE	1:a:350:GLU:OE2	2.46	0.41
1:a:266:ARG:HA	1:a:266:ARG:HD2	1.86	0.41
1:a:489:ASP:OD2	1:a:492:ASN:ND2	2.39	0.41
4:e:219:LEU:HD22	4:e:394:ILE:HD11	2.03	0.41
1:A:190:TYR:CE2	1:A:403:LEU:HD13	2.55	0.41
2:B:113:ALA:HB2	2:B:130:TRP:HH2	1.84	0.41
4:E:130:PRO:HG2	6:H:45:MET:HE1	2.03	0.41
5:G:229:MET:SD	5:G:310:THR:HA	2.60	0.41
7:Q:190:ILE:HD11	7:Q:373:SER:N	2.35	0.41
8:Z:79:LYS:HD3	8:Z:79:LYS:HA	1.91	0.41
8:Z:526:MET:SD	8:Z:526:MET:N	2.86	0.41
1:a:46:VAL:HG13	5:g:524:SER:HB3	2.03	0.41
4:e:7:LEU:HD12	4:e:7:LEU:HA	1.87	0.41
8:z:26:ALA:HB2	8:z:71:HIS:CE1	2.56	0.41
8:z:33:VAL:HG11	8:z:67:MET:SD	2.61	0.41
8:z:159:LYS:HA	8:z:159:LYS:HD3	1.74	0.41
1:A:55:THR:HA	1:A:387:GLU:OE1	2.21	0.41
4:E:284:LYS:HD2	4:E:284:LYS:HA	1.75	0.41
4:E:412:LEU:HD12	4:E:412:LEU:HA	1.94	0.41
8:Z:53:ASP:OD1	8:Z:53:ASP:N	2.53	0.41
1:a:44:MET:CE	5:g:519:ILE:HD13	2.51	0.41
1:A:353:GLN:NE2	1:A:360:GLU:HB3	2.27	0.41
2:B:390:LEU:HD23	2:B:390:LEU:HA	1.77	0.41
4:E:207:GLU:OE2	4:E:207:GLU:C	2.63	0.41
5:G:108:VAL:HG11	5:G:443:ALA:HB2	2.03	0.41
6:H:30:GLN:OE1	6:H:106:LYS:HB2	2.20	0.41
7:Q:220:GLY:HA3	7:Q:363:PHE:O	2.21	0.41
8:Z:16:ALA:N	8:Z:519:ASP:O	2.31	0.41
1:a:22:VAL:HG21	1:a:105:ASP:CB	2.50	0.41
1:a:314:ARG:NH2	9:P:289:ALA:HB3	2.36	0.41
5:g:203:LYS:HE2	5:g:385:SER:HA	2.03	0.41
5:g:249:LYS:NZ	8:z:243:GLU:O	2.44	0.41
6:h:93:GLY:HA2	11:h:601:ADP:O2B	2.21	0.41
6:h:294:PRO:HA	6:h:313:ARG:HD2	2.02	0.41
7:q:101:THR:N	13:q:603:AF3:F1	2.35	0.41
4:E:109:VAL:HG13	4:E:516:GLN:HG2	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:405:ALA:O	4:E:409:ILE:HG12	2.21	0.41
8:Z:143:MET:HE2	8:Z:143:MET:HA	2.03	0.41
8:Z:253:ALA:O	8:Z:257:GLU:HG2	2.21	0.41
2:b:189:ARG:NH2	2:b:370:ALA:O	2.53	0.41
4:e:63:ASP:OD1	4:e:67:ASP:N	2.54	0.41
4:e:387:ILE:HD11	4:e:402:LEU:HD12	2.03	0.41
4:e:460:MET:HE3	4:e:460:MET:HB3	1.79	0.41
7:q:276:MET:HE2	7:q:276:MET:HB2	1.84	0.41
1:A:28:ILE:HD13	1:A:28:ILE:HA	1.88	0.41
2:B:245:ASP:OD1	2:B:245:ASP:N	2.53	0.41
4:E:248:ILE:HG12	4:E:299:LEU:HD23	2.01	0.41
4:E:332:LEU:HD23	4:E:332:LEU:HA	1.92	0.41
6:H:94:THR:OG1	13:H:603:AF3:F3	2.28	0.41
6:H:229:PRO:HG2	6:H:232:TYR:OH	2.21	0.41
7:Q:101:THR:N	13:Q:603:AF3:F1	2.34	0.41
7:Q:277:ASP:HB2	7:Q:304:TYR:CE2	2.56	0.41
7:Q:335:ARG:HB3	7:Q:337:THR:HG23	2.01	0.41
8:Z:23:ASN:OD1	8:Z:73:THR:OG1	2.36	0.41
8:Z:190:MET:HA	8:Z:190:MET:HE2	2.03	0.41
1:a:233:LYS:HB2	1:a:283:ALA:HA	2.03	0.41
1:a:328:LEU:HD23	1:a:328:LEU:HA	1.93	0.41
1:a:410:PRO:HG3	1:a:485:TRP:HE3	1.85	0.41
2:b:445:MET:HE2	2:b:445:MET:HB2	1.83	0.41
3:d:248:LEU:HD21	3:d:333:ILE:HD12	2.03	0.41
4:e:196:VAL:HG21	4:e:209:ILE:HG13	2.03	0.41
4:e:456:GLU:O	4:e:460:MET:HG3	2.20	0.41
5:g:165:ILE:HB	5:g:390:ASN:HD22	1.85	0.41
7:q:225:LYS:HE2	7:q:225:LYS:HB3	1.84	0.41
9:P:206:ALA:HA	9:P:214:PHE:CE2	2.56	0.41
1:A:184:ILE:O	1:A:185:ARG:HG2	2.21	0.41
1:A:402:VAL:HG23	1:A:506:PRO:HG3	2.03	0.41
1:A:487:GLY:HA3	1:A:498:ASN:ND2	2.36	0.41
3:D:164:LEU:HD23	3:D:188:VAL:HG21	2.03	0.41
5:G:226:HIS:H	5:G:229:MET:HE2	1.85	0.41
5:G:473:GLU:OE1	5:G:473:GLU:N	2.54	0.41
8:Z:444:LEU:HD23	8:Z:444:LEU:HA	1.95	0.41
5:g:41:LEU:HD13	5:g:100:ILE:HD12	2.03	0.41
7:q:263:GLU:OE1	7:q:263:GLU:N	2.49	0.41
1:A:160:ILE:HG23	1:A:161:ILE:HG23	2.03	0.40
2:B:204:LYS:HA	2:B:204:LYS:HD2	1.89	0.40
3:D:435:ARG:HA	3:D:435:ARG:HD3	1.84	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:183:VAL:HG21	5:G:199:ALA:HB2	2.02	0.40
6:H:266:ILE:HD13	6:H:266:ILE:HA	1.92	0.40
1:a:321:LYS:HD2	9:P:297:ASP:O	2.21	0.40
1:a:514:LEU:HD23	1:a:514:LEU:HA	1.93	0.40
2:b:64:THR:HA	2:b:385:GLU:OE1	2.21	0.40
7:q:26:GLU:HA	7:q:30:TYR:CD2	2.56	0.40
9:P:184:MET:HE3	9:P:184:MET:C	2.46	0.40
2:B:222:LYS:HA	2:B:222:LYS:HD3	1.88	0.40
2:B:223:LYS:HB2	2:B:223:LYS:HE2	1.77	0.40
6:H:32:ILE:HD13	6:H:32:ILE:HA	1.85	0.40
6:H:277:LYS:O	6:H:281:ILE:HG13	2.21	0.40
1:a:222:SER:O	1:a:225:MET:HG3	2.21	0.40
1:a:456:ALA:HB2	1:a:490:LEU:HD12	2.04	0.40
4:e:255:PHE:HB2	4:e:306:PHE:HB3	2.03	0.40
8:z:376:ILE:HG22	8:z:384:LEU:HD22	2.03	0.40
6:H:232:TYR:HD1	6:H:348:PHE:HD2	1.68	0.40
8:Z:38:LEU:O	8:Z:454:ASN:ND2	2.48	0.40
2:b:425:ALA:HA	2:b:436:MET:HE3	2.03	0.40
7:q:163:LEU:HD22	7:q:408:LEU:HD11	2.02	0.40
7:q:235:LYS:HD3	7:q:235:LYS:HA	1.71	0.40
7:q:385:MET:HE3	7:q:385:MET:HB2	1.92	0.40
8:z:64:LEU:HD11	8:z:96:VAL:HG21	2.04	0.40
8:z:351:TYR:HE2	8:z:353:TYR:HB2	1.86	0.40
6:H:186:LEU:HD11	6:H:195:ILE:HD11	2.02	0.40
6:H:495:PRO:HB2	6:H:498:VAL:HG23	2.03	0.40
7:Q:480:LEU:HD12	7:Q:481:ASP:N	2.36	0.40
1:a:156:MET:HE1	1:a:169:ALA:N	2.37	0.40
2:b:71:LEU:HD11	2:b:103:THR:HG21	2.03	0.40
7:q:103:PHE:CE2	7:q:448:ILE:HG13	2.55	0.40
1:A:228:ARG:NE	1:A:350:GLU:OE2	2.48	0.40
4:E:203:ASP:OD2	6:H:357:ARG:NH2	2.46	0.40
5:G:50:LEU:HD13	8:Z:522:MET:HB3	2.03	0.40
6:H:26:ILE:O	6:H:30:GLN:HG2	2.22	0.40
7:Q:111:LEU:HD23	7:Q:111:LEU:HA	1.90	0.40
8:Z:520:GLU:OE1	8:Z:522:MET:HE1	2.21	0.40
3:d:233:VAL:HG22	3:d:325:ILE:HG12	2.02	0.40
4:e:101:GLU:HG2	4:e:515:GLN:CD	2.47	0.40
6:h:66:LEU:HD11	6:h:98:THR:HG21	2.04	0.40
8:z:37:ASN:ND2	8:z:58:LYS:O	2.54	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 PDB entries followed by that with respect to all EM entries.

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	534/556 (96%)	514 (96%)	20 (4%)	0	100	100
1	a	530/556 (95%)	514 (97%)	16 (3%)	0	100	100
2	B	524/535 (98%)	509 (97%)	15 (3%)	0	100	100
2	b	523/535 (98%)	511 (98%)	12 (2%)	0	100	100
3	D	518/539 (96%)	507 (98%)	11 (2%)	0	100	100
3	d	518/539 (96%)	495 (96%)	22 (4%)	1 (0%)	43	76
4	E	534/541 (99%)	521 (98%)	13 (2%)	0	100	100
4	e	539/541 (100%)	524 (97%)	15 (3%)	0	100	100
5	G	524/545 (96%)	509 (97%)	15 (3%)	0	100	100
5	g	526/545 (96%)	512 (97%)	14 (3%)	0	100	100
6	H	526/543 (97%)	509 (97%)	17 (3%)	0	100	100
6	h	523/543 (96%)	510 (98%)	13 (2%)	0	100	100
7	Q	536/548 (98%)	519 (97%)	17 (3%)	0	100	100
7	q	531/548 (97%)	511 (96%)	20 (4%)	0	100	100
8	Z	523/531 (98%)	509 (97%)	14 (3%)	0	100	100
8	z	525/531 (99%)	511 (97%)	14 (3%)	0	100	100
9	P	84/326 (26%)	77 (92%)	6 (7%)	1 (1%)	10	40
10	N	20/441 (4%)	20 (100%)	0	0	100	100
All	All	8538/9443 (90%)	8282 (97%)	254 (3%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	P	291	CYS
3	d	513	LEU

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 PDB entries followed by that with respect to all EM entries.

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	447/463 (96%)	444 (99%)	3 (1%)	76	86
1	a	444/463 (96%)	441 (99%)	3 (1%)	76	86
2	B	418/427 (98%)	416 (100%)	2 (0%)	81	89
2	b	417/427 (98%)	416 (100%)	1 (0%)	87	92
3	D	442/452 (98%)	441 (100%)	1 (0%)	87	92
3	d	441/452 (98%)	438 (99%)	3 (1%)	76	86
4	E	452/456 (99%)	452 (100%)	0	100	100
4	e	456/456 (100%)	455 (100%)	1 (0%)	87	92
5	G	456/469 (97%)	454 (100%)	2 (0%)	84	90
5	g	457/469 (97%)	453 (99%)	4 (1%)	70	85
6	H	435/443 (98%)	433 (100%)	2 (0%)	81	89
6	h	432/443 (98%)	431 (100%)	1 (0%)	87	92
7	Q	442/452 (98%)	442 (100%)	0	100	100
7	q	438/452 (97%)	436 (100%)	2 (0%)	81	89
8	Z	437/442 (99%)	431 (99%)	6 (1%)	59	80
8	z	438/442 (99%)	437 (100%)	1 (0%)	87	92
9	P	83/289 (29%)	79 (95%)	4 (5%)	23	57
10	N	22/366 (6%)	22 (100%)	0	100	100
All	All	7157/7863 (91%)	7121 (100%)	36 (0%)	78	89

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	VAL
1	A	166	ASP
1	A	358	ASP
2	B	4	LEU
2	B	493	ILE
3	D	399	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	G	278	LEU
5	G	292	THR
6	H	38	THR
6	H	251	ASP
8	Z	32	ASP
8	Z	53	ASP
8	Z	63	LEU
8	Z	179	ILE
8	Z	244	VAL
8	Z	522	MET
1	a	13	THR
1	a	46	VAL
1	a	156	MET
2	b	39	VAL
3	d	355	MET
3	d	393	SER
3	d	513	LEU
4	e	92	VAL
5	g	183	VAL
5	g	214	VAL
5	g	255	ASP
5	g	522	ILE
6	h	14	ASP
7	q	193	ASP
7	q	212	ILE
8	z	244	VAL
9	P	19	SER
9	P	24	ASP
9	P	62	VAL
9	P	295	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (65) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	135	ASN
1	A	393	HIS
1	A	450	ASN
2	B	65	ASN
2	B	227	ASN
2	B	269	HIS
2	B	381	GLN
2	B	464	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	469	HIS
2	B	502	GLN
3	D	80	GLN
4	E	55	ASN
4	E	495	HIS
4	E	515	GLN
5	G	71	GLN
5	G	111	HIS
5	G	115	GLN
5	G	396	GLN
5	G	420	HIS
6	H	17	GLN
6	H	359	ASN
6	H	431	GLN
6	H	448	GLN
6	H	501	ASN
7	Q	145	ASN
1	a	164	ASN
1	a	193	ASN
1	a	262	GLN
1	a	284	ASN
1	a	393	HIS
1	a	450	ASN
2	b	65	ASN
2	b	157	GLN
2	b	174	HIS
2	b	292	ASN
2	b	464	GLN
3	d	72	ASN
3	d	165	ASN
3	d	262	ASN
3	d	271	GLN
4	e	72	ASN
4	e	403	HIS
5	g	71	GLN
5	g	73	GLN
5	g	111	HIS
5	g	390	ASN
5	g	420	HIS
6	h	17	GLN
6	h	60	ASN
6	h	201	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	h	264	GLN
6	h	331	GLN
6	h	359	ASN
6	h	431	GLN
6	h	448	GLN
6	h	501	ASN
7	q	4	HIS
7	q	21	HIS
7	q	219	HIS
7	q	359	GLN
8	z	65	HIS
8	z	182	GLN
8	z	380	ASN
9	P	56	ASN
9	P	292	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 48 ligands modelled in this entry, 16 are monoatomic - leaving 32 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	ADP	B	601	12,13	28,29,29	1.41	5 (17%)	43,45,45	1.81	10 (23%)
11	ADP	Z	601	12,13	28,29,29	1.39	4 (14%)	43,45,45	1.84	10 (23%)
13	AF3	a	603	11,1	0,3,3	-	-	-	-	-
11	ADP	h	601	12,13	28,29,29	1.39	4 (14%)	43,45,45	1.81	10 (23%)
13	AF3	H	603	11	0,3,3	-	-	-	-	-
13	AF3	Q	603	11	0,3,3	-	-	-	-	-
11	ADP	a	601	12,13	28,29,29	1.39	4 (14%)	43,45,45	1.82	10 (23%)
13	AF3	h	603	11	0,3,3	-	-	-	-	-
13	AF3	D	603	11	0,3,3	-	-	-	-	-
13	AF3	z	603	11	0,3,3	-	-	-	-	-
13	AF3	G	603	11	0,3,3	-	-	-	-	-
11	ADP	d	601	12	28,29,29	1.39	4 (14%)	43,45,45	1.87	9 (20%)
13	AF3	B	603	11,2	0,3,3	-	-	-	-	-
13	AF3	e	603	11	0,3,3	-	-	-	-	-
11	ADP	z	601	12,13	28,29,29	1.40	4 (14%)	43,45,45	1.84	9 (20%)
11	ADP	H	601	12,13	28,29,29	1.41	4 (14%)	43,45,45	1.83	10 (23%)
11	ADP	E	601	12,13	28,29,29	1.41	4 (14%)	43,45,45	1.82	10 (23%)
11	ADP	e	601	12,13	28,29,29	1.41	5 (17%)	43,45,45	1.78	9 (20%)
11	ADP	q	601	12,13	28,29,29	1.39	4 (14%)	43,45,45	1.84	10 (23%)
11	ADP	g	601	12,13	28,29,29	1.39	5 (17%)	43,45,45	1.81	10 (23%)
13	AF3	q	603	11	0,3,3	-	-	-	-	-
11	ADP	D	601	12,13	28,29,29	1.41	4 (14%)	43,45,45	1.82	9 (20%)
13	AF3	d	603	-	0,3,3	-	-	-	-	-
13	AF3	g	603	11	0,3,3	-	-	-	-	-
11	ADP	A	601	12,13	28,29,29	1.41	4 (14%)	43,45,45	1.84	10 (23%)
13	AF3	E	603	11	0,3,3	-	-	-	-	-
13	AF3	b	603	11	0,3,3	-	-	-	-	-
11	ADP	b	601	12,13	28,29,29	1.39	4 (14%)	43,45,45	1.85	10 (23%)
11	ADP	Q	601	12,13	28,29,29	1.39	4 (14%)	43,45,45	1.86	10 (23%)
13	AF3	Z	603	11	0,3,3	-	-	-	-	-
13	AF3	A	603	11	0,3,3	-	-	-	-	-
11	ADP	G	601	12,13	28,29,29	1.39	4 (14%)	43,45,45	1.82	9 (20%)

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	ADP	B	601	12,13	-	1/16/32/32	0/3/3/3
11	ADP	A	601	12,13	-	1/16/32/32	0/3/3/3
11	ADP	Z	601	12,13	-	7/16/32/32	0/3/3/3
11	ADP	G	601	12,13	-	6/16/32/32	0/3/3/3
11	ADP	b	601	12,13	-	5/16/32/32	0/3/3/3
11	ADP	d	601	12	-	3/16/32/32	0/3/3/3
11	ADP	Q	601	12,13	-	5/16/32/32	0/3/3/3
11	ADP	E	601	12,13	-	1/16/32/32	0/3/3/3
11	ADP	e	601	12,13	-	6/16/32/32	0/3/3/3
11	ADP	h	601	12,13	-	6/16/32/32	0/3/3/3
11	ADP	q	601	12,13	-	6/16/32/32	0/3/3/3
11	ADP	a	601	12,13	-	6/16/32/32	0/3/3/3
11	ADP	g	601	12,13	-	0/16/32/32	0/3/3/3
11	ADP	z	601	12,13	-	5/16/32/32	0/3/3/3
11	ADP	D	601	12,13	-	1/16/32/32	0/3/3/3
11	ADP	H	601	12,13	-	1/16/32/32	0/3/3/3

All (67) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	z	601	ADP	C5-C4	4.64	1.47	1.39
11	A	601	ADP	C5-C4	4.61	1.47	1.39
11	Z	601	ADP	C5-C4	4.60	1.47	1.39
11	H	601	ADP	C5-C4	4.60	1.47	1.39
11	q	601	ADP	C5-C4	4.59	1.47	1.39
11	d	601	ADP	C5-C4	4.59	1.47	1.39
11	D	601	ADP	C5-C4	4.58	1.47	1.39
11	g	601	ADP	C5-C4	4.58	1.47	1.39
11	B	601	ADP	C5-C4	4.58	1.47	1.39
11	Q	601	ADP	C5-C4	4.58	1.47	1.39
11	a	601	ADP	C5-C4	4.57	1.47	1.39
11	E	601	ADP	C5-C4	4.57	1.47	1.39
11	h	601	ADP	C5-C4	4.56	1.47	1.39
11	e	601	ADP	C5-C4	4.55	1.47	1.39
11	b	601	ADP	C5-C4	4.55	1.47	1.39
11	G	601	ADP	C5-C4	4.54	1.47	1.39
11	D	601	ADP	C5-C6	2.71	1.48	1.41
11	A	601	ADP	C5-C6	2.71	1.48	1.41
11	a	601	ADP	C5-C6	2.70	1.48	1.41
11	B	601	ADP	C5-C6	2.70	1.48	1.41
11	Z	601	ADP	C5-C6	2.69	1.48	1.41

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	H	601	ADP	C5-C6	2.69	1.48	1.41
11	G	601	ADP	C5-C6	2.68	1.48	1.41
11	q	601	ADP	C5-C6	2.68	1.48	1.41
11	d	601	ADP	C5-C6	2.68	1.48	1.41
11	h	601	ADP	C5-C6	2.68	1.48	1.41
11	b	601	ADP	C5-C6	2.68	1.48	1.41
11	z	601	ADP	C5-C6	2.67	1.48	1.41
11	E	601	ADP	C5-C6	2.67	1.48	1.41
11	Q	601	ADP	C5-C6	2.66	1.48	1.41
11	e	601	ADP	C5-C6	2.66	1.48	1.41
11	g	601	ADP	C5-C6	2.66	1.48	1.41
11	Z	601	ADP	C8-N7	2.40	1.36	1.31
11	A	601	ADP	C8-N7	2.38	1.36	1.31
11	z	601	ADP	C5-N7	-2.37	1.34	1.39
11	G	601	ADP	C5-N7	-2.36	1.34	1.39
11	D	601	ADP	C8-N7	2.36	1.36	1.31
11	H	601	ADP	C5-N7	-2.35	1.34	1.39
11	Q	601	ADP	C8-N7	2.35	1.36	1.31
11	q	601	ADP	C5-N7	-2.34	1.34	1.39
11	d	601	ADP	C8-N7	2.34	1.36	1.31
11	a	601	ADP	C5-N7	-2.34	1.34	1.39
11	H	601	ADP	C8-N7	2.33	1.36	1.31
11	E	601	ADP	C5-N7	-2.33	1.34	1.39
11	b	601	ADP	C5-N7	-2.33	1.34	1.39
11	a	601	ADP	C8-N7	2.33	1.36	1.31
11	Q	601	ADP	C5-N7	-2.33	1.34	1.39
11	e	601	ADP	C8-N7	2.33	1.36	1.31
11	G	601	ADP	C8-N7	2.32	1.36	1.31
11	h	601	ADP	C8-N7	2.32	1.36	1.31
11	A	601	ADP	C5-N7	-2.31	1.34	1.39
11	Z	601	ADP	C5-N7	-2.31	1.34	1.39
11	q	601	ADP	C8-N7	2.31	1.36	1.31
11	g	601	ADP	C8-N7	2.31	1.36	1.31
11	e	601	ADP	C5-N7	-2.31	1.34	1.39
11	g	601	ADP	C5-N7	-2.31	1.34	1.39
11	h	601	ADP	C5-N7	-2.30	1.34	1.39
11	D	601	ADP	C5-N7	-2.30	1.34	1.39
11	B	601	ADP	C8-N7	2.30	1.36	1.31
11	b	601	ADP	C8-N7	2.30	1.36	1.31
11	B	601	ADP	C5-N7	-2.29	1.34	1.39
11	d	601	ADP	C5-N7	-2.29	1.34	1.39
11	E	601	ADP	C8-N7	2.25	1.36	1.31

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	z	601	ADP	C8-N7	2.25	1.36	1.31
11	B	601	ADP	C4-N9	-2.04	1.33	1.37
11	g	601	ADP	C4-N9	-2.04	1.33	1.37
11	e	601	ADP	C4-N9	-2.01	1.33	1.37

All (155) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	Q	601	ADP	C5-C4-N3	-5.87	118.63	126.72
11	d	601	ADP	C5-C4-N3	-5.86	118.64	126.72
11	z	601	ADP	C5-C4-N3	-5.83	118.69	126.72
11	H	601	ADP	C5-C4-N3	-5.82	118.70	126.72
11	E	601	ADP	C5-C4-N3	-5.81	118.71	126.72
11	h	601	ADP	C5-C4-N3	-5.81	118.72	126.72
11	D	601	ADP	C5-C4-N3	-5.80	118.73	126.72
11	Z	601	ADP	C5-C4-N3	-5.78	118.75	126.72
11	A	601	ADP	C5-C4-N3	-5.76	118.78	126.72
11	e	601	ADP	C5-C4-N3	-5.75	118.80	126.72
11	q	601	ADP	C5-C4-N3	-5.75	118.80	126.72
11	b	601	ADP	C5-C4-N3	-5.75	118.81	126.72
11	G	601	ADP	C5-C4-N3	-5.72	118.84	126.72
11	a	601	ADP	C5-C4-N3	-5.70	118.87	126.72
11	g	601	ADP	C5-C4-N3	-5.64	118.95	126.72
11	B	601	ADP	C5-C4-N3	-5.58	119.03	126.72
11	z	601	ADP	N3-C4-N9	4.65	135.07	127.17
11	E	601	ADP	N3-C4-N9	4.64	135.07	127.17
11	h	601	ADP	N3-C4-N9	4.57	134.94	127.17
11	Q	601	ADP	N3-C4-N9	4.56	134.92	127.17
11	H	601	ADP	N3-C4-N9	4.53	134.87	127.17
11	a	601	ADP	N3-C4-N9	4.53	134.87	127.17
11	D	601	ADP	N3-C4-N9	4.53	134.87	127.17
11	d	601	ADP	N3-C4-N9	4.53	134.87	127.17
11	b	601	ADP	N3-C4-N9	4.53	134.87	127.17
11	q	601	ADP	N3-C4-N9	4.52	134.86	127.17
11	A	601	ADP	N3-C4-N9	4.50	134.82	127.17
11	Z	601	ADP	N3-C4-N9	4.48	134.79	127.17
11	e	601	ADP	N3-C4-N9	4.48	134.79	127.17
11	G	601	ADP	N3-C4-N9	4.45	134.73	127.17
11	B	601	ADP	N3-C4-N9	4.41	134.66	127.17
11	g	601	ADP	N3-C4-N9	4.41	134.66	127.17
11	Q	601	ADP	C2-N3-C4	3.76	121.01	111.83
11	h	601	ADP	C2-N3-C4	3.74	120.96	111.83

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	d	601	ADP	C2-N3-C4	3.73	120.94	111.83
11	D	601	ADP	C2-N3-C4	3.72	120.92	111.83
11	Z	601	ADP	C2-N3-C4	3.72	120.91	111.83
11	H	601	ADP	C2-N3-C4	3.71	120.90	111.83
11	E	601	ADP	C2-N3-C4	3.70	120.88	111.83
11	A	601	ADP	C2-N3-C4	3.70	120.88	111.83
11	q	601	ADP	C2-N3-C4	3.70	120.86	111.83
11	z	601	ADP	C2-N3-C4	3.69	120.84	111.83
11	b	601	ADP	C2-N3-C4	3.69	120.84	111.83
11	a	601	ADP	C2-N3-C4	3.67	120.79	111.83
11	e	601	ADP	C2-N3-C4	3.67	120.79	111.83
11	G	601	ADP	C2-N3-C4	3.64	120.72	111.83
11	B	601	ADP	C2-N3-C4	3.63	120.69	111.83
11	g	601	ADP	C2-N3-C4	3.62	120.67	111.83
11	G	601	ADP	C4-C5-N7	-3.62	106.44	110.58
11	Q	601	ADP	C4-C5-N7	-3.61	106.45	110.58
11	Z	601	ADP	C4-C5-N7	-3.56	106.51	110.58
11	d	601	ADP	C4-C5-N7	-3.53	106.54	110.58
11	H	601	ADP	C4-C5-N7	-3.53	106.55	110.58
11	A	601	ADP	C4-C5-N7	-3.52	106.56	110.58
11	h	601	ADP	C4-C5-N7	-3.51	106.57	110.58
11	g	601	ADP	C4-C5-N7	-3.50	106.58	110.58
11	D	601	ADP	C4-C5-N7	-3.49	106.59	110.58
11	b	601	ADP	C4-C5-N7	-3.47	106.61	110.58
11	e	601	ADP	C4-C5-N7	-3.47	106.62	110.58
11	q	601	ADP	C4-C5-N7	-3.47	106.62	110.58
11	B	601	ADP	C4-C5-N7	-3.45	106.63	110.58
11	a	601	ADP	C4-C5-N7	-3.43	106.66	110.58
11	z	601	ADP	C4-C5-N7	-3.39	106.71	110.58
11	E	601	ADP	C4-C5-N7	-3.38	106.72	110.58
11	h	601	ADP	N3-C2-N1	-3.31	123.57	128.58
11	Q	601	ADP	N3-C2-N1	-3.29	123.60	128.58
11	d	601	ADP	N3-C2-N1	-3.28	123.61	128.58
11	A	601	ADP	N3-C2-N1	-3.27	123.62	128.58
11	q	601	ADP	N3-C2-N1	-3.27	123.63	128.58
11	H	601	ADP	N3-C2-N1	-3.27	123.63	128.58
11	b	601	ADP	N3-C2-N1	-3.27	123.64	128.58
11	D	601	ADP	N3-C2-N1	-3.26	123.64	128.58
11	Z	601	ADP	N3-C2-N1	-3.26	123.65	128.58
11	a	601	ADP	N3-C2-N1	-3.25	123.67	128.58
11	E	601	ADP	N3-C2-N1	-3.23	123.69	128.58
11	z	601	ADP	N3-C2-N1	-3.21	123.73	128.58

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	B	601	ADP	N3-C2-N1	-3.20	123.74	128.58
11	e	601	ADP	N3-C2-N1	-3.19	123.75	128.58
11	g	601	ADP	N3-C2-N1	-3.16	123.80	128.58
11	G	601	ADP	N3-C2-N1	-3.13	123.84	128.58
11	B	601	ADP	C4-N9-C8	2.79	108.67	105.74
11	a	601	ADP	C4-N9-C8	2.78	108.65	105.74
11	b	601	ADP	C4-N9-C8	2.75	108.62	105.74
11	E	601	ADP	C4-N9-C8	2.72	108.59	105.74
11	G	601	ADP	C4-N9-C8	2.72	108.59	105.74
11	h	601	ADP	C4-N9-C8	2.71	108.58	105.74
11	g	601	ADP	C4-N9-C8	2.70	108.58	105.74
11	A	601	ADP	C4-N9-C8	2.67	108.55	105.74
11	q	601	ADP	C4-N9-C8	2.67	108.54	105.74
11	G	601	ADP	C5-N7-C8	2.67	107.64	103.45
11	Q	601	ADP	C5-N7-C8	2.66	107.63	103.45
11	D	601	ADP	C4-N9-C8	2.65	108.52	105.74
11	Q	601	ADP	C4-N9-C8	2.65	108.52	105.74
11	e	601	ADP	C4-N9-C8	2.63	108.50	105.74
11	Z	601	ADP	C4-N9-C8	2.61	108.48	105.74
11	z	601	ADP	C4-N9-C8	2.61	108.48	105.74
11	Z	601	ADP	C5-N7-C8	2.60	107.54	103.45
11	h	601	ADP	C5-N7-C8	2.60	107.53	103.45
11	A	601	ADP	C5-N7-C8	2.59	107.51	103.45
11	H	601	ADP	C4-N9-C8	2.59	108.45	105.74
11	H	601	ADP	C5-N7-C8	2.57	107.50	103.45
11	b	601	ADP	C5-N7-C8	2.56	107.47	103.45
11	a	601	ADP	C5-N7-C8	2.55	107.45	103.45
11	D	601	ADP	C5-N7-C8	2.55	107.45	103.45
11	q	601	ADP	C5-N7-C8	2.54	107.44	103.45
11	g	601	ADP	C5-N7-C8	2.52	107.41	103.45
11	d	601	ADP	C5-N7-C8	2.51	107.40	103.45
11	B	601	ADP	C5-N7-C8	2.51	107.39	103.45
11	E	601	ADP	C5-N7-C8	2.51	107.39	103.45
11	d	601	ADP	C4-N9-C8	2.50	108.36	105.74
11	e	601	ADP	C5-N7-C8	2.47	107.33	103.45
11	z	601	ADP	C5-N7-C8	2.46	107.31	103.45
11	Z	601	ADP	O4'-C1'-N9	2.44	112.77	108.09
11	d	601	ADP	C3'-C2'-C1'	2.43	106.07	101.46
11	b	601	ADP	C3'-C2'-C1'	2.35	105.90	101.46
11	B	601	ADP	C3'-C2'-C1'	2.27	105.75	101.46
11	Q	601	ADP	O4'-C1'-N9	2.26	112.42	108.09
11	z	601	ADP	C3'-C2'-C1'	2.24	105.71	101.46

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	e	601	ADP	C3'-C2'-C1'	2.20	105.62	101.46
11	B	601	ADP	C6-C5-N7	2.20	136.32	132.09
11	G	601	ADP	C6-C5-N7	2.19	136.31	132.09
11	Z	601	ADP	C6-C5-N7	2.19	136.31	132.09
11	Q	601	ADP	C6-C5-N7	2.18	136.30	132.09
11	A	601	ADP	C6-C5-N7	2.18	136.28	132.09
11	g	601	ADP	C6-C5-N7	2.15	136.23	132.09
11	H	601	ADP	C6-C5-N7	2.15	136.23	132.09
11	G	601	ADP	N9-C8-N7	-2.14	110.90	113.94
11	h	601	ADP	C6-C5-N7	2.14	136.21	132.09
11	D	601	ADP	C6-C5-N7	2.13	136.20	132.09
11	a	601	ADP	C6-C5-N7	2.11	136.17	132.09
11	q	601	ADP	C6-C5-N7	2.11	136.16	132.09
11	a	601	ADP	C3'-C2'-C1'	2.11	105.45	101.46
11	b	601	ADP	C6-C5-N7	2.11	136.15	132.09
11	d	601	ADP	C6-C5-N7	2.11	136.15	132.09
11	Q	601	ADP	N9-C8-N7	-2.10	110.96	113.94
11	e	601	ADP	C6-C5-N7	2.09	136.13	132.09
11	b	601	ADP	N9-C8-N7	-2.09	110.97	113.94
11	h	601	ADP	N9-C8-N7	-2.09	110.97	113.94
11	a	601	ADP	N9-C8-N7	-2.08	110.98	113.94
11	A	601	ADP	N9-C8-N7	-2.08	110.99	113.94
11	B	601	ADP	N9-C8-N7	-2.07	111.00	113.94
11	Z	601	ADP	N9-C8-N7	-2.06	111.02	113.94
11	h	601	ADP	C3'-C2'-C1'	2.05	105.35	101.46
11	E	601	ADP	C3'-C2'-C1'	2.05	105.34	101.46
11	q	601	ADP	C3'-C2'-C1'	2.05	105.33	101.46
11	g	601	ADP	C3'-C2'-C1'	2.04	105.33	101.46
11	g	601	ADP	N9-C8-N7	-2.04	111.04	113.94
11	E	601	ADP	C6-C5-N7	2.04	136.03	132.09
11	H	601	ADP	C3'-C2'-C1'	2.04	105.32	101.46
11	D	601	ADP	N9-C8-N7	-2.04	111.05	113.94
11	q	601	ADP	N9-C8-N7	-2.03	111.05	113.94
11	A	601	ADP	O4'-C1'-N9	2.01	111.96	108.09
11	H	601	ADP	N9-C8-N7	-2.01	111.08	113.94
11	z	601	ADP	C6-C5-N7	2.01	135.97	132.09
11	E	601	ADP	N9-C8-N7	-2.01	111.08	113.94

There are no chirality outliers.

All (60) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	G	601	ADP	C5'-O5'-PA-O2A
11	G	601	ADP	O4'-C4'-C5'-O5'
11	Q	601	ADP	C5'-O5'-PA-O1A
11	Z	601	ADP	C5'-O5'-PA-O1A
11	Z	601	ADP	C5'-O5'-PA-O2A
11	Z	601	ADP	C5'-O5'-PA-O3A
11	Z	601	ADP	O4'-C4'-C5'-O5'
11	a	601	ADP	C5'-O5'-PA-O1A
11	a	601	ADP	C5'-O5'-PA-O2A
11	a	601	ADP	C5'-O5'-PA-O3A
11	b	601	ADP	PA-O3A-PB-O3B
11	b	601	ADP	C5'-O5'-PA-O1A
11	d	601	ADP	C5'-O5'-PA-O2A
11	d	601	ADP	C5'-O5'-PA-O3A
11	e	601	ADP	PA-O3A-PB-O3B
11	e	601	ADP	C5'-O5'-PA-O1A
11	e	601	ADP	C5'-O5'-PA-O3A
11	h	601	ADP	PA-O3A-PB-O3B
11	h	601	ADP	C5'-O5'-PA-O1A
11	h	601	ADP	C5'-O5'-PA-O2A
11	h	601	ADP	C5'-O5'-PA-O3A
11	q	601	ADP	C5'-O5'-PA-O2A
11	z	601	ADP	C5'-O5'-PA-O2A
11	G	601	ADP	C3'-C4'-C5'-O5'
11	Q	601	ADP	O4'-C4'-C5'-O5'
11	Q	601	ADP	C3'-C4'-C5'-O5'
11	b	601	ADP	O4'-C4'-C5'-O5'
11	b	601	ADP	C3'-C4'-C5'-O5'
11	h	601	ADP	O4'-C4'-C5'-O5'
11	h	601	ADP	C3'-C4'-C5'-O5'
11	Z	601	ADP	C3'-C4'-C5'-O5'
11	q	601	ADP	C3'-C4'-C5'-O5'
11	z	601	ADP	C3'-C4'-C5'-O5'
11	b	601	ADP	PA-O3A-PB-O1B
11	B	601	ADP	PB-O3A-PA-O5'
11	D	601	ADP	PB-O3A-PA-O5'
11	H	601	ADP	PB-O3A-PA-O5'
11	A	601	ADP	O4'-C4'-C5'-O5'
11	e	601	ADP	O4'-C4'-C5'-O5'
11	G	601	ADP	C5'-O5'-PA-O1A
11	G	601	ADP	C5'-O5'-PA-O3A
11	Q	601	ADP	C5'-O5'-PA-O2A
11	Q	601	ADP	C5'-O5'-PA-O3A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
11	e	601	ADP	C5'-O5'-PA-O2A
11	q	601	ADP	C5'-O5'-PA-O1A
11	q	601	ADP	C5'-O5'-PA-O3A
11	z	601	ADP	C5'-O5'-PA-O1A
11	z	601	ADP	C5'-O5'-PA-O3A
11	q	601	ADP	O4'-C4'-C5'-O5'
11	e	601	ADP	C3'-C4'-C5'-O5'
11	a	601	ADP	O4'-C4'-C5'-O5'
11	E	601	ADP	PB-O3A-PA-O5'
11	a	601	ADP	C3'-C4'-C5'-O5'
11	d	601	ADP	O4'-C4'-C5'-O5'
11	z	601	ADP	O4'-C4'-C5'-O5'
11	G	601	ADP	PB-O3A-PA-O2A
11	Z	601	ADP	PB-O3A-PA-O1A
11	Z	601	ADP	PB-O3A-PA-O2A
11	a	601	ADP	PB-O3A-PA-O2A
11	q	601	ADP	PB-O3A-PA-O1A

There are no ring outliers.

28 monomers are involved in 51 short contacts:

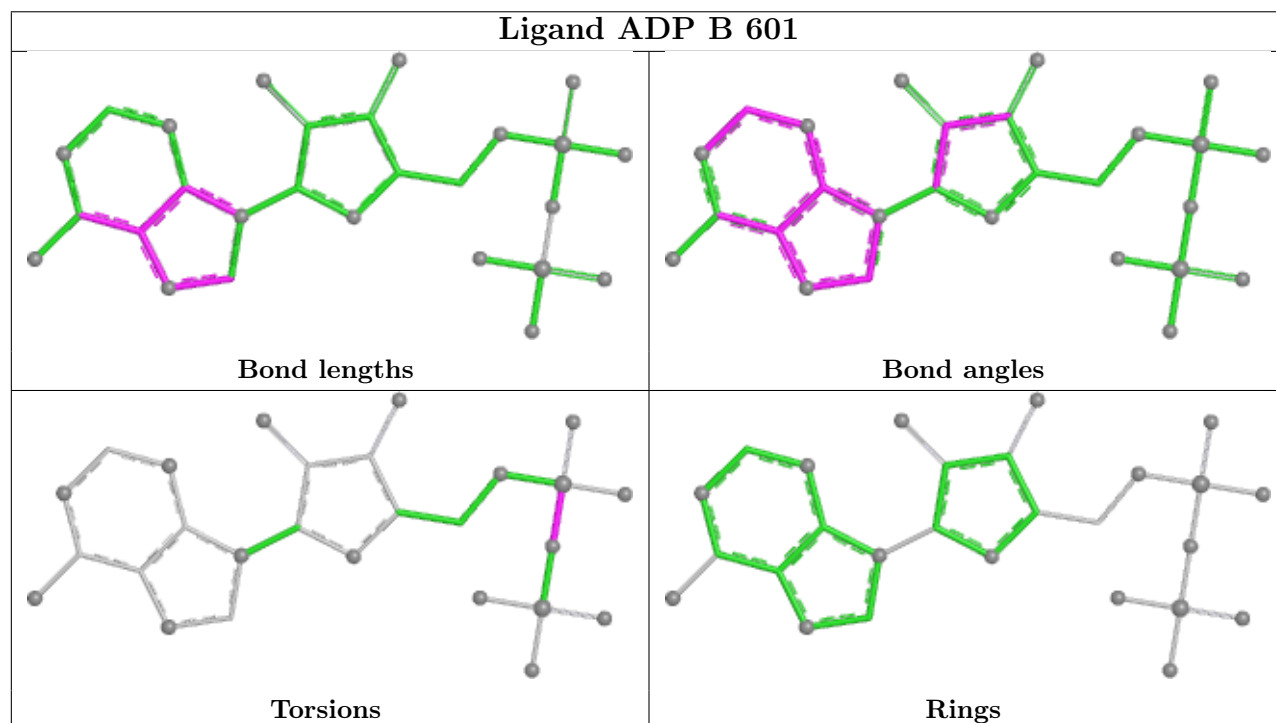
Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	B	601	ADP	2	0
11	Z	601	ADP	1	0
13	a	603	AF3	2	0
11	h	601	ADP	3	0
13	H	603	AF3	2	0
13	Q	603	AF3	2	0
11	a	601	ADP	4	0
13	h	603	AF3	3	0
13	D	603	AF3	1	0
13	z	603	AF3	3	0
13	G	603	AF3	2	0
11	d	601	ADP	1	0
13	e	603	AF3	1	0
11	z	601	ADP	2	0
11	H	601	ADP	2	0
11	e	601	ADP	3	0
11	q	601	ADP	2	0
11	g	601	ADP	4	0
13	q	603	AF3	2	0
13	d	603	AF3	1	0

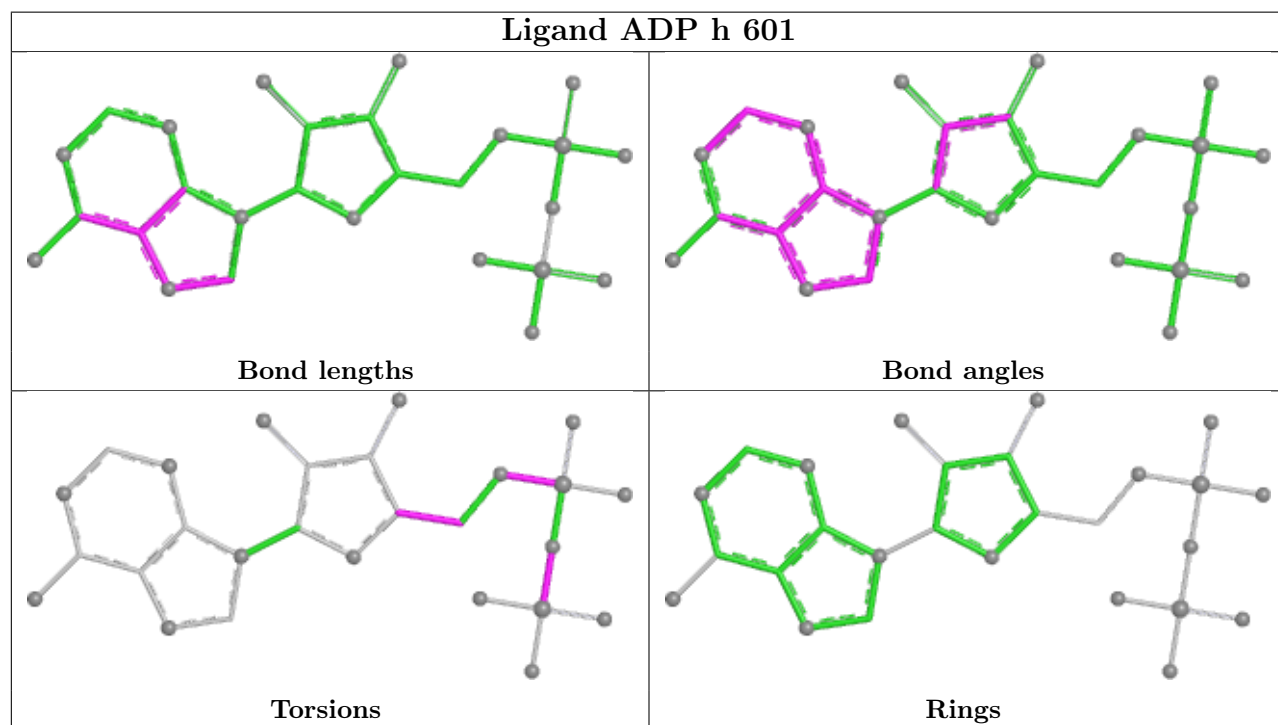
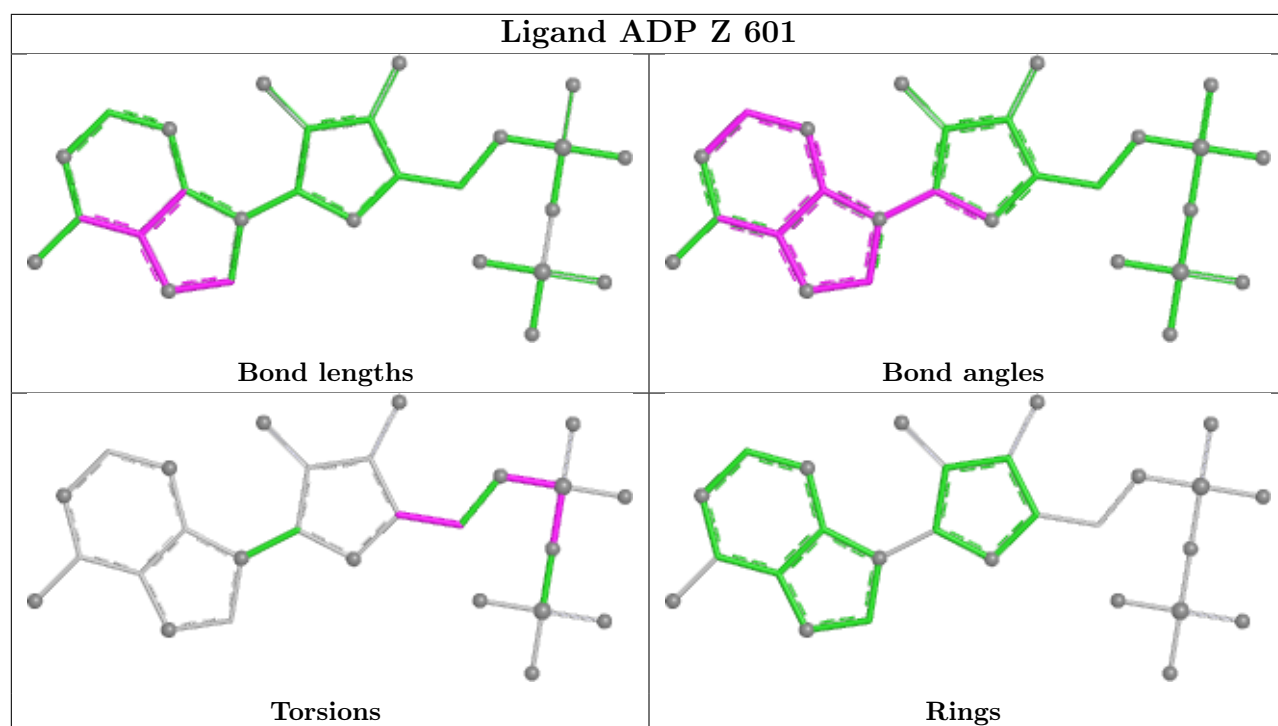
Continued on next page...

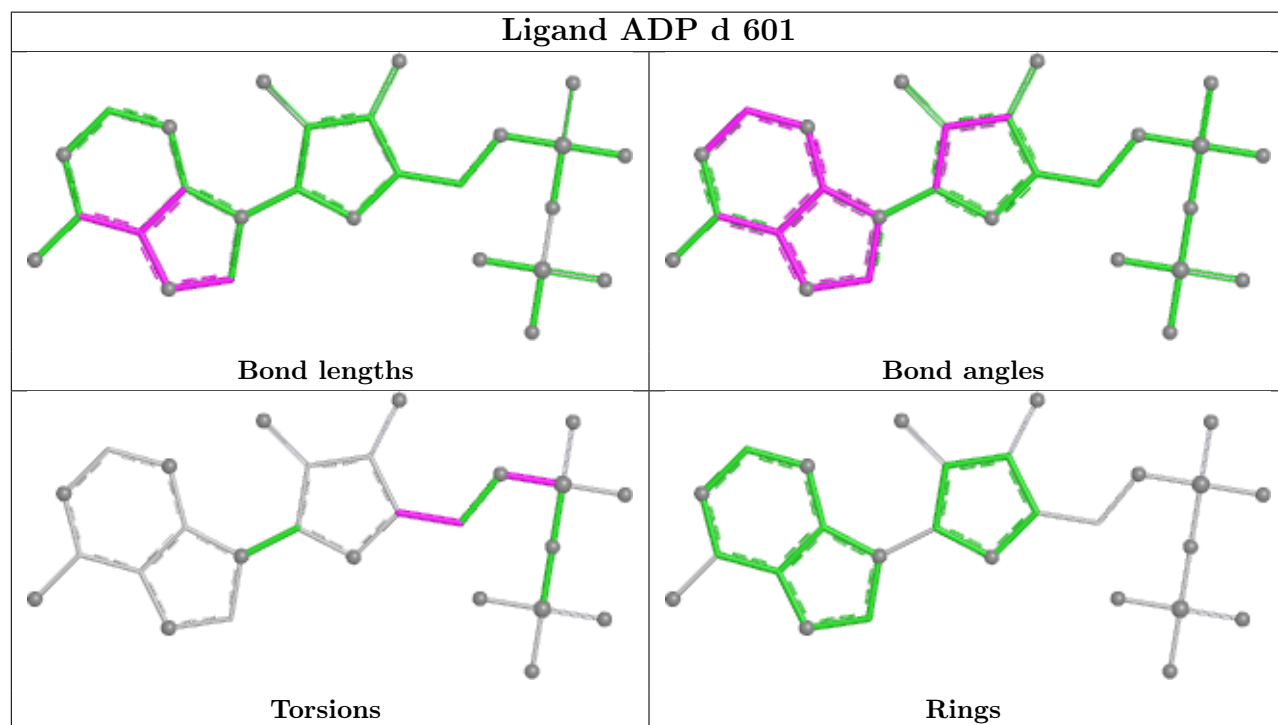
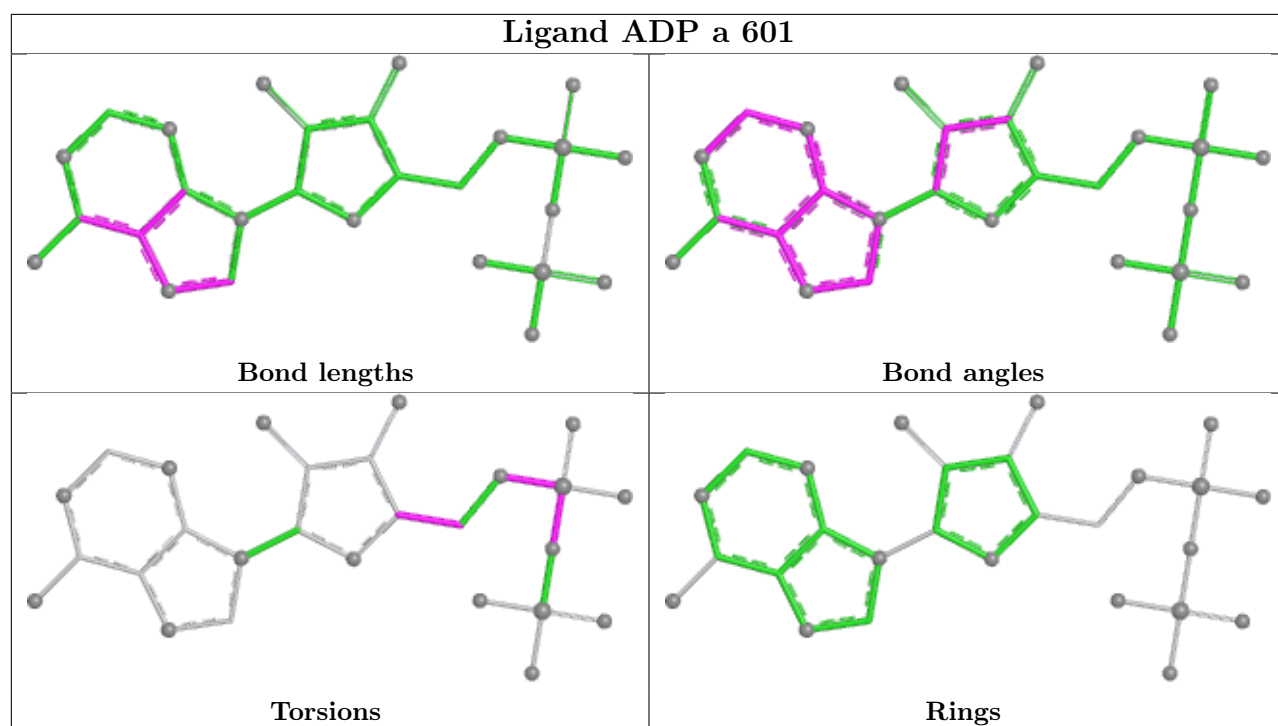
Continued from previous page...

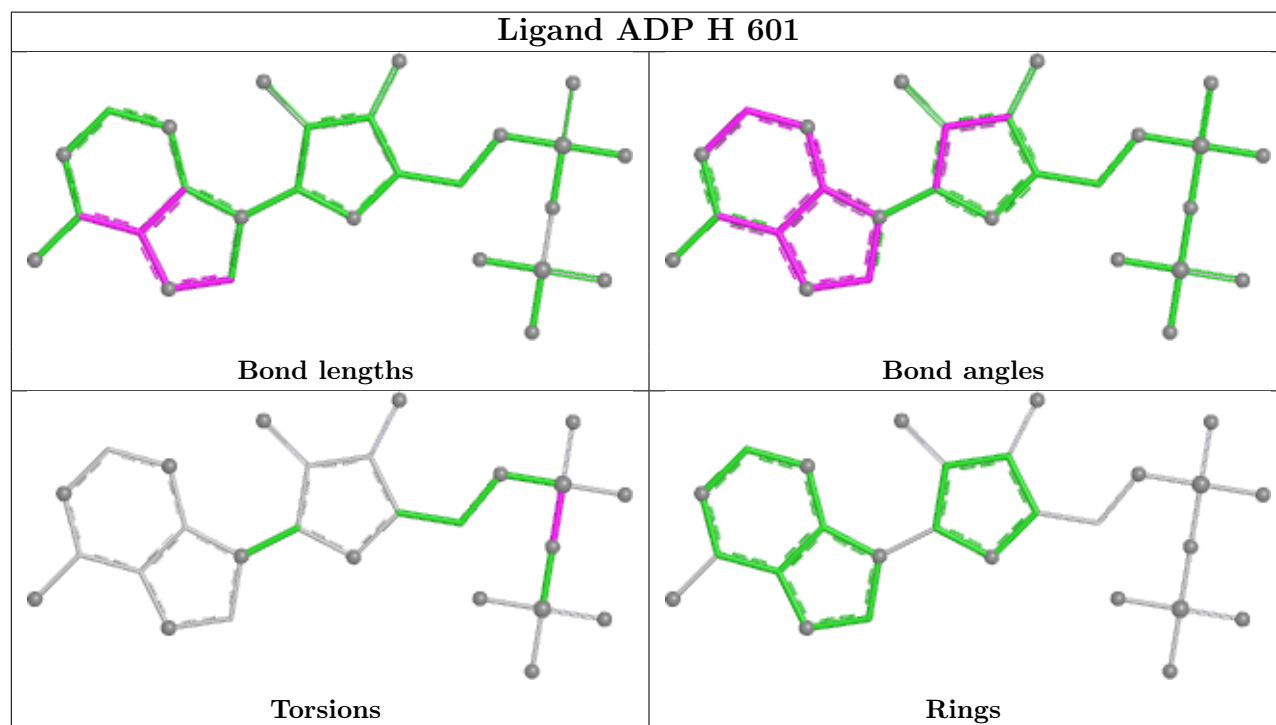
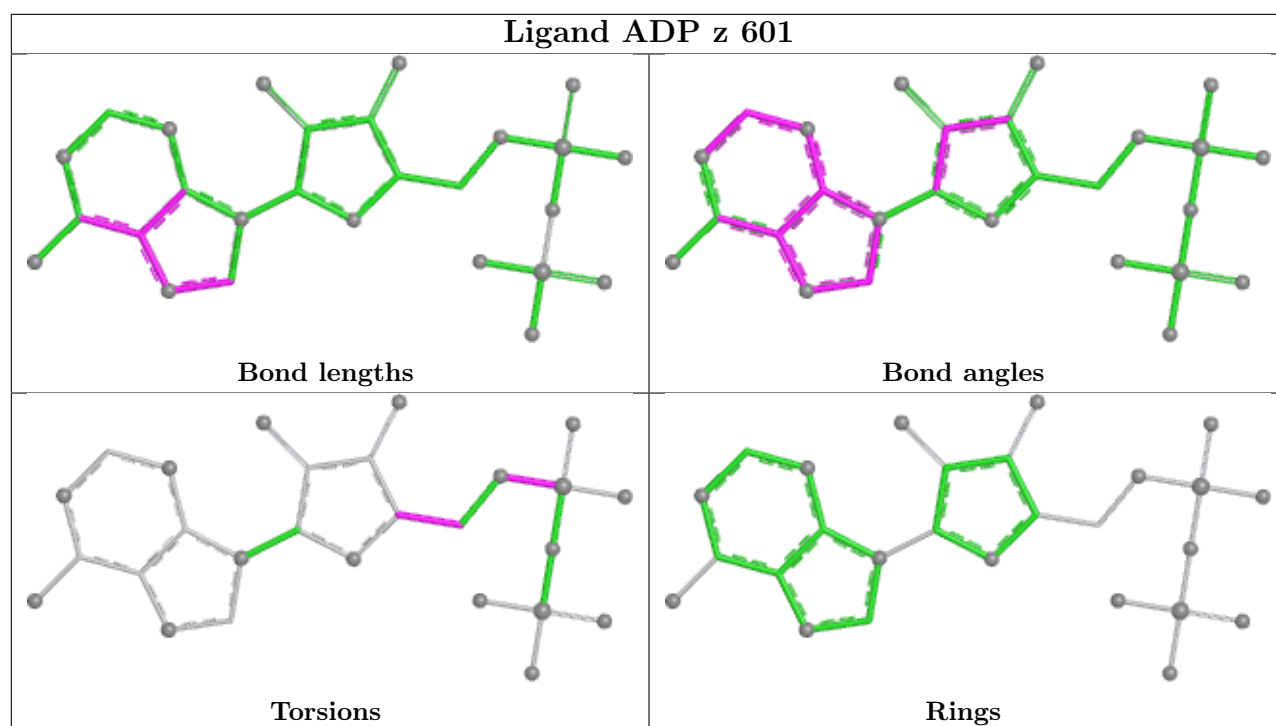
Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	g	603	AF3	4	0
11	A	601	ADP	2	0
13	b	603	AF3	1	0
11	b	601	ADP	5	0
11	Q	601	ADP	3	0
13	Z	603	AF3	3	0
13	A	603	AF3	2	0
11	G	601	ADP	2	0

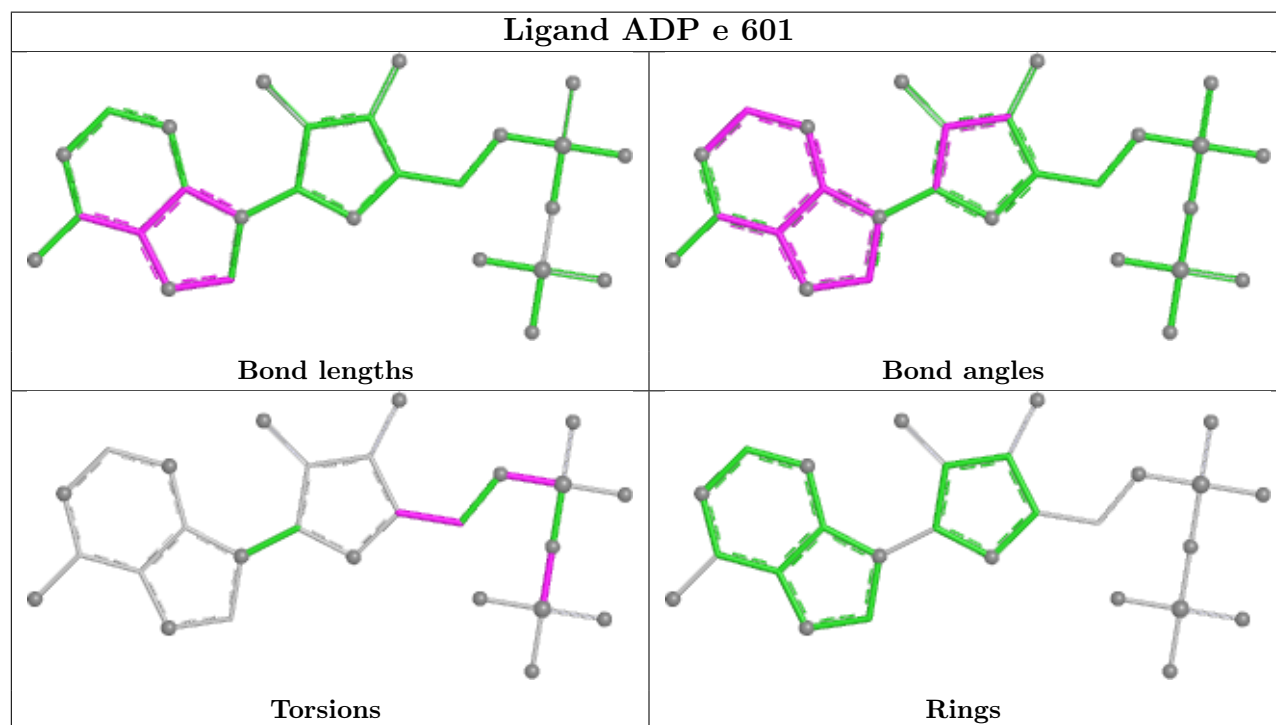
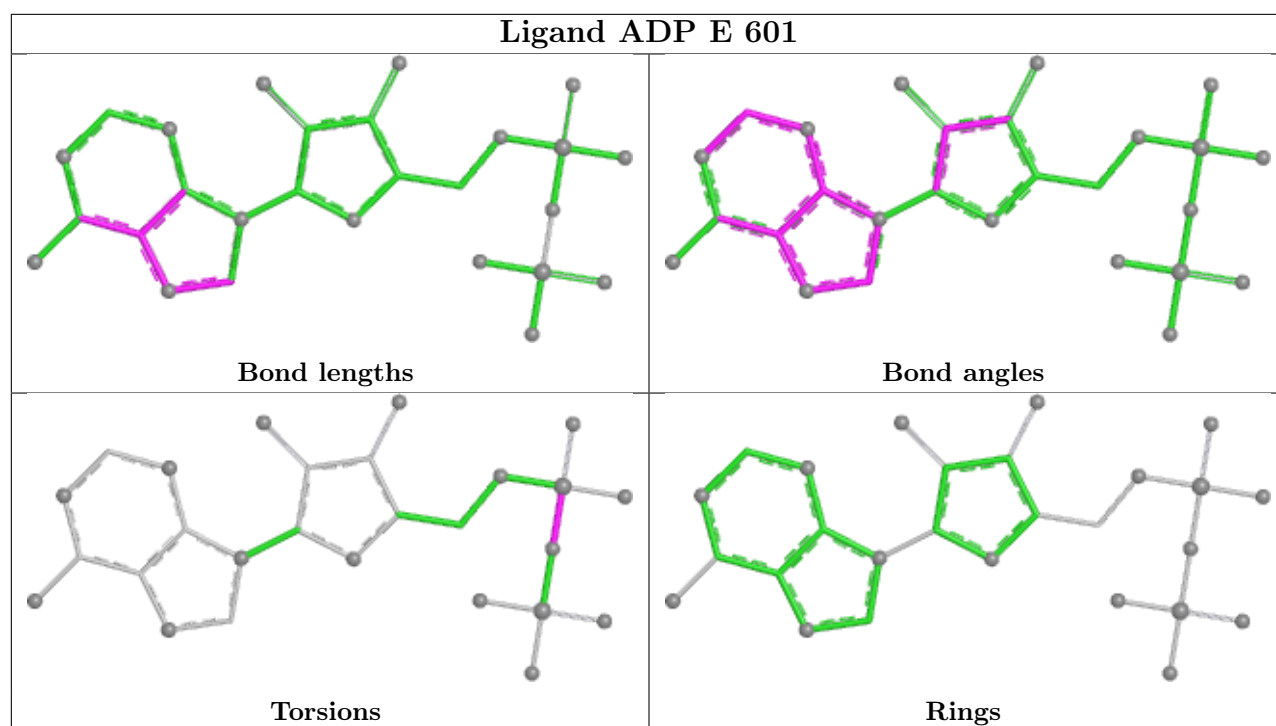
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

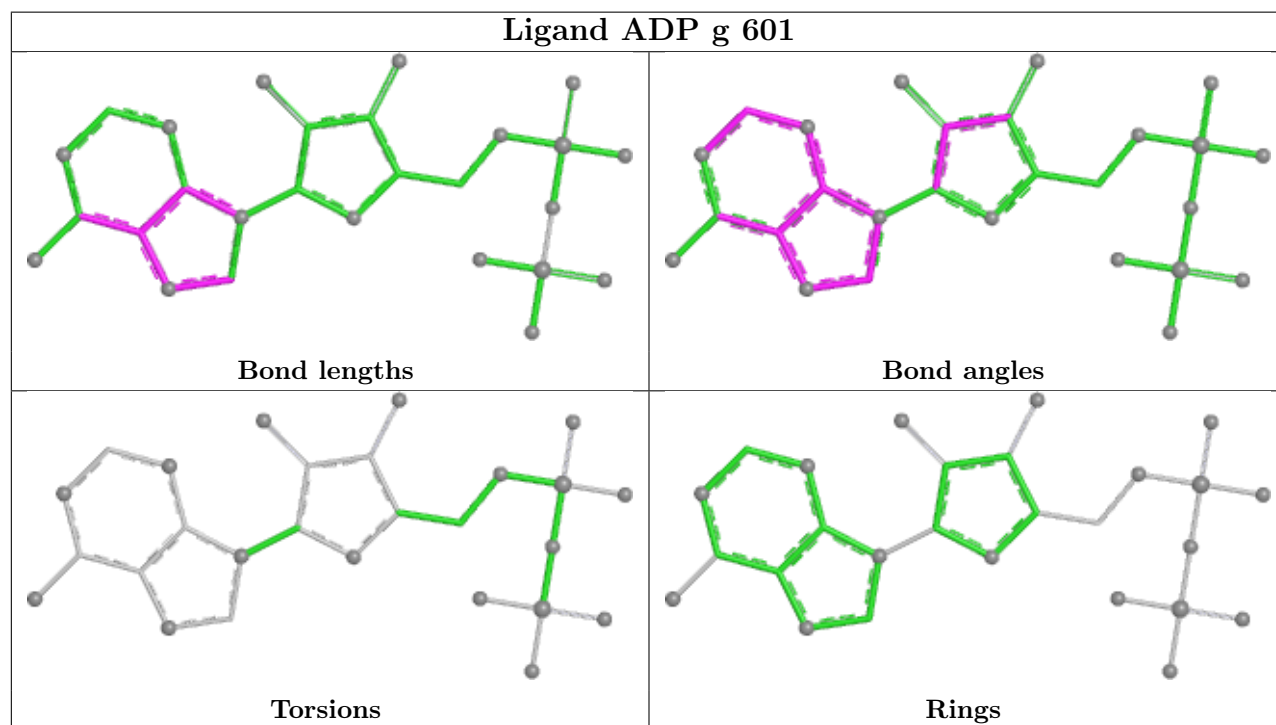
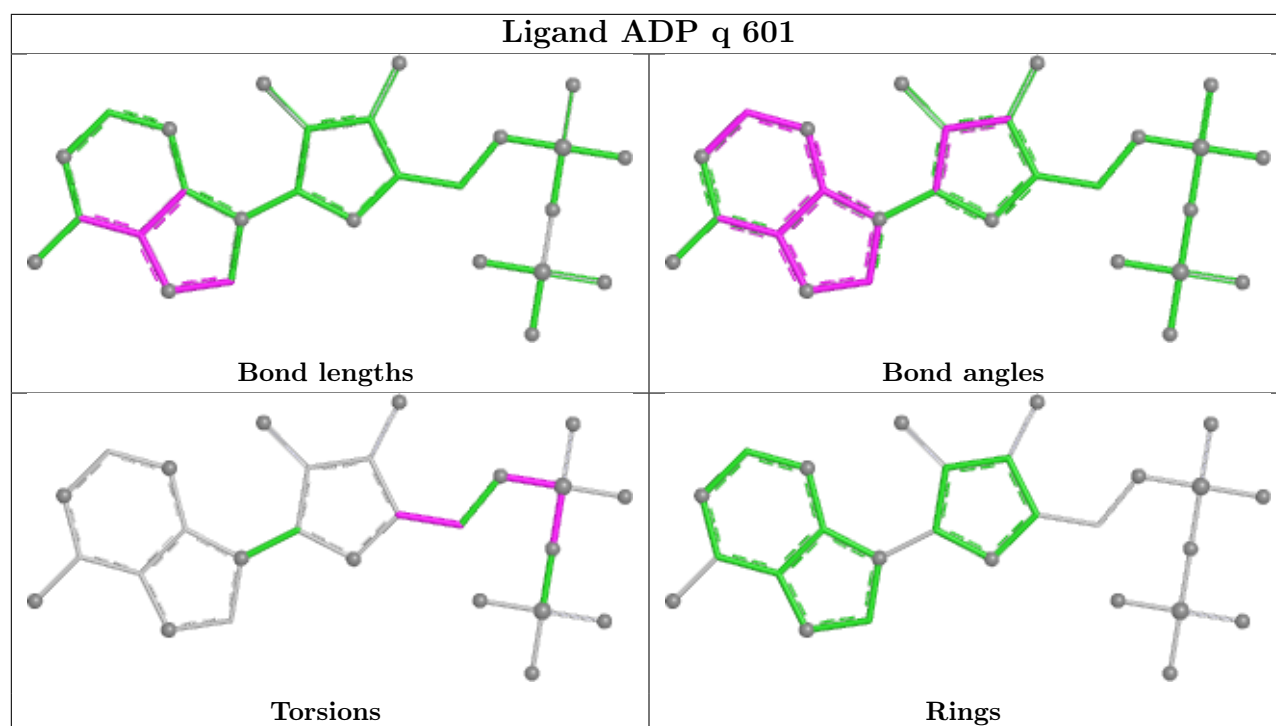


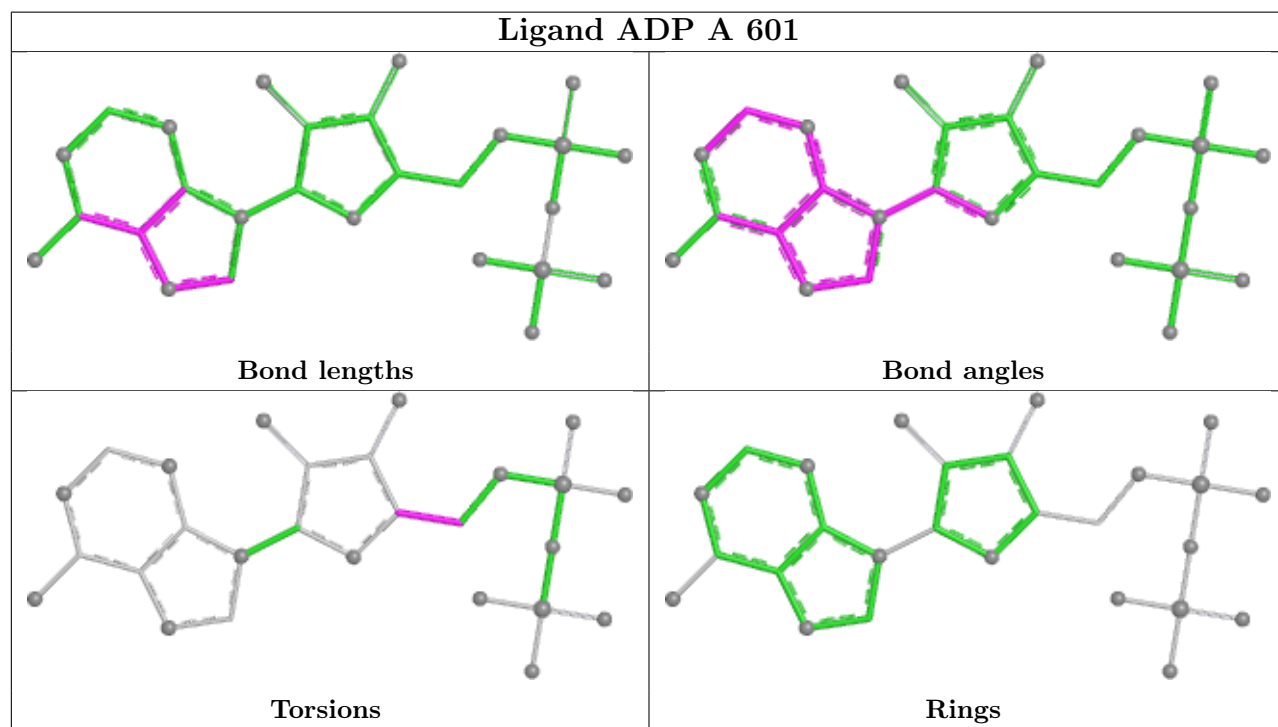
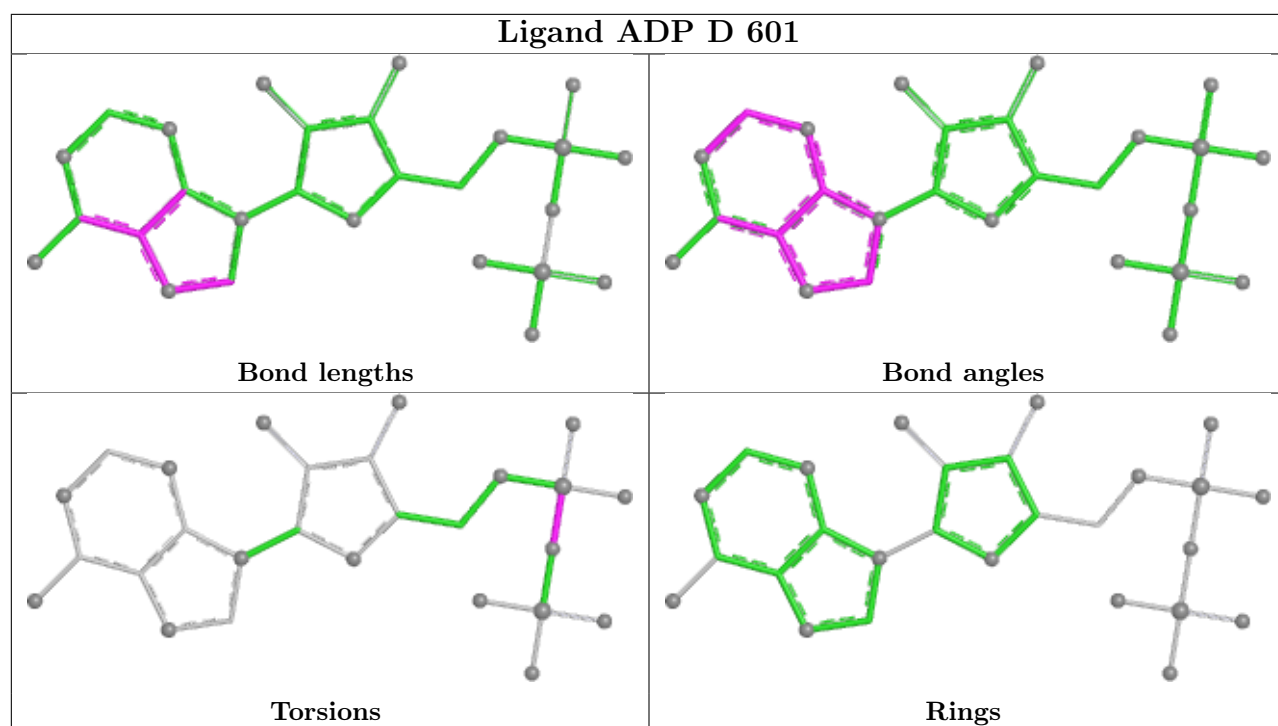


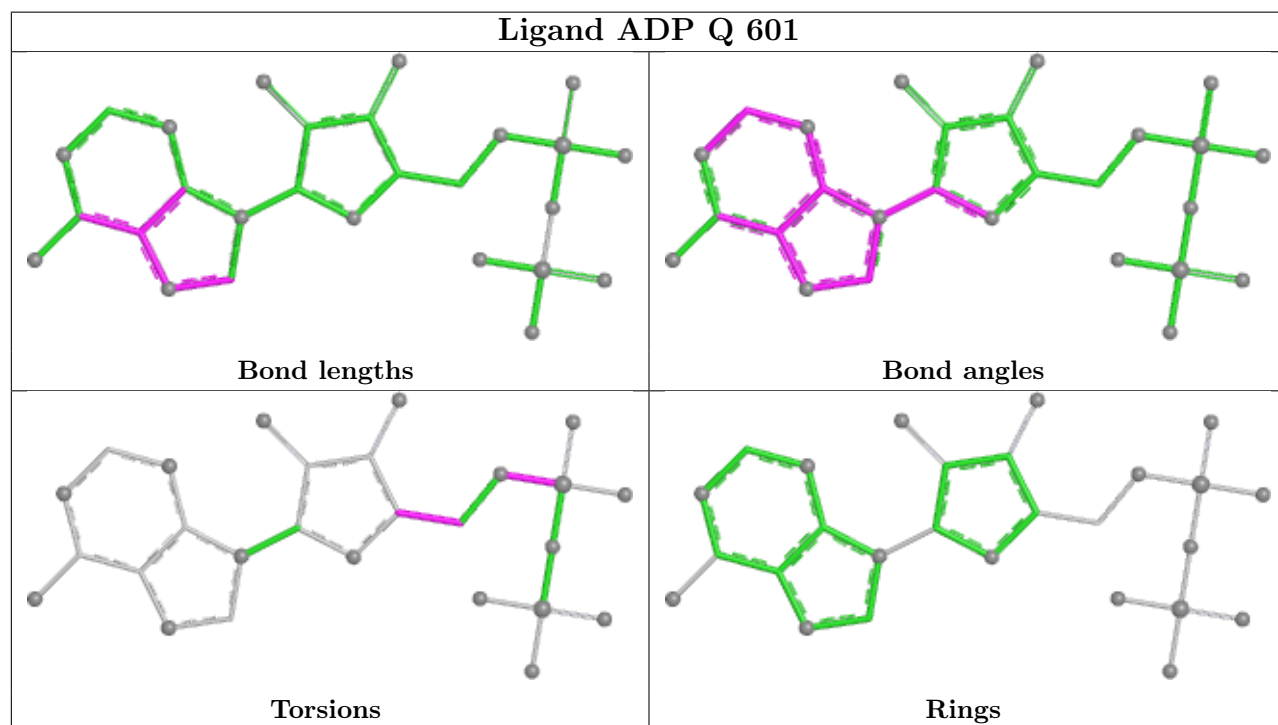
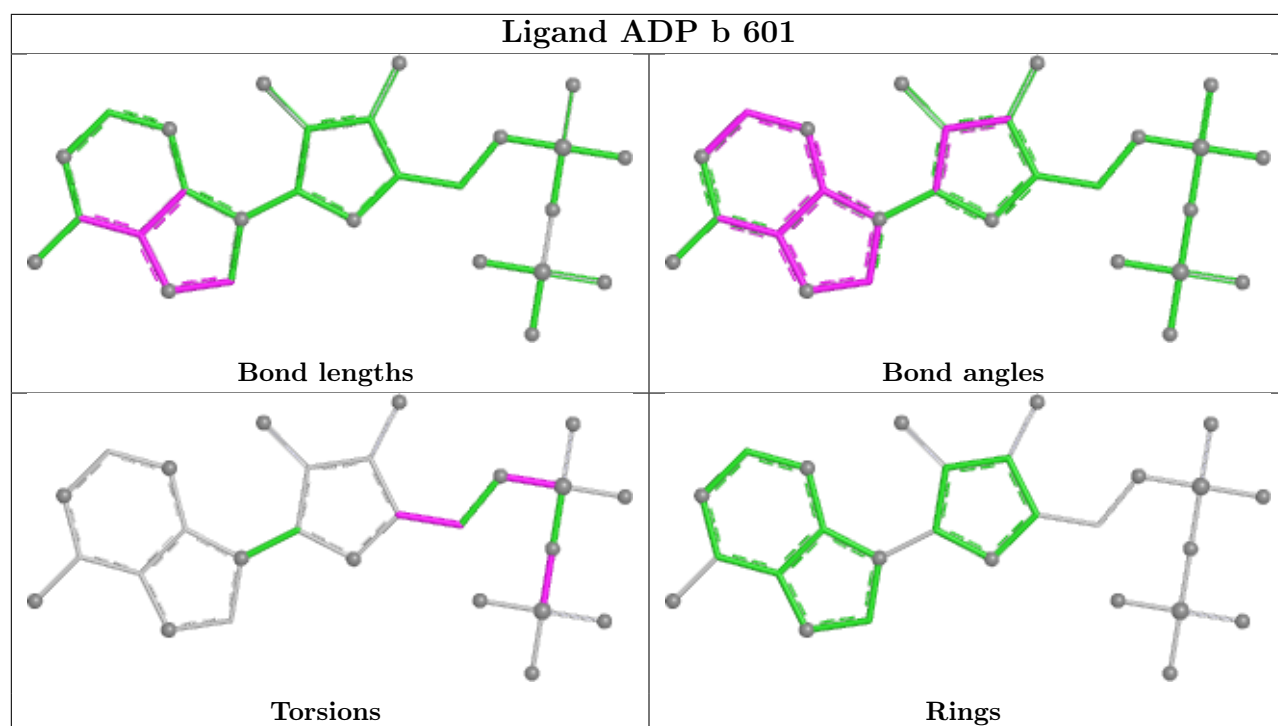


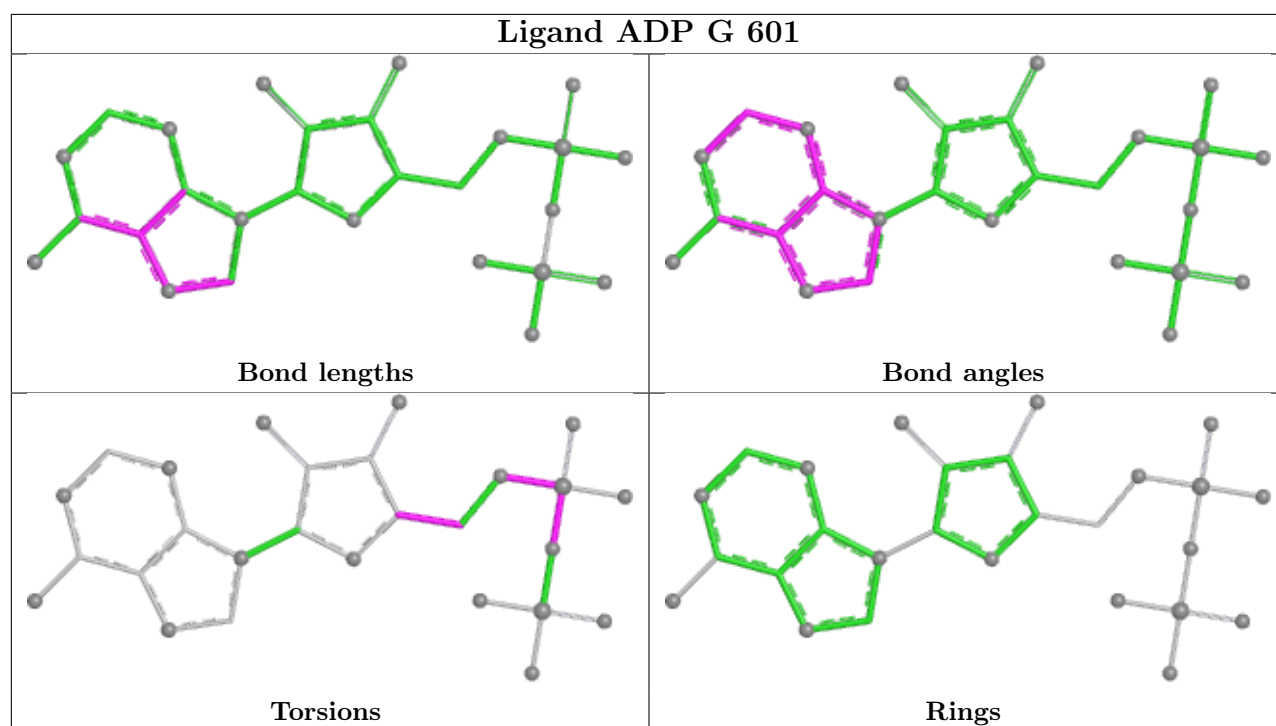












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

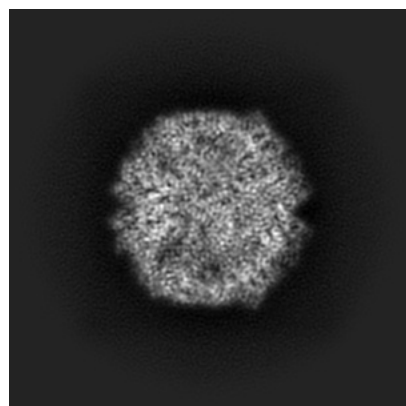
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49634. These allow visual inspection of the internal detail of the map and identification of artifacts.

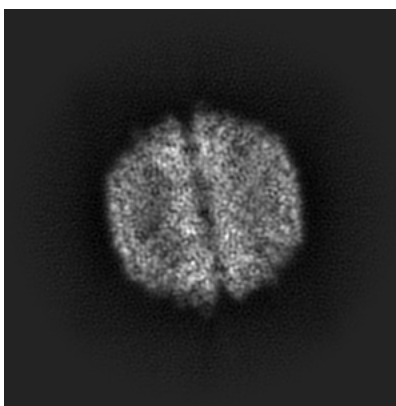
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

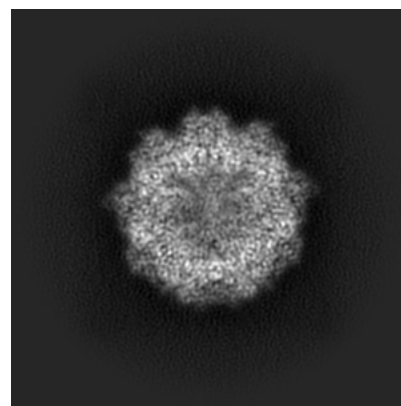
6.1.1 Primary map



X

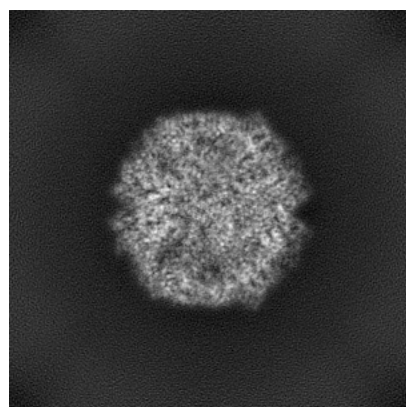


Y

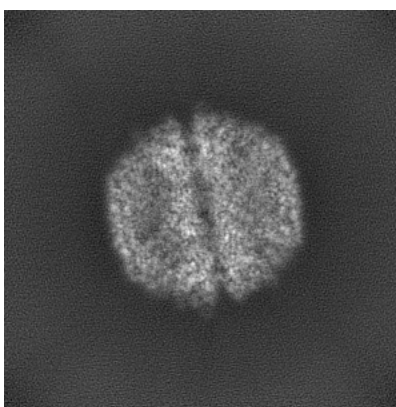


Z

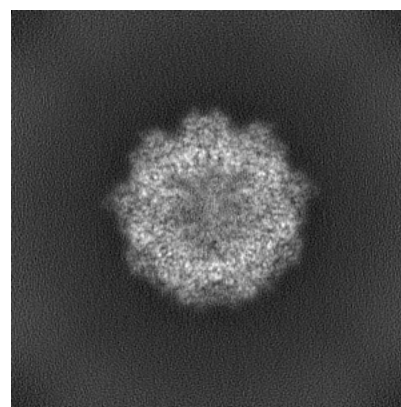
6.1.2 Raw map



X



Y

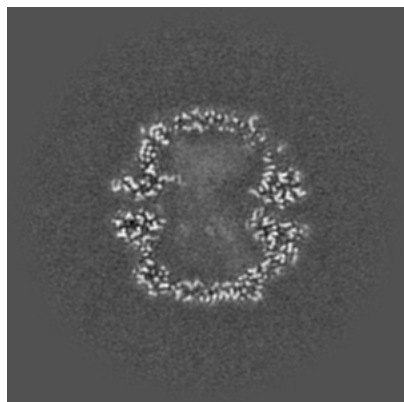


Z

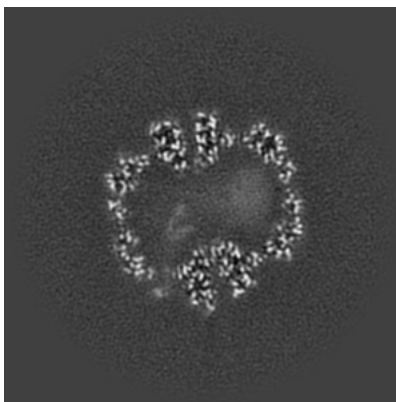
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

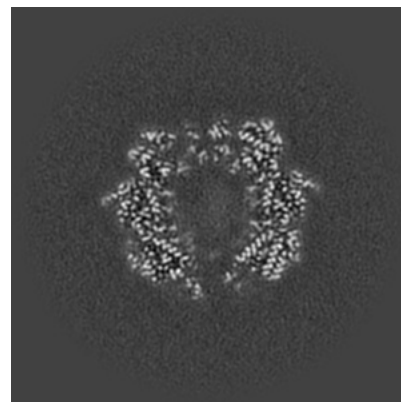
6.2.1 Primary map



X Index: 150

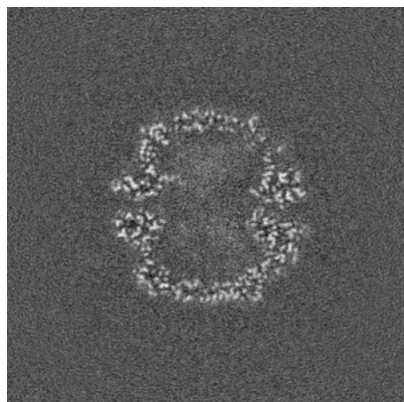


Y Index: 150

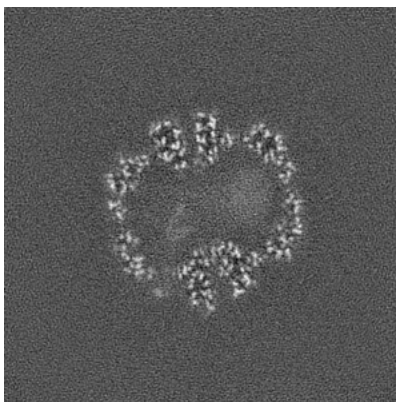


Z Index: 150

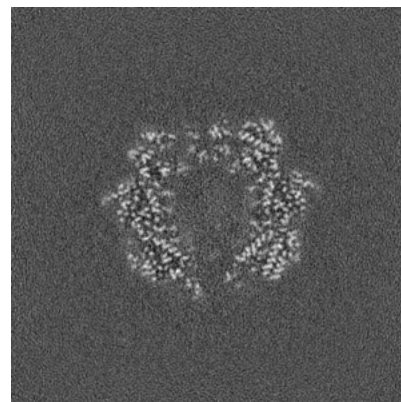
6.2.2 Raw map



X Index: 150



Y Index: 150

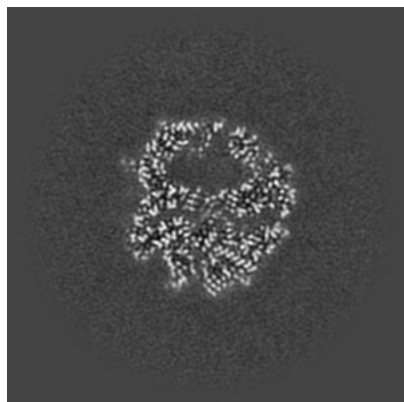


Z Index: 150

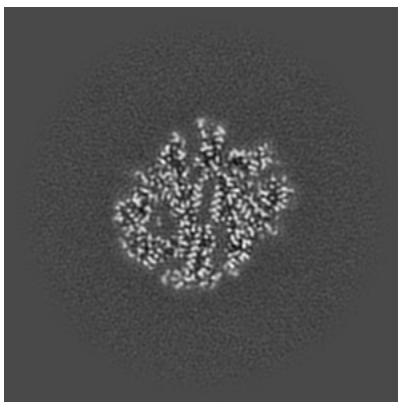
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

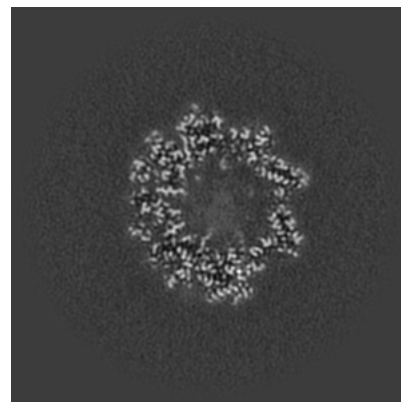
6.3.1 Primary map



X Index: 185

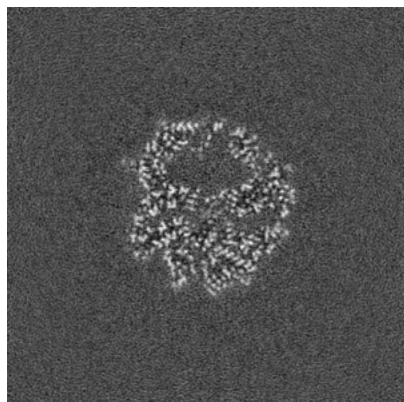


Y Index: 109

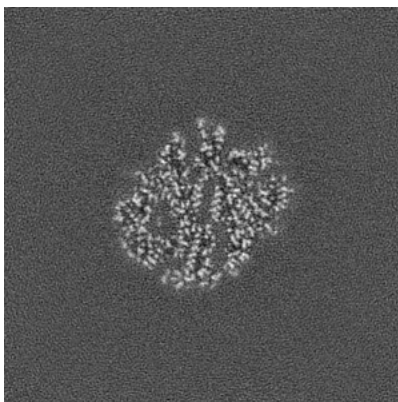


Z Index: 167

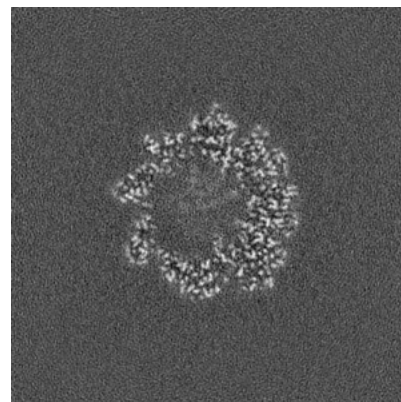
6.3.2 Raw map



X Index: 185



Y Index: 109

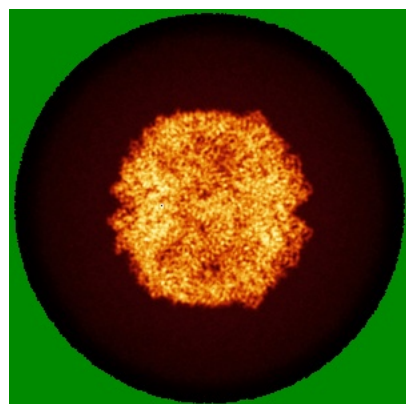


Z Index: 130

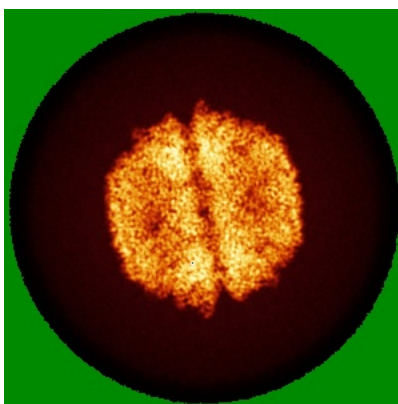
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

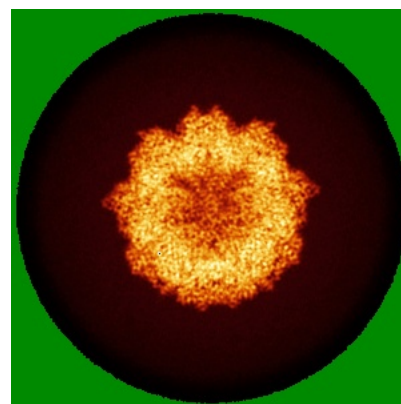
6.4.1 Primary map



X

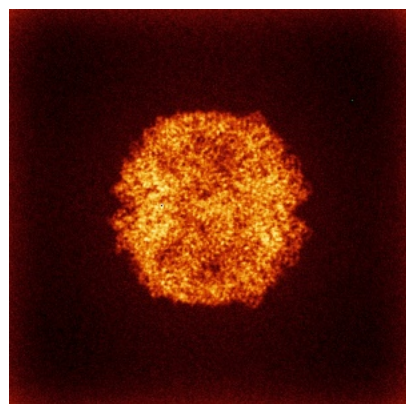


Y

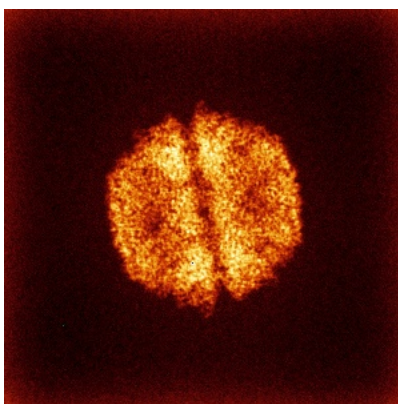


Z

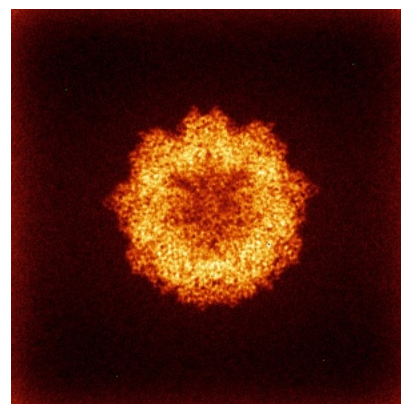
6.4.2 Raw map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



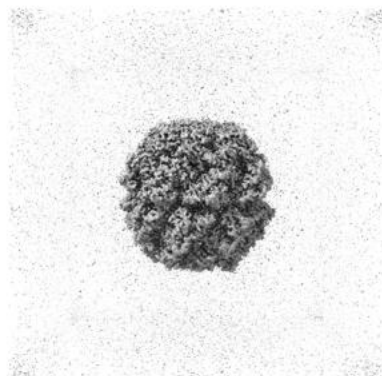
Y



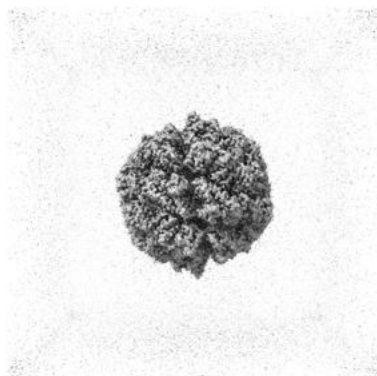
Z

The images above show the 3D surface view of the map at the recommended contour level 0.103. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

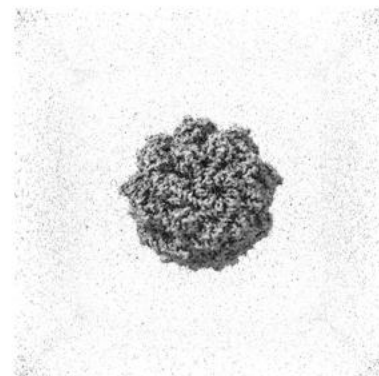
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

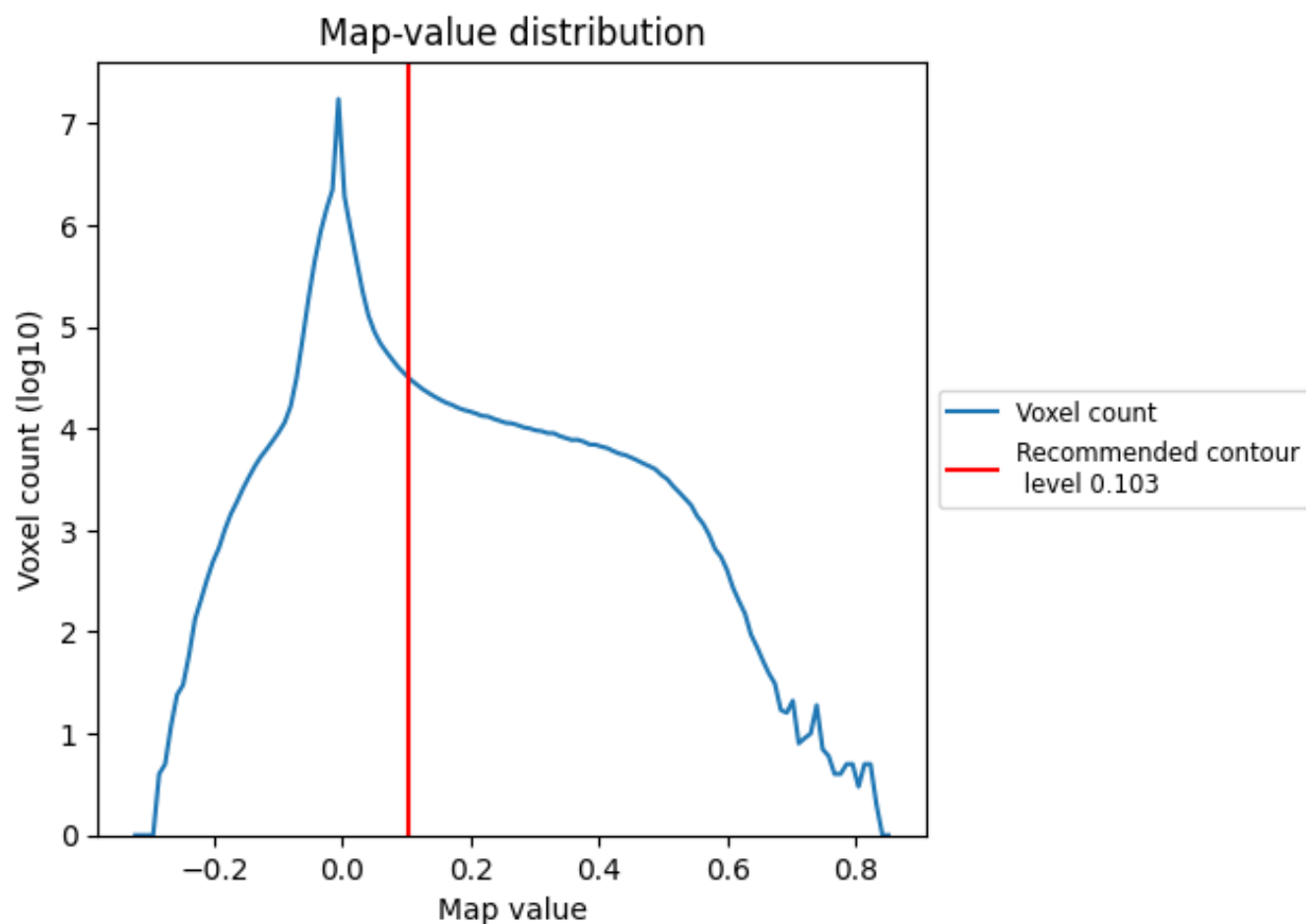
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

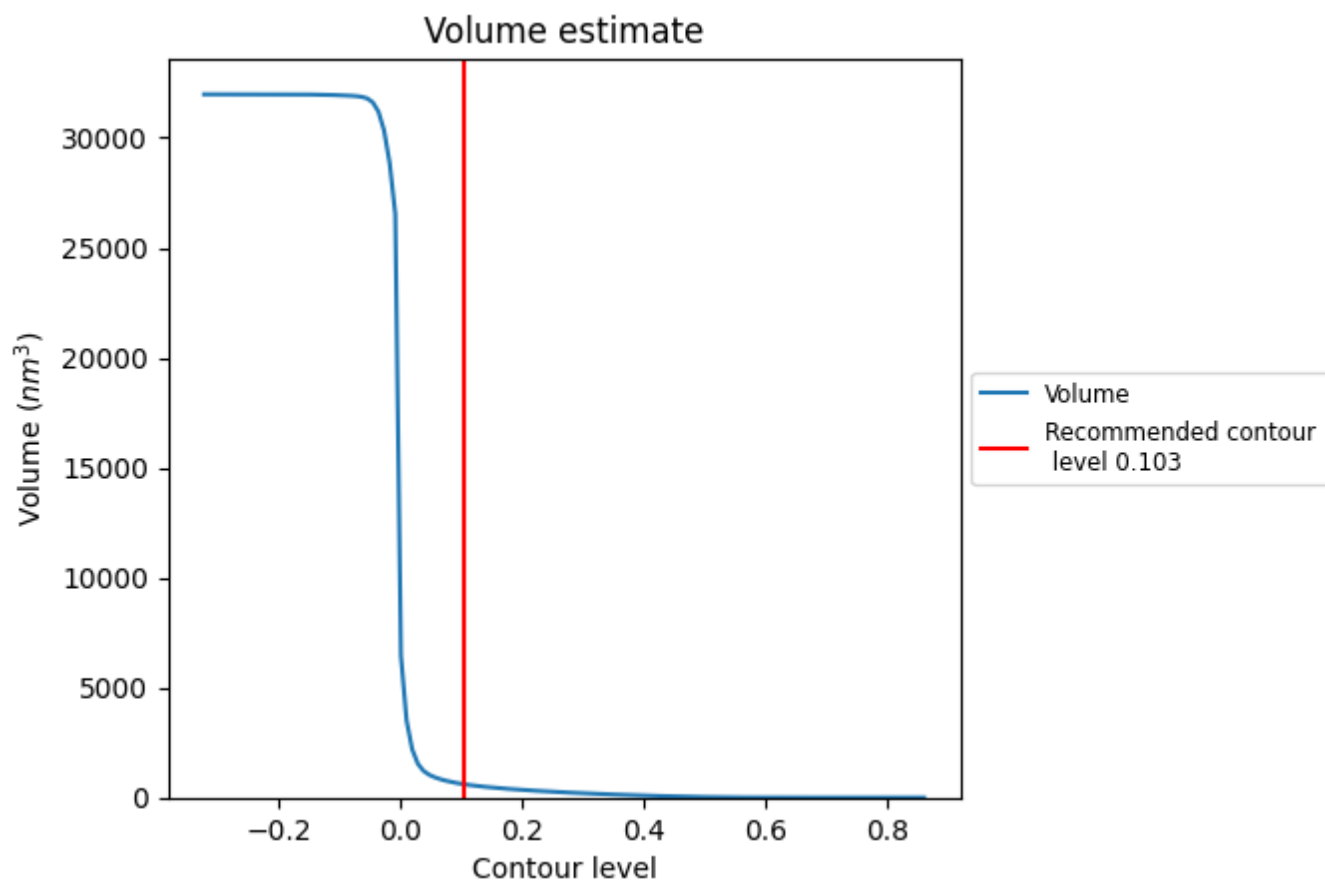
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

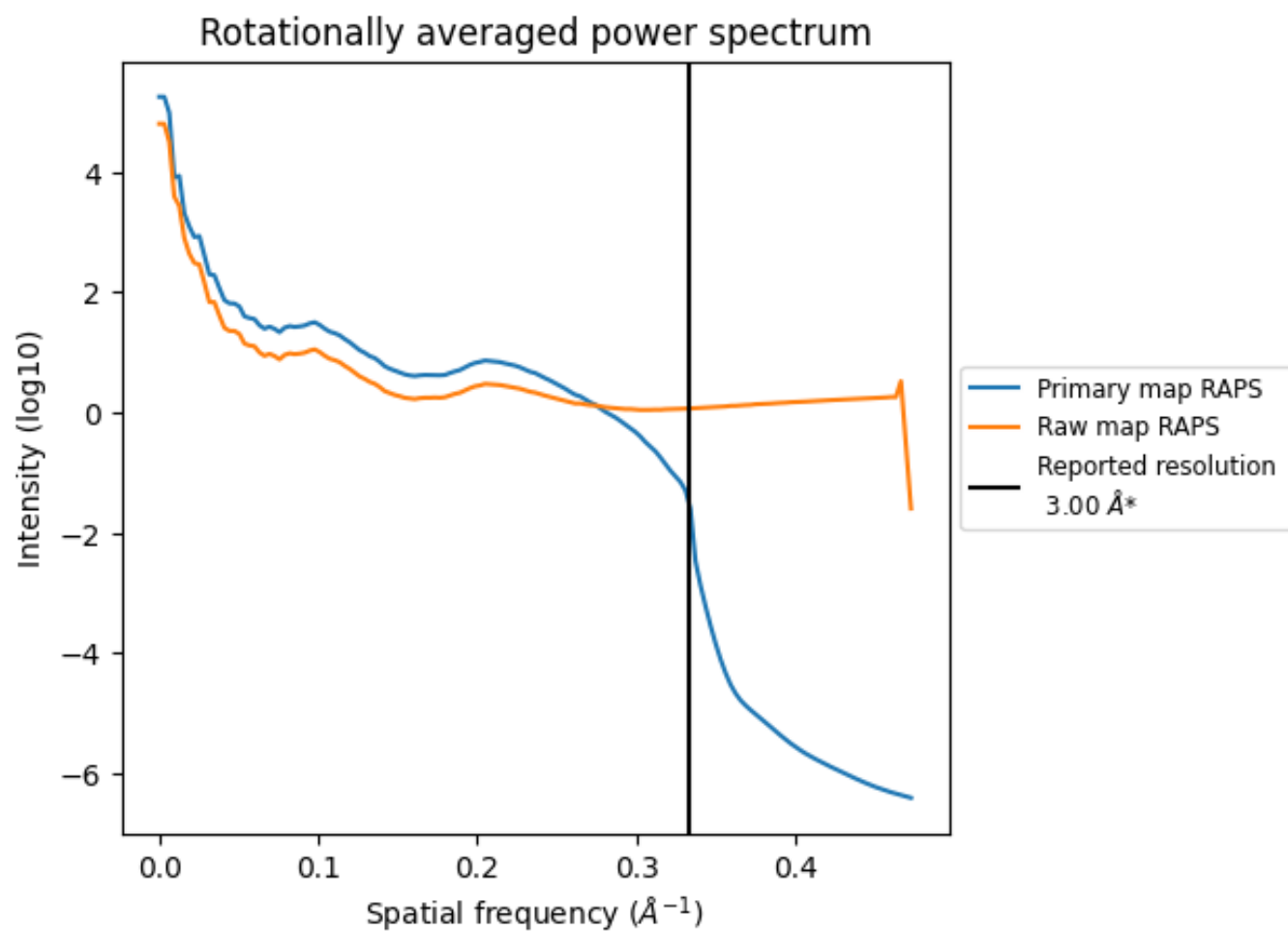
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 612 nm³; this corresponds to an approximate mass of 553 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

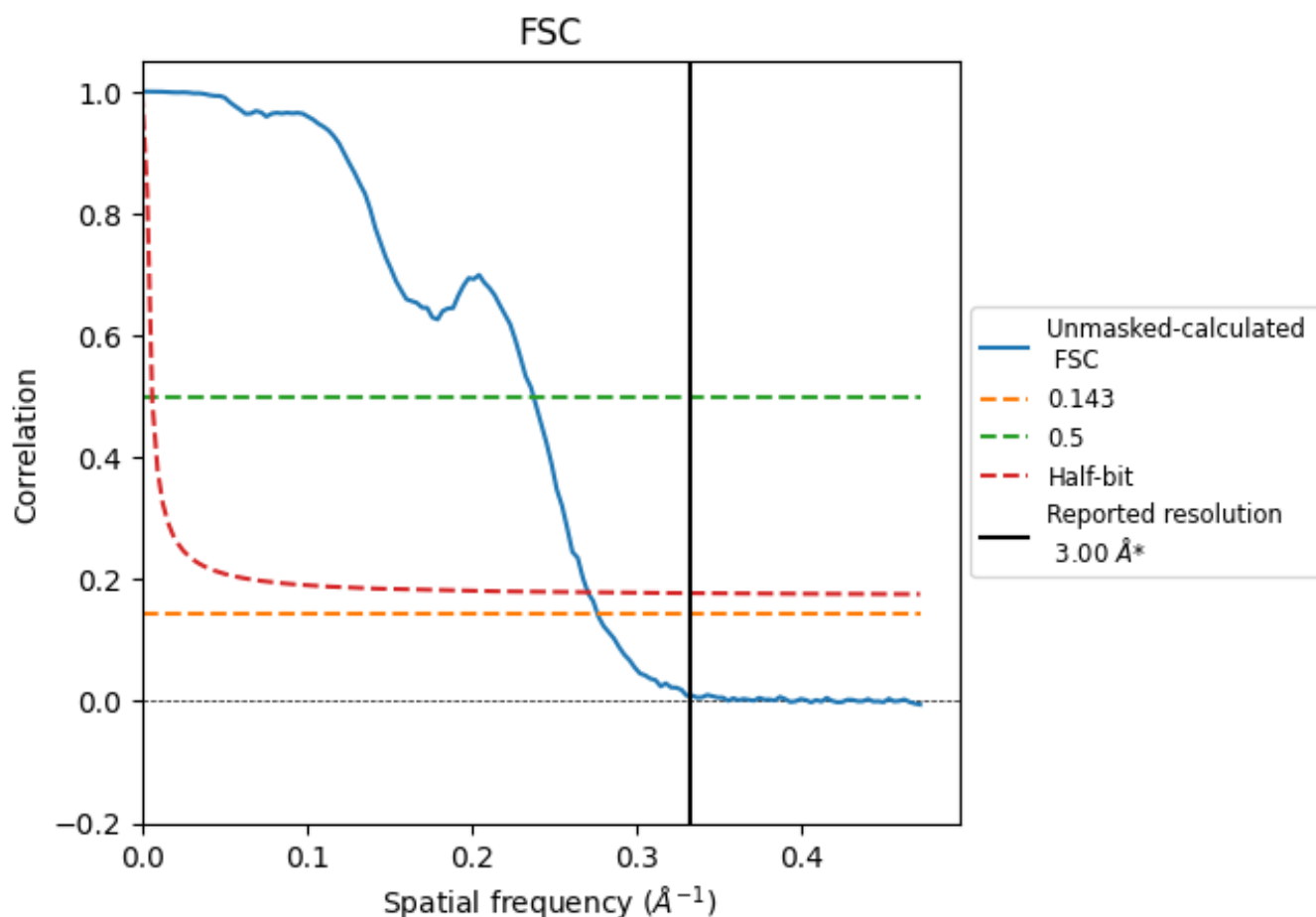


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.333 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

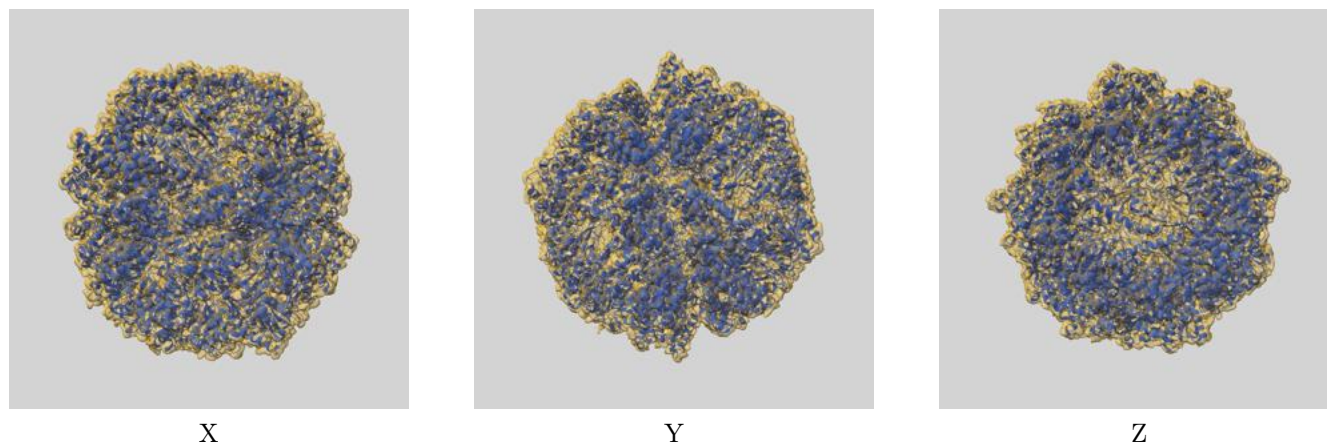
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.61	4.21	3.69

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.61 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

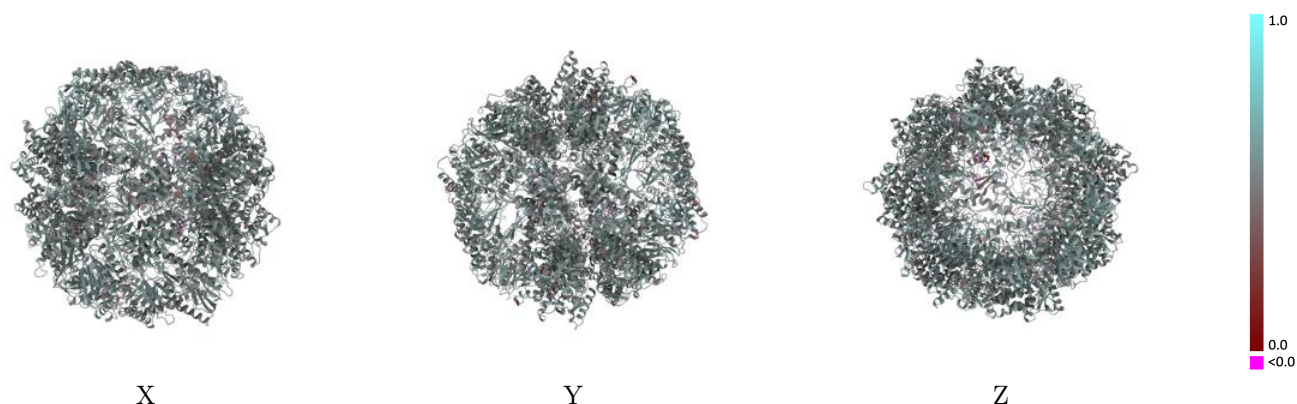
This section contains information regarding the fit between EMDB map EMD-49634 and PDB model 9NPW. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



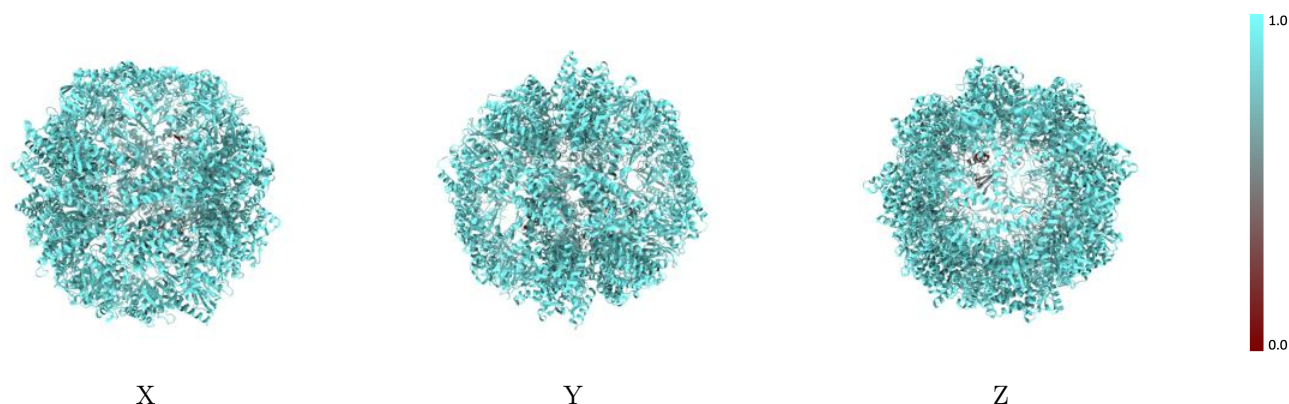
The images above show the 3D surface view of the map at the recommended contour level 0.103 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



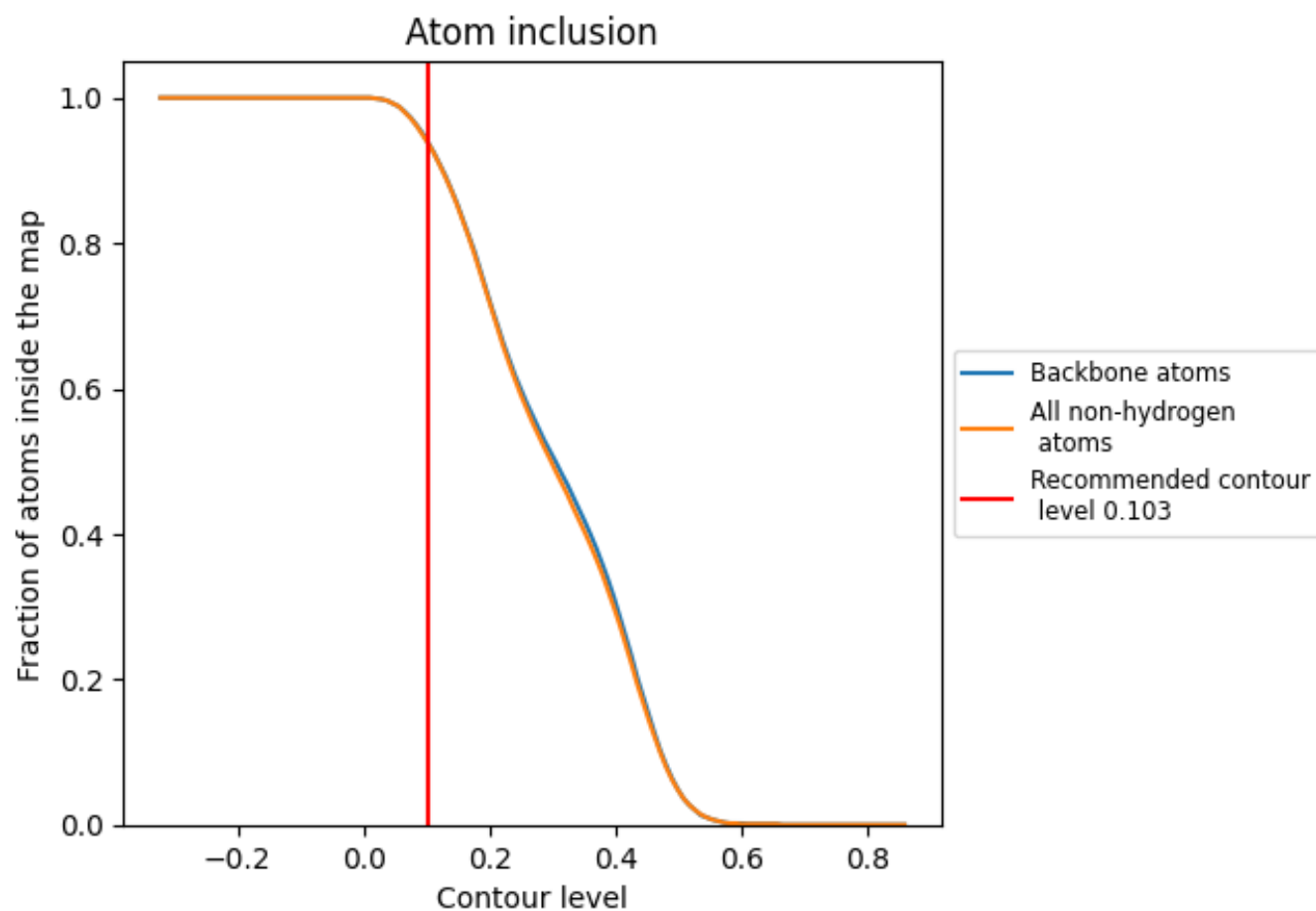
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.103).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.103) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9370	0.5260
A	0.9410	0.5240
B	0.9520	0.5340
D	0.9510	0.5330
E	0.9440	0.5310
G	0.9400	0.5290
H	0.9450	0.5310
N	0.6440	0.4030
P	0.5540	0.3840
Q	0.9330	0.5210
Z	0.9460	0.5250
a	0.9470	0.5260
b	0.9560	0.5340
d	0.9460	0.5290
e	0.9380	0.5260
g	0.9380	0.5240
h	0.9490	0.5310
q	0.9400	0.5250
z	0.9440	0.5250

