



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 03:02 AM UTC

PDB ID : 7Q55 / pdb_00007q55
EMDB ID : EMD-13826
Title : Single Particle Cryo-EM structure of photosynthetic A8B8 glyceraldehyde
-3-phosphate dehydrogenase hexadecamer (major conformer) from *Spinacia
oleracea*.
Authors : Marotta, R.; Fermani, S.; Sparla, F.; Trost, P.; Del Giudice, A.
Deposited on : 2021-11-02
Resolution : 5.70 Å(reported)

This is a wwPDB EM Validation Summary 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.dev132
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) : 2.49

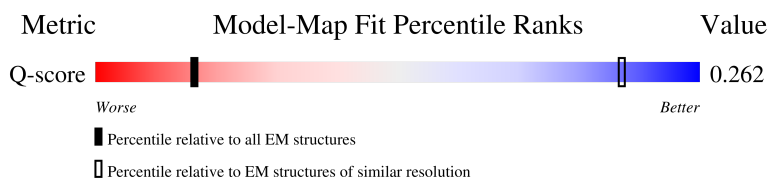
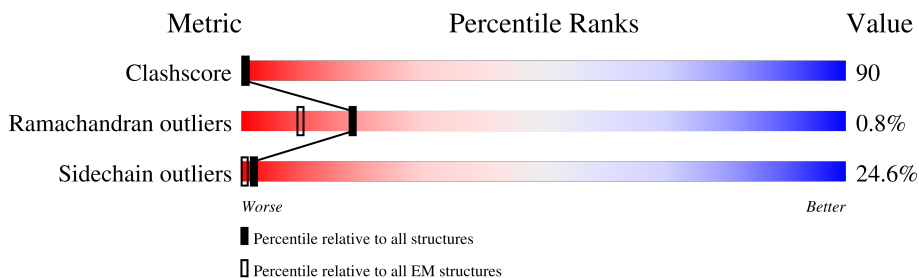
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.70 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.



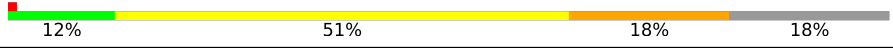
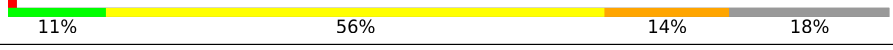
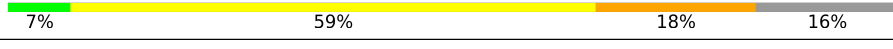
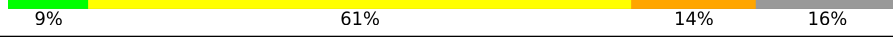
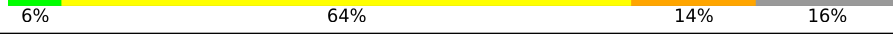
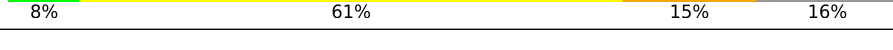
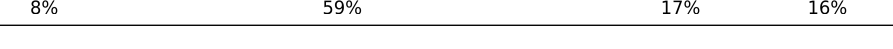
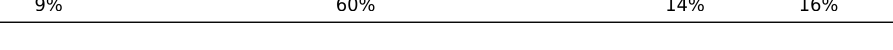
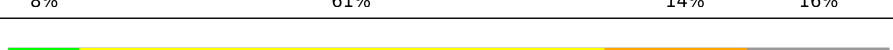
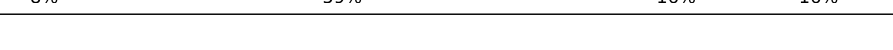
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	503 (5.20 - 6.20)

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	451	
1	C	451	
1	E	451	
1	G	451	

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Mol	Chain	Length	Quality of chain
1	I	451	
1	K	451	
1	O	451	
1	Q	451	
2	B	402	
2	D	402	
2	F	402	
2	H	402	
2	J	402	
2	L	402	
2	P	402	
2	R	402	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 42608 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 Glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	O	368	Total	C	N	O	S	0	0
			2694	1700	473	510	11		
1	Q	368	Total	C	N	O	S	0	0
			2694	1700	473	510	11		
1	A	368	Total	C	N	O	S	0	0
			2694	1700	473	510	11		
1	C	368	Total	C	N	O	S	0	0
			2694	1700	473	510	11		
1	E	368	Total	C	N	O	S	0	0
			2694	1700	473	510	11		
1	G	368	Total	C	N	O	S	0	0
			2694	1700	473	510	11		
1	I	368	Total	C	N	O	S	0	0
			2694	1700	473	510	11		
1	K	368	Total	C	N	O	S	0	0
			2694	1700	473	510	11		

- Molecule 2 is a protein called Glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	P	337	Total	C	N	O	S	0	0
			2544	1600	445	488	11		
2	R	337	Total	C	N	O	S	0	0
			2544	1600	445	488	11		
2	B	337	Total	C	N	O	S	0	0
			2544	1600	445	488	11		
2	D	337	Total	C	N	O	S	0	0
			2544	1600	445	488	11		
2	F	337	Total	C	N	O	S	0	0
			2544	1600	445	488	11		
2	H	337	Total	C	N	O	S	0	0
			2544	1600	445	488	11		
2	J	337	Total	C	N	O	S	0	0
			2544	1600	445	488	11		

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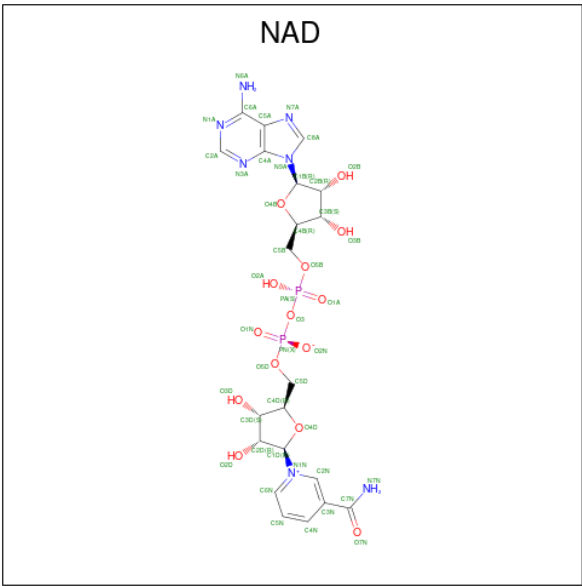
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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	L	337	2544	1600	445	488	11	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	334	UNK	-	insertion	UNP P19866
R	334	UNK	-	insertion	UNP P19866
B	334	UNK	-	insertion	UNP P19866
D	334	UNK	-	insertion	UNP P19866
F	334	UNK	-	insertion	UNP P19866
H	334	UNK	-	insertion	UNP P19866
J	334	UNK	-	insertion	UNP P19866
L	334	UNK	-	insertion	UNP P19866

- Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
3	O	1	44	21	7	14	2	0
3	P	1	44	21	7	14	2	0
3	Q	1	44	21	7	14	2	0
3	R	1	44	21	7	14	2	0

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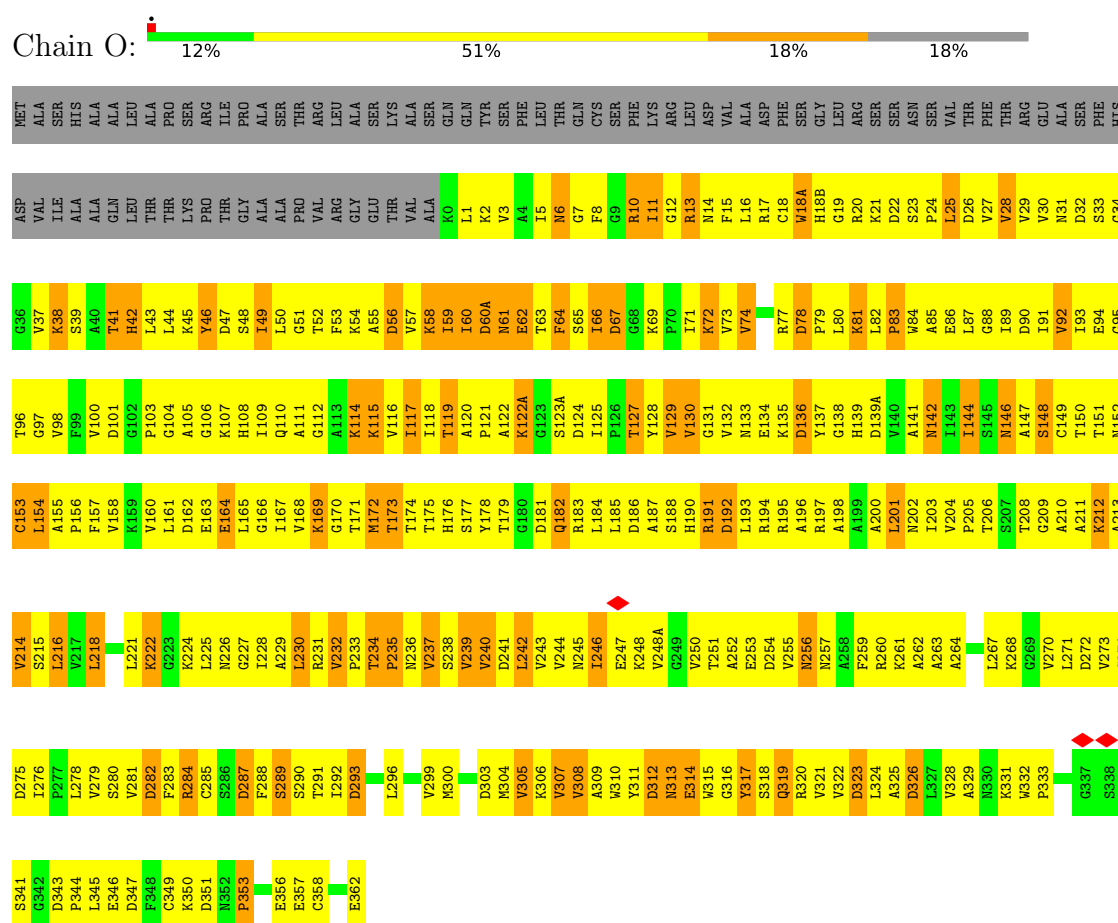
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Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total 44	C 21	N 7	O 14	P 2	0
3	B	1	Total 44	C 21	N 7	O 14	P 2	0
3	C	1	Total 44	C 21	N 7	O 14	P 2	0
3	D	1	Total 44	C 21	N 7	O 14	P 2	0
3	E	1	Total 44	C 21	N 7	O 14	P 2	0
3	F	1	Total 44	C 21	N 7	O 14	P 2	0
3	G	1	Total 44	C 21	N 7	O 14	P 2	0
3	H	1	Total 44	C 21	N 7	O 14	P 2	0
3	I	1	Total 44	C 21	N 7	O 14	P 2	0
3	J	1	Total 44	C 21	N 7	O 14	P 2	0
3	K	1	Total 44	C 21	N 7	O 14	P 2	0
3	L	1	Total 44	C 21	N 7	O 14	P 2	0

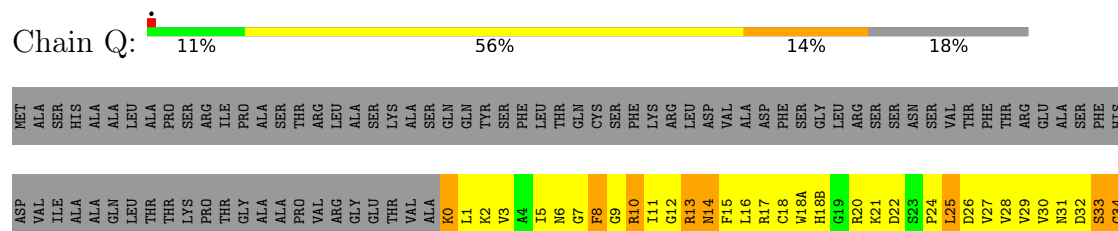
3 Residue-property plots

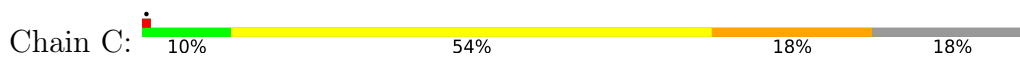
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic



- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic



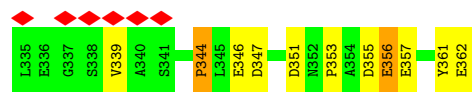


MET	ASP	G36	L154	D275	S338	D287	ASP	G36	G95	N152	V214
ALA	VAL	V37	A155	I276	V339	D288	VAL	V37	T96	C153	
SER	ILE	K38	P156	P277	V340	D289	ILE	K38	G97		
HIS	ALA	S39	F157	L278	S341	D290	ALA	S39	V98		
ALA	ALA	F99	V158	L218	S342	D291	ALA	A40	F99		
ALA	GLN	T41	K159	Q220	G343	D292	GLN	V100	D101		
LEU	LEU	H42	V160	L221	G344	D293	LEU	D101	G102		
ALA	THR	L43	L161	D282	P344	D294	THR	G102	D101		
PRO	THR	L44	L162	P283	P345	D295	PRO	L44	P103		
SER	LYS	K45	E163	R284	L346	D296	SER	K45	G104		
ARG	PRO	Y46	C285	R285	E347	D297	ARG	Y46	A105		
ILE	THR	D47	S286	G286	F347	D298	ILE	D47	G106		
PRO	GLY	S48	D287	F287	F348	D299	PRO	S48	K107		
ALA	ALA	I49	F288	P288	C349	D300	ALA	I49	H108		
SER	ALA	L50	S289	S290	K350	D301	SER	L50	H109		
THR	PRO	G51	S290	L296	C351	D302	THR	G51	Q110		
ARG	VAL	T52	N351	T297	D352	D303	ARG	T52	A111		
LEU	ARG	F53	P352	M298	E353	D304	LEU	F53	G112		
ALA	GLY	K54	L354	M299	E356	D305	ALA	K54	A113		
SER	GLU	A55	E357	M300	E358	D306	SER	A55	K114		
LYS	THR	D56	E359	G301	C359	D307	LYS	D56	K115		
ALA	VAL	V57	C358	G302	E361	D308	ALA	V57	V116		
ALA	VAL	K58	K359	D303	E362	D309	ALA	K58	T117		
SER	ALA	I59		D304		D310	SER	I59	I117		
GLN	KO	I60		M304		D311	GLN	I60	T118		
THR	L1	D60A		V305		D312	THR	D60A	G119		
GLN	K2	N61		K306		D313	GLN	N61	T119		
CYS	V3	E62		V307		D314	CYS	V3	G120		
SER	A4	T63		V308		D315	SER	A4	A121		
PHE	I5	F64		A309		D316	PHE	I5	K122A		
LEU	N6	S65		W310		D317	LEU	N6			
THR	G7	I66		Y311		D318	THR	G7	D124		
GLN	G8	D67		X312		D319	GLN	G8	I125		
ARG	G9	G68		D320		D321	ARG	G9	P126		
LEU	R10	K69		R321		D322	LEU	R10	T127		
ASP	I11	P70		V322		D323	ASP	I11	G128		
VAL	G12	I71		L324		D324	VAL	G12	V129		
ASP	R13	K72		A325		D325	ASP	R13	A130		
VAL	F15	V73		D326		D327	VAL	F15	G131		
ALA	L16	S75		D327		D328	ALA	L16	V132		
ASP	R17	N76		L327		D329	ASP	R17	N133		
PHE	C18	R77		L328		D330	PHE	C18	E134		
SER	W18A	D78		L329		D331	SER	W18A	R135		
GLY	H18B	P79		A326		D332	GLY	H18B	D136		
LEU	G19	L80		D326		D333	LEU	G19	Y137		
ARG	R20	K81		D327		D334	ARG	R20	G138		
SER	K21	P82		L327		D335	SER	K21	D139A		
SER	D22	P83		L328		D336	SER	D22	V140		
ASN	S23	W84		A327		D337	ASN	S23	A141		
SER	P24	A85		D326		D338	SER	P24	N142		
VAL	L25	E86		D327		D339	VAL	L25	N143		
THR	D26	L87		L327		D340	THR	D26	P205		
PHE	V27	G88		L328		D341	PHE	V27	T206		
THR	V28	I89		L329		D342	THR	V28	S207		
THR	V29	D90		A328		D343	THR	V29	G209		
ARG	V30	I91		D326		D344	ARG	V30	A147		
GLU	N31	V92		D327		D345	GLU	N31	S148		
ALA	D32	I93		L327		D346	ALA	D32	C149		
SER	P33	E94		L328		D347	SER	P33	T150		
PHE	G34	G95		L329		D348	PHE	G34	T151		

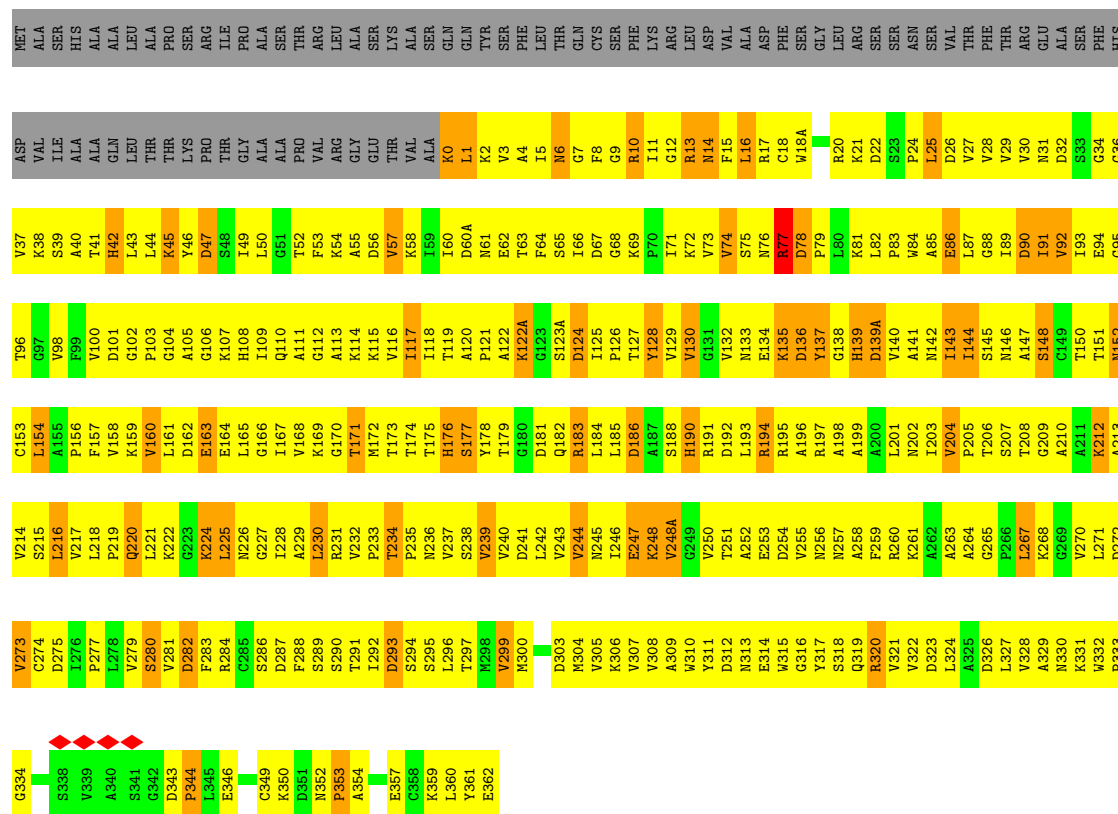
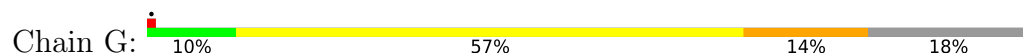
- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic



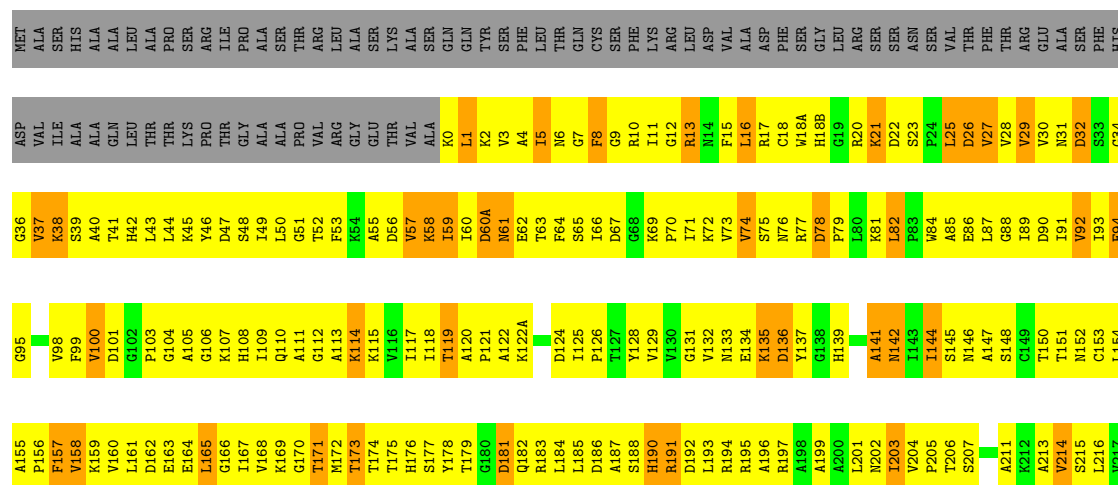
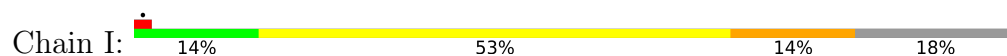
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SER	ILE	K38	L154	V216	I276
HIS	ALA	S39	A155	V217	P277
ALA	ALA	F99	P156	L218	L278
ALA	GLN	T41	F157	P219	V279
LEU	LEU	H42	V158	Q220	S280
ALA	THR	L43	K159	L221	V281
PRO	THR	L44	D101	K222	D282
SER	THR	L45	G102	G223	F283
ARG	PRO	K45	P103	G224	R284
ILE	THR	Y46	G104	L225	
PRO	GLY	D47	A105	L226	
ALA	GLY	S48	G106	N226	
ALA	ALA	I49	K107	G227	
SER	ALA	L50	H108	I228	
THR	PRO	G51	I109	A229	
ARG	PRO	T52	Q110	S290	
LEU	VAL	F53	V168	T291	
ALA	VAL	K54	A111	R292	
SER	GLY	F53	G112	D331	
LYS	GLY	A55	A113	P332	
THR	GLU	D56	K114	P333	
ALA	THR	V57	K115	T234	
ALA	VAL	K58	V116	P335	
SER	VAL	I59	T117	N236	
GLN	KO	I60	T118	V237	
THR	L1	D60A	T119	S238	
GLN	K2	N61	G120	V239	
CYS	V3	E62	A121	P240	
SER	A4	T63	K122A	D241	
PHE	I5	F64	D181	G242	
LEU	N6	S65	G123	L243	
THR	G7	I66	G124	V244	
GLN	G8	D67	S123A	N245	
ARG	G9	G68	D124	K246	
LEU	R10	K69	I125	E247	
ASP	I11	P70	P126	K248	
VAL	G12	I71	Y128	V248A	
ASP	R13	K72	Y129		
VAL	F15	V73	V130	T251	
ALA	L16	S75	G131	A252	
ASP	R17	N76	N132	E253	
PHE	C18	R77	N133	D254	
SER	W18A	D78	E134	V255	
GLY	H18B	P79	R135	N256	
LEU	G19	L80	D136	N257	
ARG	R20	K81	Y137	A258	
SER	K21	P82	G138	F259	
SER	D22	P83	H139	R260	
ASN	S23	W84	D139A	K261	
SER	P24	A85	V140	L262	
VAL	L25	E86	A141	A263	
THR	D26	L87	N142	A264	
PHE	V27	G88	N143	G265	
THR	V28	I89	T144	P266	
THR	V29	D90	S145	L267	
ARG	V30	I91	G146	G268	
GLU	N31	V92	A147	K269	
ALA	D32	I93	S148	V270	
SER	P33	E94	C149	L271	
HIS	G34	G95	T150	D272	
			T151	V273	

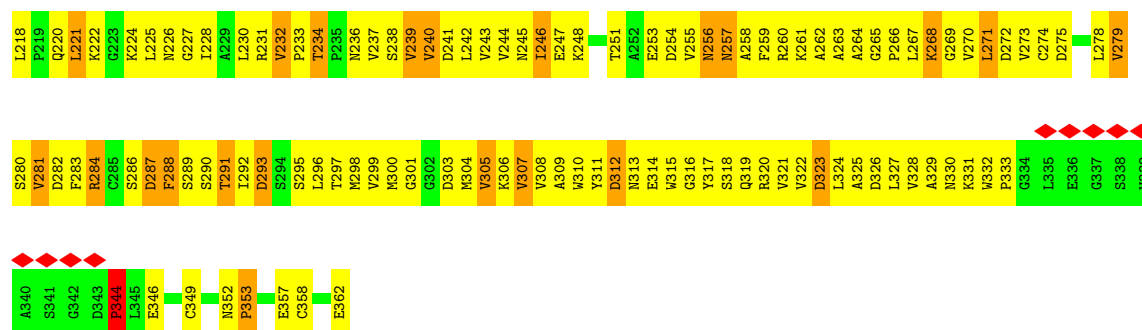


• Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic

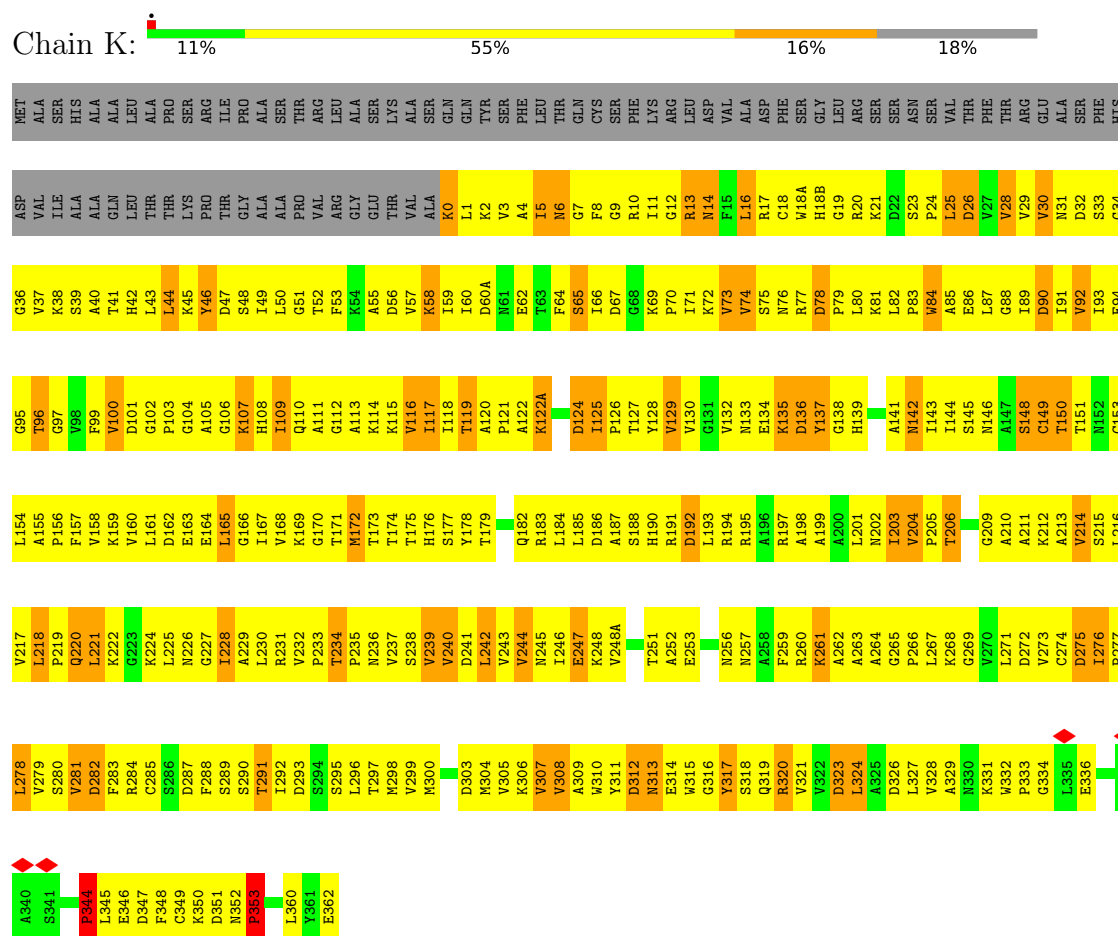


• Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic

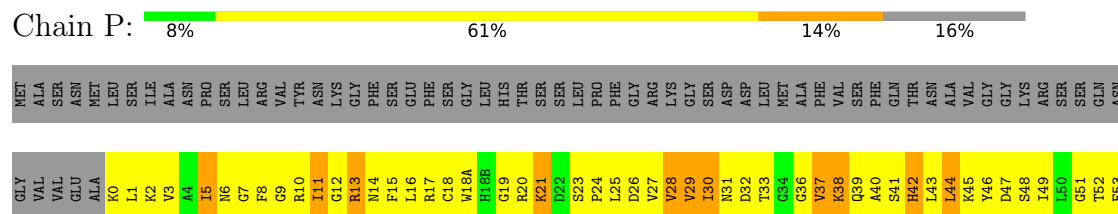




• Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic



• Molecule 2: Glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic



L296	L297	L298	L299	M300	G301	D302	D303	M304	M305	K306	V307	I308	A309	W310	Y311	D312	M313	E314	W315	G316	Y317	S318	K319	R320	Y321	V322	D323	L324	A325	D326	V328	A329	N330	K331	W332	K333	X334	T175	T176	M236	V237	S238	V239	V240	D241	L242	V243	V244	V245	V246	S247	K248	K249	T250	F251	A252	E253	E254	V255	M256	F257	A258	F259	R260	E261	S262	D263	D264	M265	E266	T267	G268	G269	I270	L271	S272	V273	T274	D275	E276	P277	L278	V279	S280	L281	D282	F283	R284	C285	T286	D287	V288	S289	S290	T291	I292	D293	S294	S295	A113	K114	K115	V116	L117	L118	T119	A120	P121	D124	I125	P126	T127	Y128	V129	V130	G131	V132	N133	E134	E135	E136	Y137	T138	H139	A140	D141	T142	I143	I144	S145	N146	A147	S148	C149	T150	T151	N152	C153	L154	F157	V158	K159	V160	L161	D162	Q163	K164	F165	G166	I167	I168	R169	K170	T171	M172	T173	T174
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• Molecule 2: Glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic

Chain D: 9% 61% 14% 16%

M298	M299	M300	G301	D302	D303	M304	M305	M306	V307	I308	A309	M310	F251	A252	E253	E254	V255	M256	A257	A258	Q319	R260	E261	S262	A263	D264	M265	E266	L267	K268	G269	L270	L271	S272	V273	C274	D275	E276	P277	L278	V279	S280	L281	D282	D283	R284	C285	T286	D287	S288	S289	S290	T291	L292	D293	S294	S295	L296	T297								
L117	L118	T119	A120	P121	G122	K122A	G123	D124	I125	P126	T127	Y128	V129		M130	N133	E134	E135	G136	Y137	T138	H139	A140	D141	T142	I143	P143	S144	S145	N146	A147	S148	C149	T150	T151	M152	C153	L154	A155	P156	F157	V158	K159	L160	L161	D162	O163	K164	F165	G166	T167	I168	K169	G170	T171	M172	T173	L174	T175	H176							
S177	Y178	T179	G180	D181	O182	R183	L184	L185	D186	A187	S188	H190	R191	D192	L193	R194	R195	A196	G197	A198	A199	G200	L201	N202	T203	V204	P205	T206	S207	T208	G209	A210	A211	K212	A213	V214	A215	L216	V217	L218	P219	N220	L221	K222	G223	K224	L225	N226	G227	T228	A229	L230	R231	V232	P233	T234	P235	N236	T237								
D54	A55	D56	V57	K58	G59	T59				D61	S62	A63	I64	S65	V66	D67	G68	K69	V70	I71	K72	V73			R77	N78	P79	V80	N81	L82	P83	W84	G85	D86	M87	G88	I89	D90	L91	V92	I93	E94	G95	T96	G97	V98	F99	V37	K38	Q39	D101	R102	D103	G104	A105	G106	L43	K45	H107	K108	L109	Q110	A111		K114	L115	V116
MET	ALA	SER	ASN	MET	LEU	SER	ILE	ALA	ASN	PRO	SER	LEU	ARG	ARG	VAL	THR	TYR	VAL	ASN	LYS	GLY	PHE	SER	GLU	GLY	GLY	LEU	HIS	THR	THR	SER	SER	LEU	PRO	PHE	GLY	ARG	LYS	GLY	SER	ASP	ASP	LEU	MET	ALA	PHE	VAL	SER	PHE	GLN	THR	ASN	ALA	VAL	GLY	ARG	LYS	SER	GLN	ASN							

• Molecule 2: Glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic

Chain F: 6% 64% 14% 16%

MET	ALA	SER	ASN	MET	LEU	SER	ILE	ALA	ASN	PRO	SER	LEU	ARG	ARG	VAL	THR	TYR	VAL	ASN	LYS	GLY	PHE	SER	GLU	GLY	GLY	LEU	HIS	THR	THR	SER	SER	LEU	PRO	PHE	GLY	ARG	LYS	GLY	SER	ASP	ASP	LEU	MET	ALA	PHE	VAL	SER	PHE	GLN	THR	ASN	ALA	VAL	GLY	GLY	LYS	ARG	SER	SER	GLN	ASN																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
D54	A55	D56	V57	K58	T59		D61	G62	A63	I64	S65	V66		K69	V70	I71	K72	V73	V74	S75	D76	R77	N78	P79	N80	N81	L82	P83	V84	G85	D86	M87	G88	I89	D90	L91	V92	N93	E94	G95	T96	G97	V98	F99	V100	D101	R102	D103	G104	A105	G106	K107	H108	L109	Q110	A111	G112	T113	L114																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															</

T174	T175	H176	S177	Y178	T179	G180	D181	Q182	R183	L184	L185	D186	A187	S188	H190	R191	D192	L193	R194	R195	A196	R197	A198	A199	C200	L201	N202	T203	V204	P205	T206	S207	T208	G209	A210	A211	K212	A213	V214	A215	L216	V217	L218	P219	N220	L221	K222	G223	K224	L225	N226	G227	V228	S229	L230	R231	V232	P233	T234	
P235	N236	V237	S238	V239	V240	D241	L242	V243	V244	Q245	V246	S247	K248	K249	T250	Y311	A252	E253	E254	V255	N256	A257	S316	S317	S318	Q319	R320	V321	V322	D323	L324	A325	D326	L327	K288	I270	L271	S272	V273	C274	D275	E276	P277	L278	V279	S280	I281	L282	D283	R284	C285	T286	D287	V288	S289	L290	T291	I292	P293	S294
S295	L296	P297	P298	M300	M301	D302	D303	M304	A305	Q306	K307	G308	A309	W310	Y311	D312	N313	E314	W315	G316	Y317	S318	Q319	R320	V321	V322	D323	L324	A325	D326	L327	K288	I270	L271	S272	V273	C274	D275	E276	P277	L278	V279	S280	I281	L282	D283	R284	C285	T286	D287	V288	S289	L290	T291	I292	P293	S294			

• Molecule 2: Glyceraldehyde-3-phosphate dehydrogenase A, chloroplasic

Chain H: 8% 61% 15% 16%

T297	M298	V299	M300	G301	D302	D303	M304	V305	K306	V307	I308	A309	W310	Y311	D312	N313	E314	V315	G316	Y317	S318	Q319	R320	V321	V322	D323	L324	A325	D326	L327	V328	A329	N330	K331	V332	Q333	X334																						
P235	N236	V237	M238	V239	D240	D241	L242	V243	V244	Q245	V246	S247	K248	K249	T250	Y251	A252	E253	E254	V255	N256	A257	S258	F259	R260	E261		D264	N265	E266	L267	K268	G269	L270	L271	S272	V273	C274	D275	E276	P277	L278	V279	S280	I281	L282	D283	R284		D287	V288	S289	L290	T291	I292	P293	S294	L295	N296
T174	T175	H176	S177	Y178	T179	G180	D181	Q182	R183	L184	L185	D186	A187	S188	H190	R191	D192	L193	R194	R195	A196	R197	A198	A199	C200	L201	N202	T203	V204	P205	T206	S207	T208	G209	A210	A211	K212	A213	V214	A215	L216	V217	L218	P219	N220	L221	K222	G223	K224	L225	N226	G227	V228	S229	L230	R231	V232	P233	T234
K114	K115	V116	L117	T118	T119	A120	P121	G122	K123	A124	G125	D126	I127	T128	V129	V130	G131	V132	N133	E134	E135	G136	Y137	T138	H139	A140	D141	T142	P143	I144	S145	M146	A147	S148	C149	T150	T151	N152	C153	G154		F157	V158	K159	V160	L161	D162	Q163	K164	F165	G166	I167	T168	K169	L170	G171	T172		
A55	D56	K58	T59	A60	G60A	D61	S62	A63	I64	S65	V66	D67	G68	K69	I70	I71	K72	V73	S75	D76	R77	N78	P79	V80	N81	L82	P83	W84	G85	D86	M87	I88	G89	D90	L91	V92	E93	G94	G95	T96	G97	V98	F99	V100	D101	R102	D103	G104	A105	K106	I107	H108	I109	Q110	A111	G112	D113	E114	
GLY	VAL	VAL	GLU	ALA	KO	L1	K2	V3	A4	I5	N6	G7	F8	G9	R10	I11	G12	R13	N14	F15	L16	R17	C18	W18A	H18B	G19	R20	L21	D22	L23	V24	D25	D26	V27	V28	I29	V30	G31	G32	V33	T34	K35	Q36	A40	S41	H42	L43	L44	K45	Y46	G106	K107	H108	I109	Q110	G51	L112	D54	
MET	ALA	SER	ASN	LEU	MET	ILE	ALA	ASN	PRO	SER	LEU	ARG	VAL	TYR	ASN	LYS	GLY	PHE	SER	GLU	PHE	SER	GLY	LEU	HIS	THR	SER	SER	LEU	PRO	PHE	PHE	GLY	LYS	ARG	GLY	ASP	ASP	LEU	MET	ALA	PHE	VAL	PHE	GLN	THR	ASN	ALA	VAL	GLY	LYS	ARG	SER	SER	GLN	ASN			

• Molecule 2: Glyceraldehyde-3-phosphate dehydrogenase A, chloroplasic

Chain J: 8% 59% 17% 16%

MET	ALA	SER	ASN	LEU	SER	ILE	ALA	ASN	PRO	SER	LEU	ARG	VAL	TYR	ASN	LYS	GLY	PHE	SER	GLU	PHE	SER	GLY	LEU	HIS	THR	SER	SER	LEU	PRO	PHE	GLY	LYS	ARG	GLY	ASP	ASP	LEU	MET	ALA	PHE	VAL	PHE	GLN	THR	ASN	ALA	VAL	GLY	LYS	ARG	SER	SER	GLN	ASN		
GLY	VAL	VAL	GLU	ALA	KO	L1	K2	V3	I5	N6	G7	F8	G9	R10	I11	L12	R13	N14	F15	L16	R17	C18	W18A	H18B	G19	R20	L21	D22	L23	V24	D25	D26	V27	V28	I29	V30	G31	G32	V33	T34	K35	Q36	A40	S41	H42	L43	L44	K45	Y46	G106	K107	H108	I109	Q110	A111	G112	F53
D54	A55	D56	V57	K58	T59	A60	G60A	A63	I64	S65	V66	D67	G68	K69	I70	I71	K72	V73	S75	D76	R77	N78	P79	V80	N81	L82	P83	W84	G85	D86	M87	I89	D90	L91	V92	E94	G95	T96	G97	V98	F99	V100	D101	R102	D103	G104	A105	K106	I107	H108	I109	Q110	A111	G112	A113		
K114	K115	V116	L117	T118	T119	A120	P121	D124	I125	P126	T127	Y128	V129	V130	G131	V132	N133	E134	E135	G136	Y137	T138	H139	A140	D141	T142	P143	I144	S145	M146	A147	S148	C149	T150	T151	N152	C153	L154	F157	V158	K159	V160	L161	D162	Q163	K164	F165	G166	I167	T168	K169	L170	G171	T172	M173	T174	T175
H176	S177	Y178	T179	G180	D181	Q182	L184	L185	D186	A187	S188	H190	R191	D192	L193	R194	R195	A196	R197	A198	A199	C200	L201	N202	I203	V204	P205	T206	S207	T208	G209	A210	A211	K212	A213	V214	A215	L216	V217	L218	P219	N220	L221	K222	G223	K224	L225	N226	G227	V228	S229	L230	R231	V232	P233	T234	N236

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	23611	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	42	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.050	Depositor
Minimum map value	-0.016	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.012	Depositor
Map size (Å)	363.0, 363.0, 363.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.21, 1.21, 1.21	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: NAD

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	0.38	0/2739	0.64	2/3726 (0.1%)
1	C	0.48	0/2739	0.72	2/3726 (0.1%)
1	E	0.48	0/2739	0.71	2/3726 (0.1%)
1	G	0.48	0/2739	0.70	4/3726 (0.1%)
1	I	0.45	0/2739	0.67	2/3726 (0.1%)
1	K	0.45	0/2739	0.71	4/3726 (0.1%)
1	O	0.46	0/2739	0.66	2/3726 (0.1%)
1	Q	0.48	0/2739	0.67	2/3726 (0.1%)
2	B	0.39	0/2579	0.58	1/3502 (0.0%)
2	D	0.40	0/2579	0.59	0/3502
2	F	0.39	0/2579	0.57	0/3502
2	H	0.40	0/2579	0.58	0/3502
2	J	0.38	0/2579	0.57	1/3502 (0.0%)
2	L	0.39	0/2579	0.59	0/3502
2	P	0.39	0/2579	0.59	0/3502
2	R	0.41	0/2579	0.59	0/3502
All	All	0.43	0/42544	0.64	22/57824 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	G	0	1

There are no bond length outliers.

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	344	PRO	N-CA-CB	8.20	111.86	103.25
1	A	344	PRO	N-CA-CB	7.72	111.36	103.25
1	I	344	PRO	N-CA-CB	7.70	111.34	103.25
1	K	353	PRO	N-CA-CB	7.20	110.81	103.25
1	E	344	PRO	N-CA-CB	7.02	110.62	103.25

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	G	248	LYS	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2694	0	2681	496	0
1	C	2694	0	2681	550	0
1	E	2694	0	2681	534	0
1	G	2694	0	2681	562	0
1	I	2694	0	2681	483	0
1	K	2694	0	2681	498	0
1	O	2694	0	2681	579	0
1	Q	2694	0	2681	487	0
2	B	2544	0	2577	506	0
2	D	2544	0	2577	470	0
2	F	2544	0	2577	513	0
2	H	2544	0	2577	498	0
2	J	2544	0	2577	498	0
2	L	2544	0	2577	471	0
2	P	2544	0	2577	463	0
2	R	2544	0	2577	490	0
3	A	44	0	26	7	0
3	B	44	0	25	11	0
3	C	44	0	25	12	0
3	D	44	0	25	12	0
3	E	44	0	25	9	0
3	F	44	0	25	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	44	0	25	16	0
3	H	44	0	25	10	0
3	I	44	0	26	9	0
3	J	44	0	26	9	0
3	K	44	0	26	11	0
3	L	44	0	25	10	0
3	O	44	0	26	10	0
3	P	44	0	26	14	0
3	Q	44	0	25	12	0
3	R	44	0	26	13	0
All	All	42608	0	42471	7684	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 90.

The worst 5 of 7684 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:37:VAL:HB	1:O:59:ILE:CG2	1.27	1.55
2:F:10:ARG:NH2	1:G:185:LEU:HD13	1.32	1.42
1:Q:37:VAL:CG1	1:Q:59:ILE:HG23	1.55	1.35
2:F:10:ARG:CZ	1:G:185:LEU:HD13	1.58	1.33
1:E:17:ARG:CD	1:E:44:LEU:HG	1.60	1.32

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	366/451 (81%)	278 (76%)	85 (23%)	3 (1%)	16 53
1	C	366/451 (81%)	262 (72%)	100 (27%)	4 (1%)	11 45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	366/451 (81%)	286 (78%)	71 (19%)	9 (2%)	4	25
1	G	366/451 (81%)	257 (70%)	104 (28%)	5 (1%)	9	39
1	I	366/451 (81%)	268 (73%)	94 (26%)	4 (1%)	11	45
1	K	366/451 (81%)	264 (72%)	100 (27%)	2 (0%)	24	63
1	O	366/451 (81%)	265 (72%)	94 (26%)	7 (2%)	6	31
1	Q	366/451 (81%)	273 (75%)	87 (24%)	6 (2%)	7	37
2	B	335/402 (83%)	263 (78%)	72 (22%)	0	100	100
2	D	335/402 (83%)	254 (76%)	80 (24%)	1 (0%)	36	72
2	F	335/402 (83%)	251 (75%)	82 (24%)	2 (1%)	21	59
2	H	335/402 (83%)	259 (77%)	76 (23%)	0	100	100
2	J	335/402 (83%)	263 (78%)	72 (22%)	0	100	100
2	L	335/402 (83%)	256 (76%)	78 (23%)	1 (0%)	36	72
2	P	335/402 (83%)	248 (74%)	86 (26%)	1 (0%)	36	72
2	R	335/402 (83%)	257 (77%)	77 (23%)	1 (0%)	36	72
All	All	5608/6824 (82%)	4204 (75%)	1358 (24%)	46 (1%)	18	53

5 of 46 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	O	18(A)	TRP
1	O	61	ASN
1	Q	60	ILE
1	Q	352	ASN
1	A	352	ASN

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	282/370 (76%)	219 (78%)	63 (22%)	1	6
1	C	282/370 (76%)	197 (70%)	85 (30%)	0	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	282/370 (76%)	201 (71%)	81 (29%)	0	3
1	G	282/370 (76%)	216 (77%)	66 (23%)	1	5
1	I	282/370 (76%)	218 (77%)	64 (23%)	1	6
1	K	282/370 (76%)	210 (74%)	72 (26%)	0	4
1	O	282/370 (76%)	203 (72%)	79 (28%)	0	3
1	Q	282/370 (76%)	219 (78%)	63 (22%)	1	6
2	B	279/332 (84%)	207 (74%)	72 (26%)	0	3
2	D	279/332 (84%)	216 (77%)	63 (23%)	1	6
2	F	279/332 (84%)	215 (77%)	64 (23%)	1	6
2	H	279/332 (84%)	215 (77%)	64 (23%)	1	6
2	J	279/332 (84%)	207 (74%)	72 (26%)	0	3
2	L	279/332 (84%)	218 (78%)	61 (22%)	1	6
2	P	279/332 (84%)	215 (77%)	64 (23%)	1	6
2	R	279/332 (84%)	210 (75%)	69 (25%)	1	4
All	All	4488/5616 (80%)	3386 (75%)	1102 (25%)	2	4

5 of 1102 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	J	142	THR
2	J	271	LEU
2	J	141	ASP
1	K	323	ASP
2	B	256	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 97 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	108	HIS
1	I	14	ASN
2	F	202	ASN
1	G	61	ASN
1	I	220	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

16 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	NAD	K	401	-	46,48,48	0.62	1 (2%)	64,73,73	0.60	1 (1%)
3	NAD	L	401	-	46,48,48	4.09	22 (47%)	64,73,73	2.18	13 (20%)
3	NAD	P	401	-	46,48,48	0.58	1 (2%)	64,73,73	0.56	1 (1%)
3	NAD	G	401	-	46,48,48	4.06	21 (45%)	64,73,73	2.05	13 (20%)
3	NAD	H	401	-	46,48,48	4.03	21 (45%)	64,73,73	2.19	14 (21%)
3	NAD	Q	401	-	46,48,48	4.01	20 (43%)	64,73,73	2.13	14 (21%)
3	NAD	B	401	-	46,48,48	4.05	22 (47%)	64,73,73	2.20	16 (25%)
3	NAD	R	401	-	46,48,48	0.59	1 (2%)	64,73,73	0.54	1 (1%)
3	NAD	I	401	-	46,48,48	0.58	1 (2%)	64,73,73	0.56	1 (1%)
3	NAD	F	401	-	46,48,48	4.07	21 (45%)	64,73,73	2.22	15 (23%)
3	NAD	O	401	-	46,48,48	0.62	1 (2%)	64,73,73	0.53	1 (1%)
3	NAD	D	401	-	46,48,48	4.09	22 (47%)	64,73,73	2.18	13 (20%)
3	NAD	C	401	-	46,48,48	3.98	21 (45%)	64,73,73	2.23	16 (25%)
3	NAD	J	401	-	46,48,48	0.56	1 (2%)	64,73,73	0.54	1 (1%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAD	E	401	-	46,48,48	4.00	21 (45%)	64,73,73	2.27	16 (25%)
3	NAD	A	401	-	46,48,48	0.59	1 (2%)	64,73,73	0.55	1 (1%)

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
3	NAD	K	401	-	-	14/30/62/62	0/5/5/5
3	NAD	L	401	-	-	12/30/62/62	0/5/5/5
3	NAD	P	401	-	-	13/30/62/62	0/5/5/5
3	NAD	G	401	-	-	12/30/62/62	0/5/5/5
3	NAD	H	401	-	-	14/30/62/62	0/5/5/5
3	NAD	Q	401	-	-	9/30/62/62	0/5/5/5
3	NAD	B	401	-	-	14/30/62/62	0/5/5/5
3	NAD	R	401	-	-	14/30/62/62	0/5/5/5
3	NAD	I	401	-	-	13/30/62/62	0/5/5/5
3	NAD	F	401	-	-	13/30/62/62	0/5/5/5
3	NAD	O	401	-	-	15/30/62/62	0/5/5/5
3	NAD	D	401	-	-	12/30/62/62	0/5/5/5
3	NAD	C	401	-	-	11/30/62/62	0/5/5/5
3	NAD	J	401	-	-	9/30/62/62	0/5/5/5
3	NAD	E	401	-	-	10/30/62/62	0/5/5/5
3	NAD	A	401	-	-	15/30/62/62	0/5/5/5

The worst 5 of 198 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	401	NAD	O4D-C1D	-10.91	1.26	1.40
3	L	401	NAD	O4D-C1D	-10.90	1.26	1.40
3	B	401	NAD	O4D-C1D	-10.70	1.26	1.40
3	F	401	NAD	O4D-C1D	-10.69	1.26	1.40
3	H	401	NAD	O4D-C1D	-10.54	1.27	1.40

The worst 5 of 137 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	401	NAD	C4A-N9A-C1B	-7.23	109.73	126.63
3	E	401	NAD	C4A-N9A-C1B	-7.13	109.96	126.63
3	L	401	NAD	C4A-N9A-C1B	-7.08	110.06	126.63
3	D	401	NAD	C4A-N9A-C1B	-7.08	110.08	126.63
3	H	401	NAD	C4A-N9A-C1B	-6.91	110.47	126.63

There are no chirality outliers.

5 of 200 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	O	401	NAD	C5B-O5B-PA-O2A
3	O	401	NAD	C5B-O5B-PA-O3
3	O	401	NAD	O4B-C4B-C5B-O5B
3	O	401	NAD	C5D-O5D-PN-O1N
3	O	401	NAD	C5D-O5D-PN-O2N

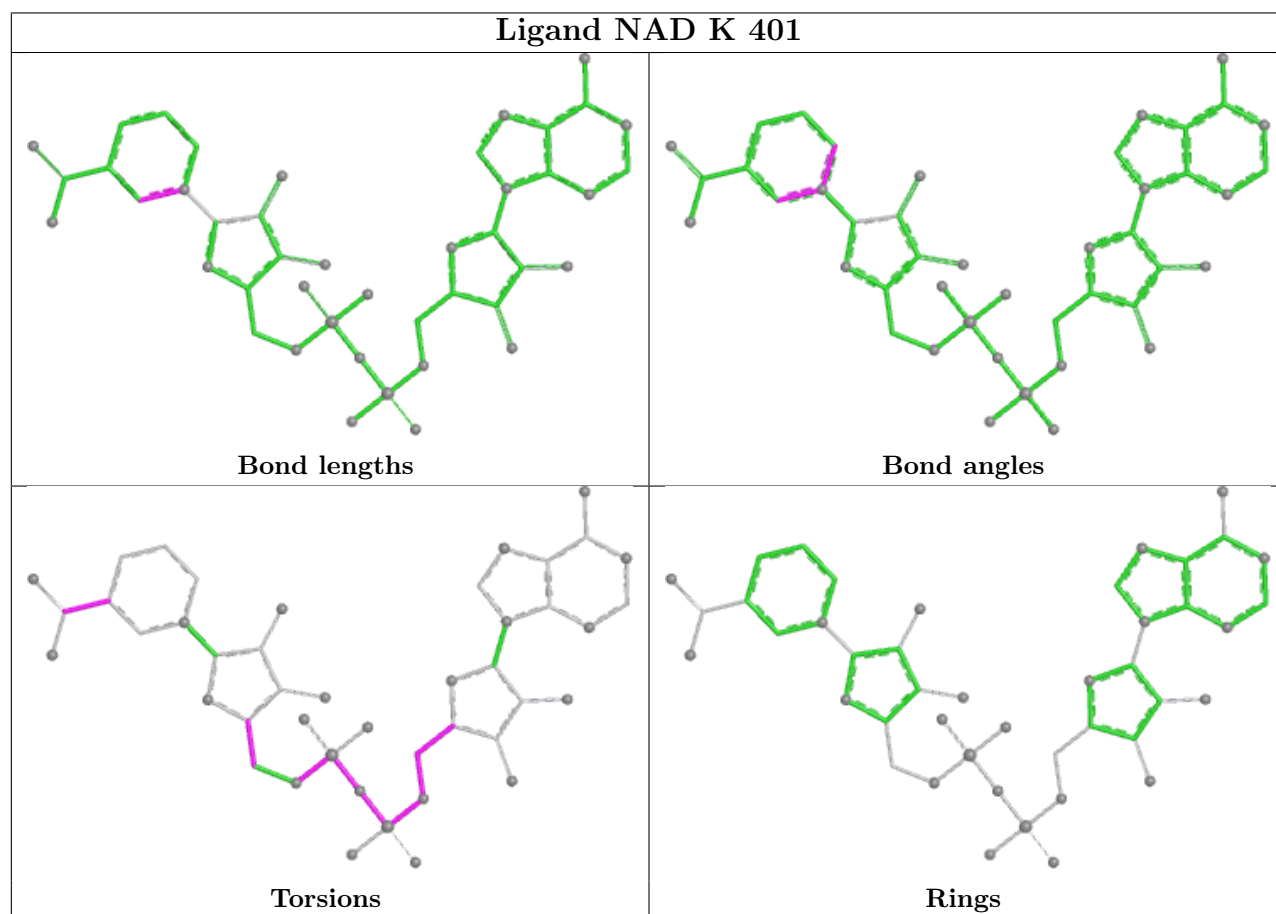
There are no ring outliers.

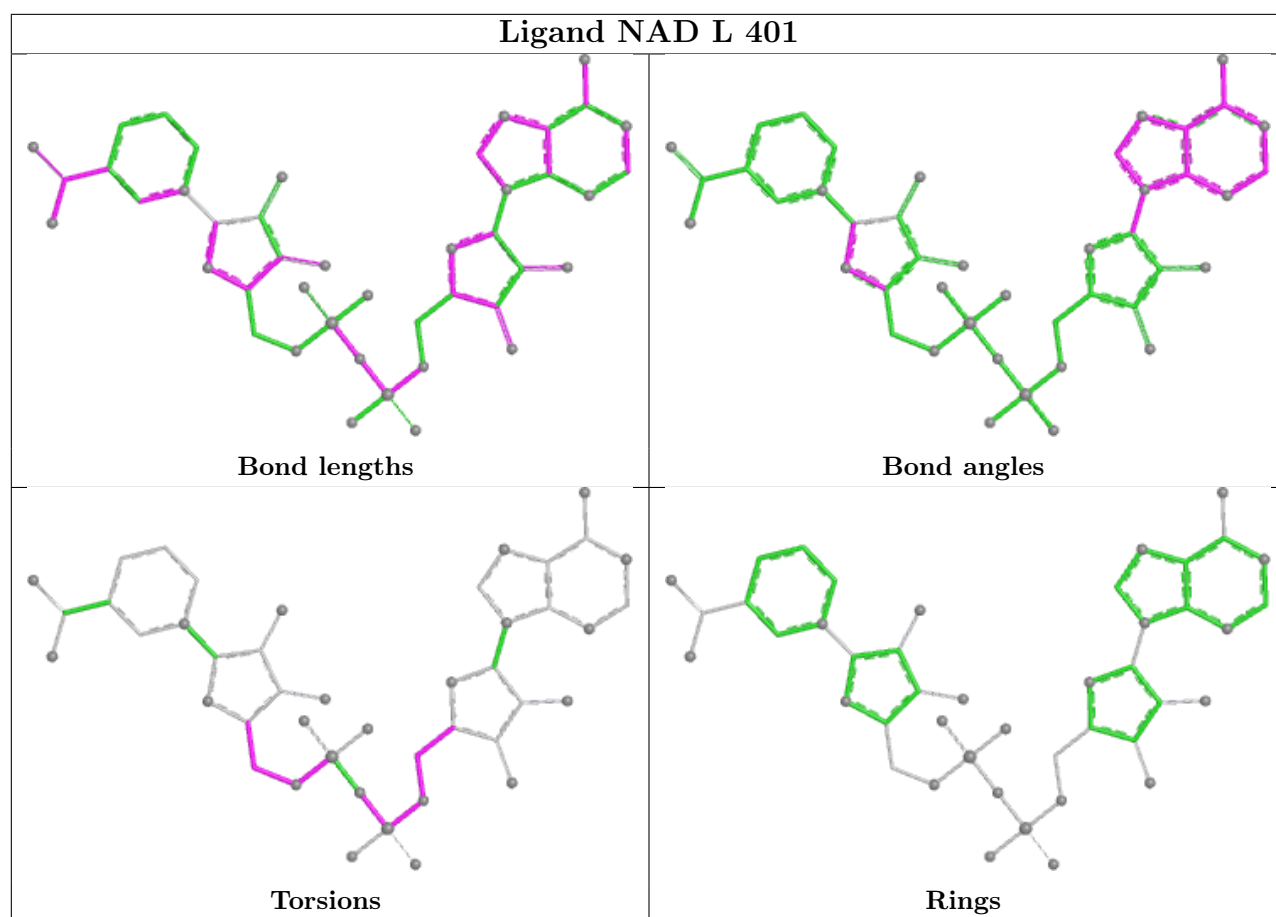
16 monomers are involved in 175 short contacts:

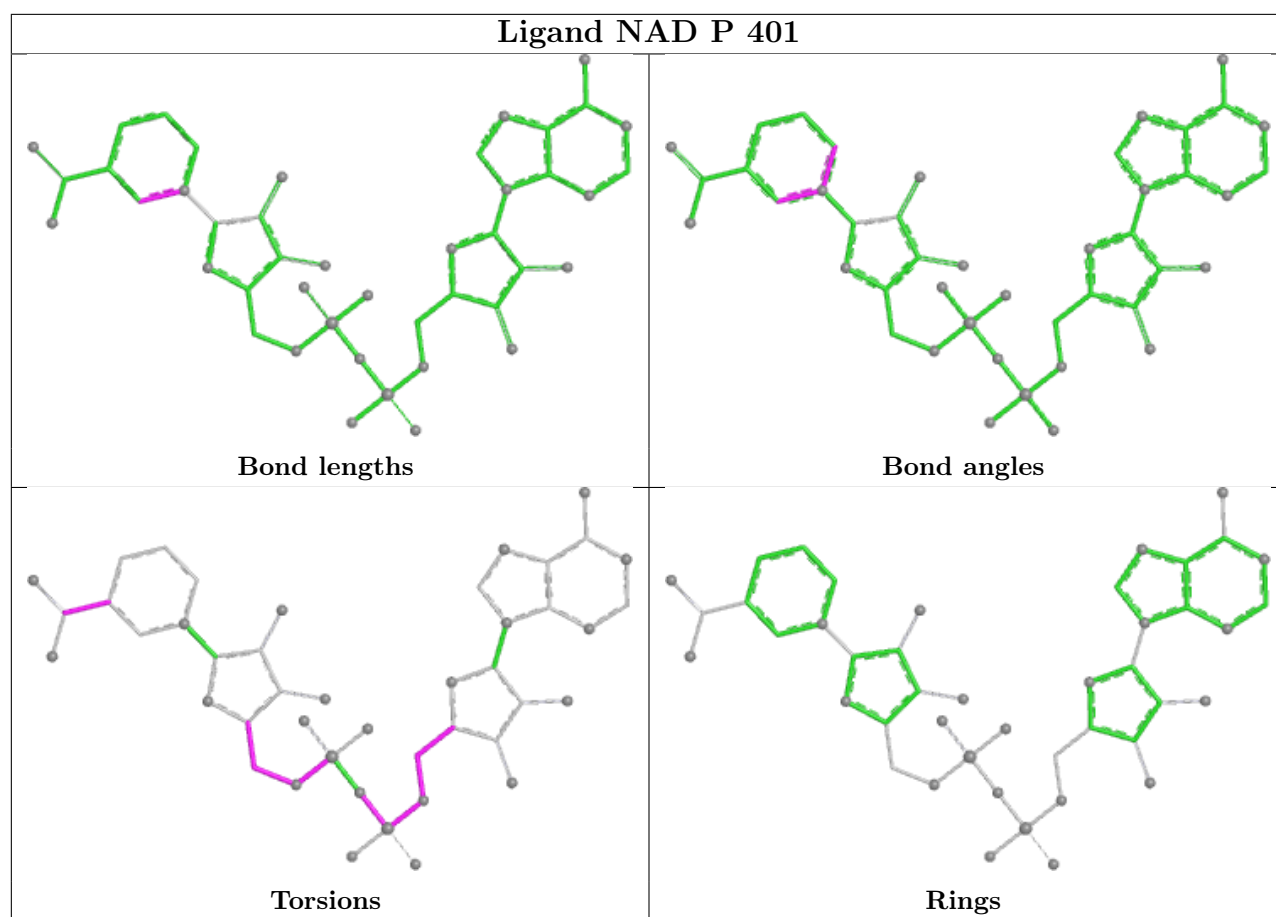
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	K	401	NAD	11	0
3	L	401	NAD	10	0
3	P	401	NAD	14	0
3	G	401	NAD	16	0
3	H	401	NAD	10	0
3	Q	401	NAD	12	0
3	B	401	NAD	11	0
3	R	401	NAD	13	0
3	I	401	NAD	9	0
3	F	401	NAD	10	0
3	O	401	NAD	10	0
3	D	401	NAD	12	0
3	C	401	NAD	12	0
3	J	401	NAD	9	0
3	E	401	NAD	9	0
3	A	401	NAD	7	0

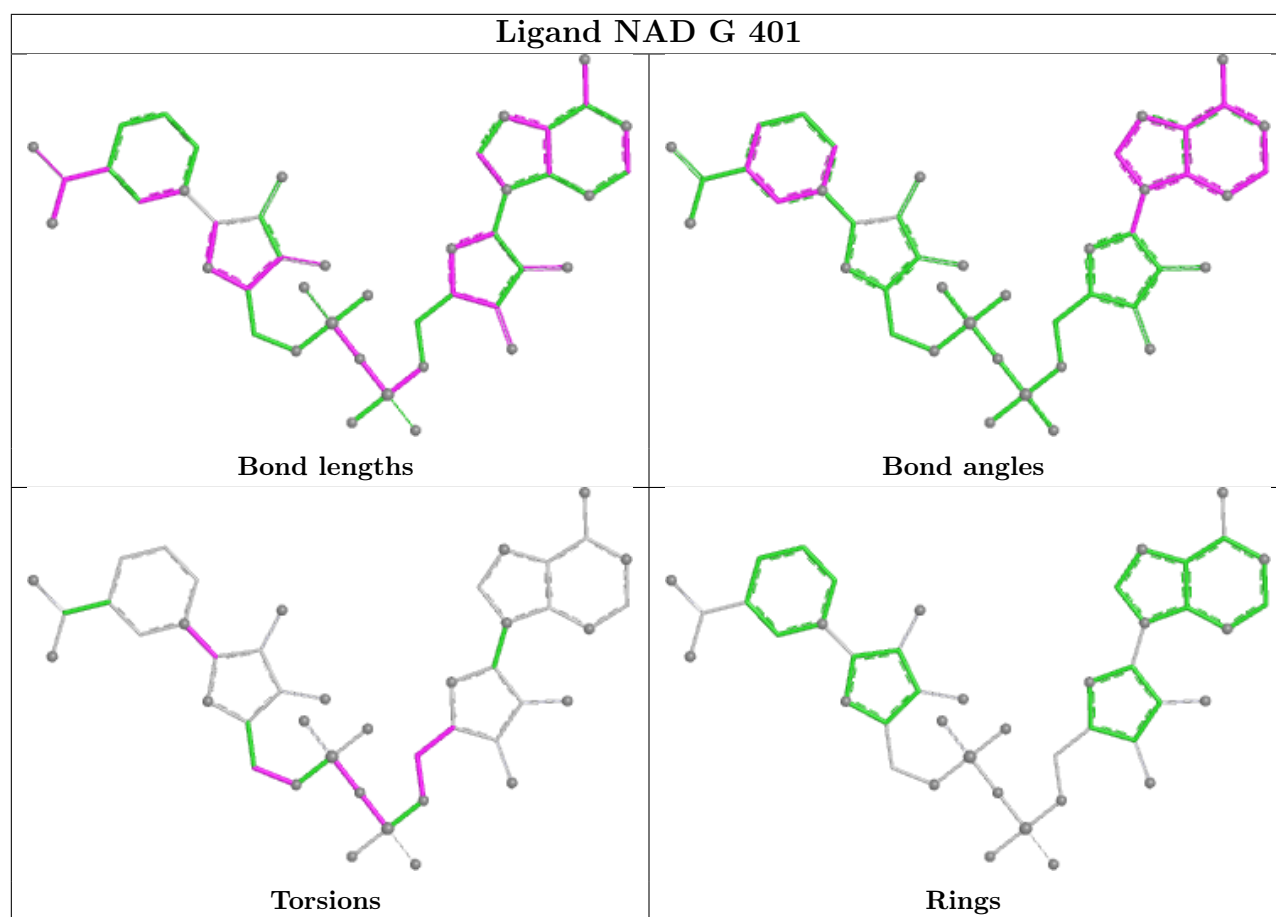
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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

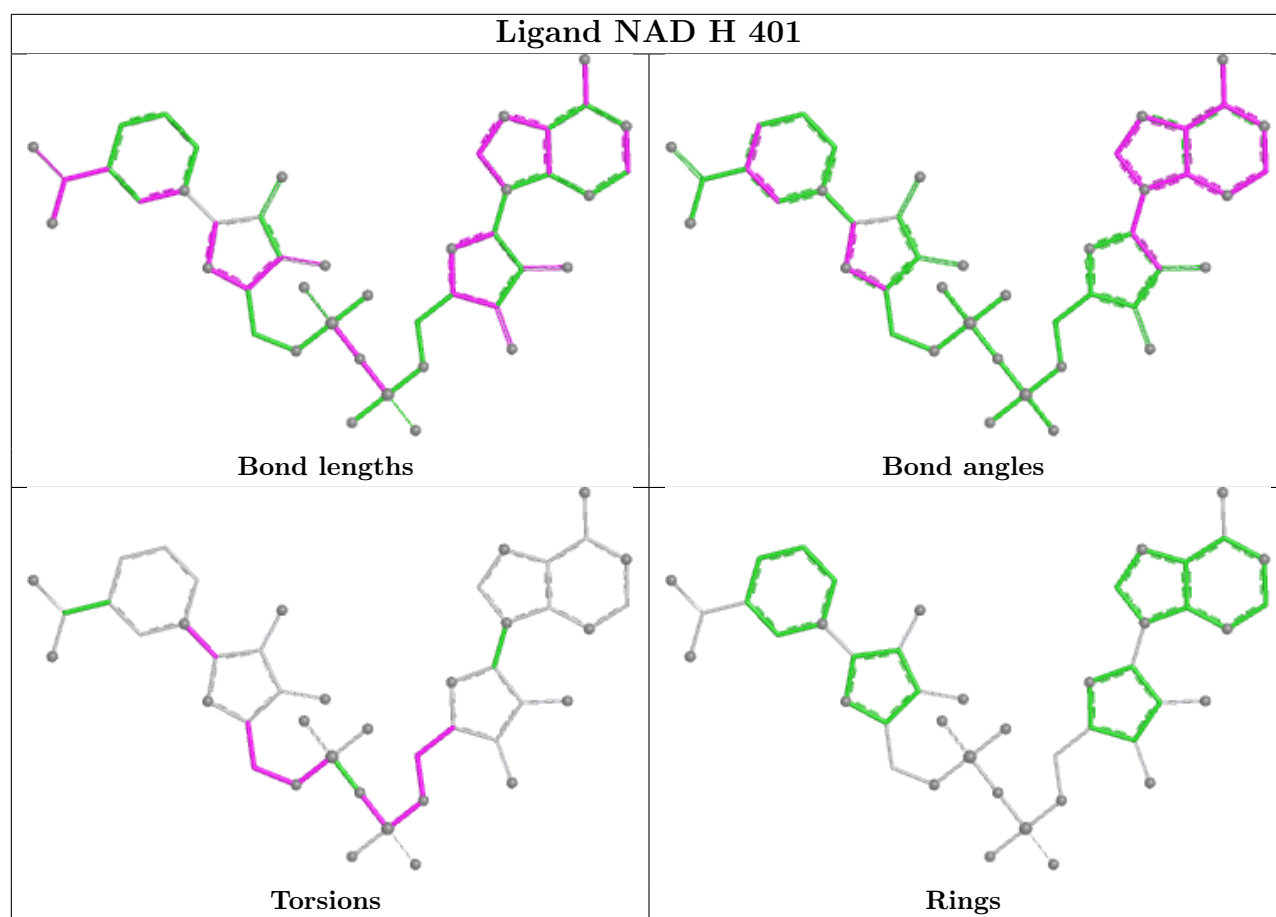
highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified 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.

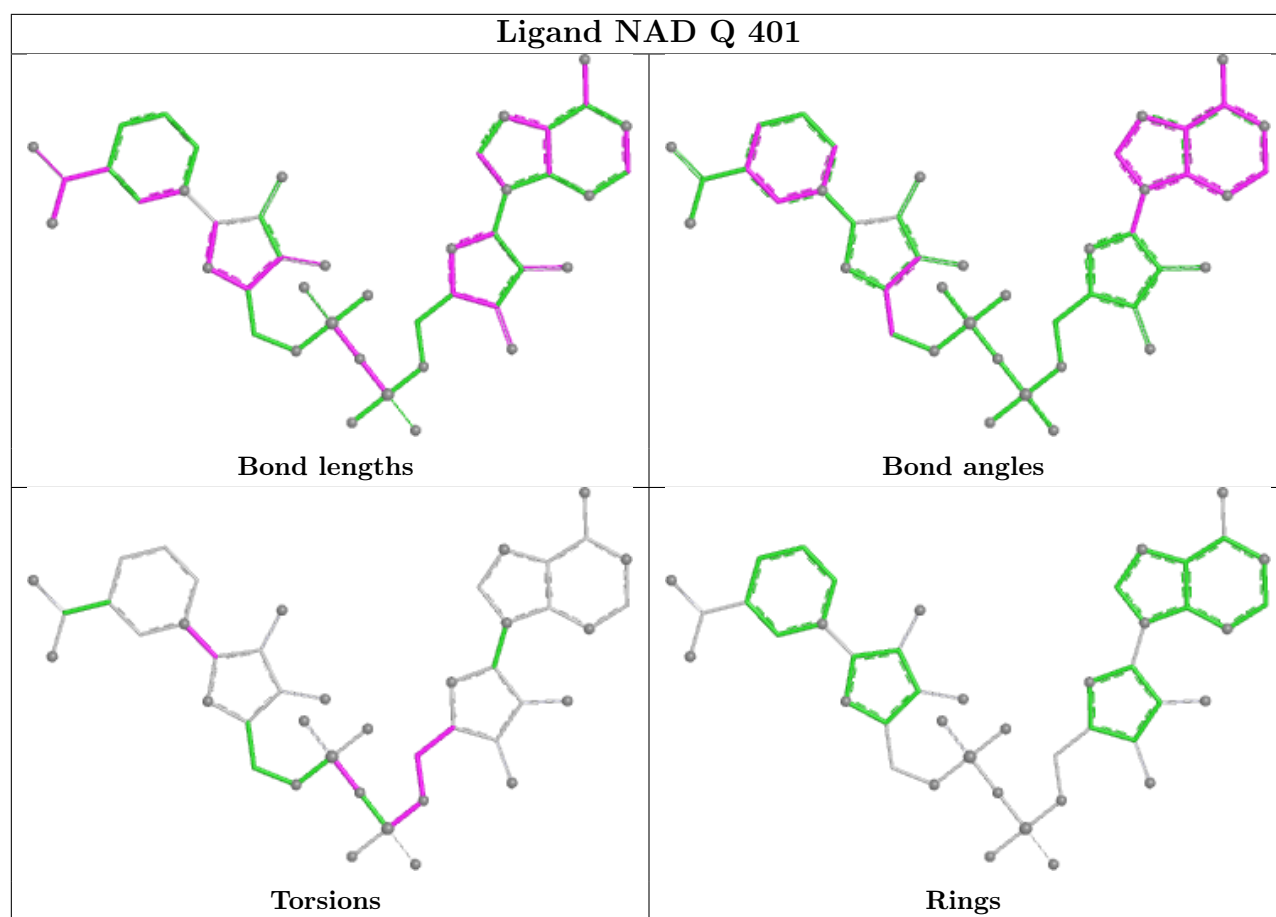


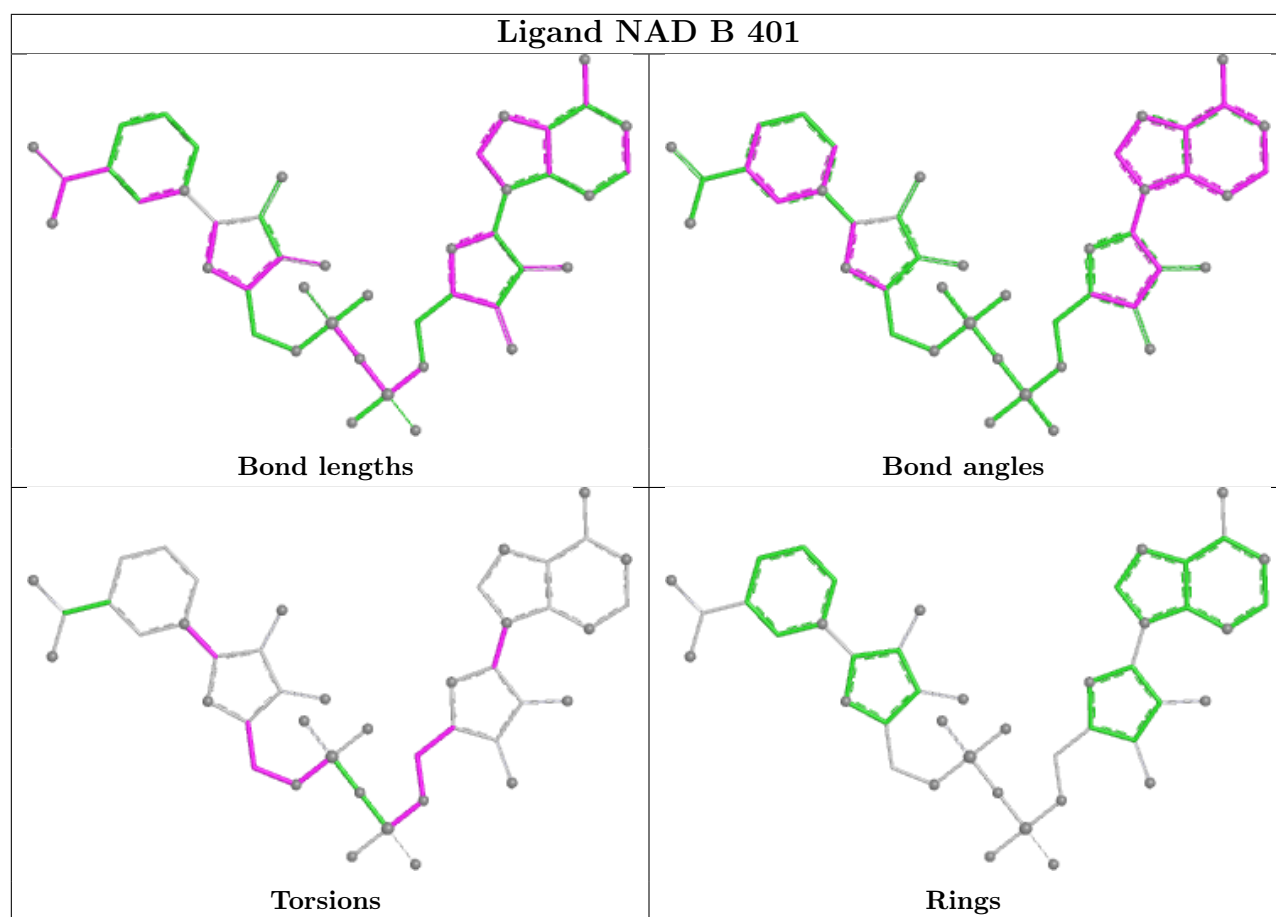


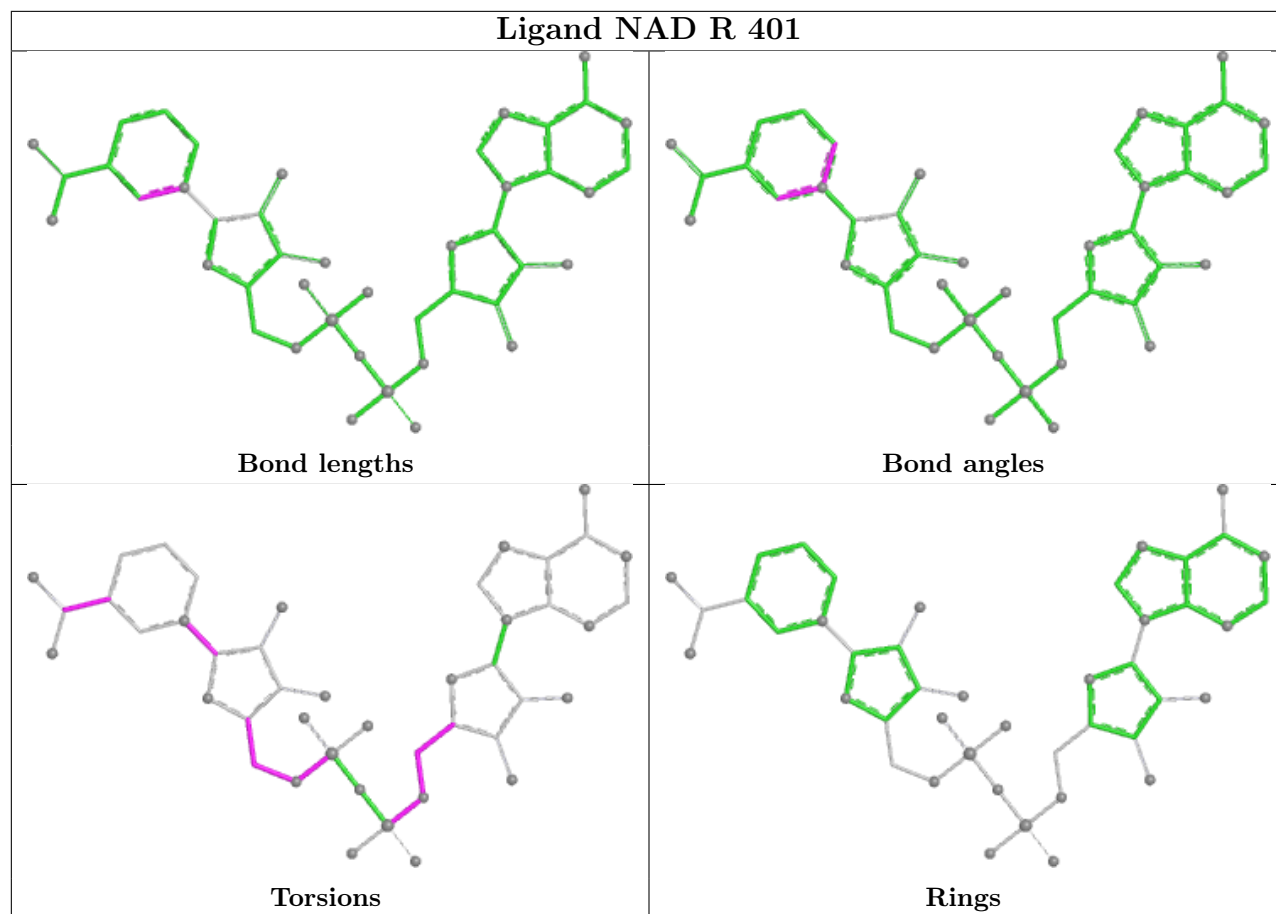


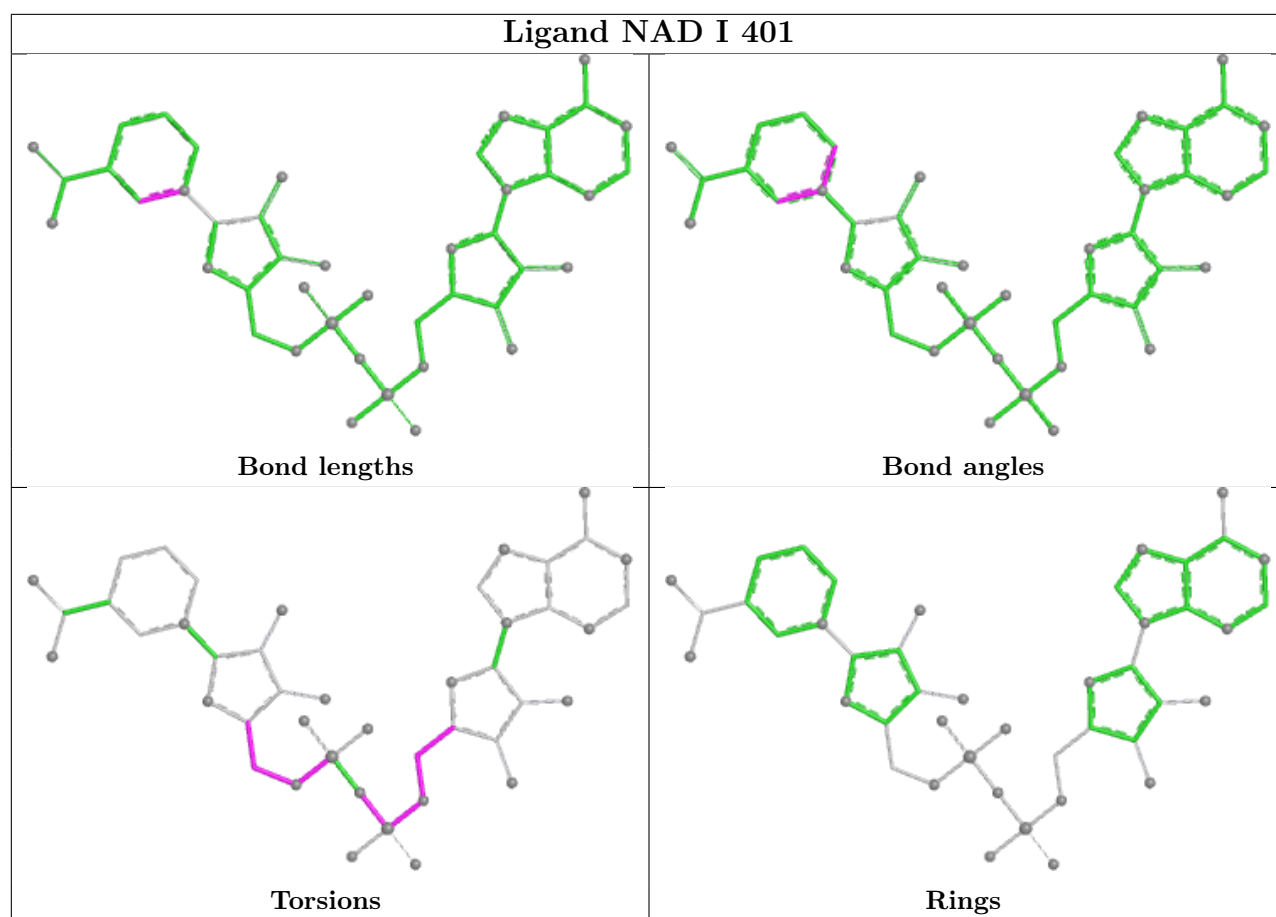


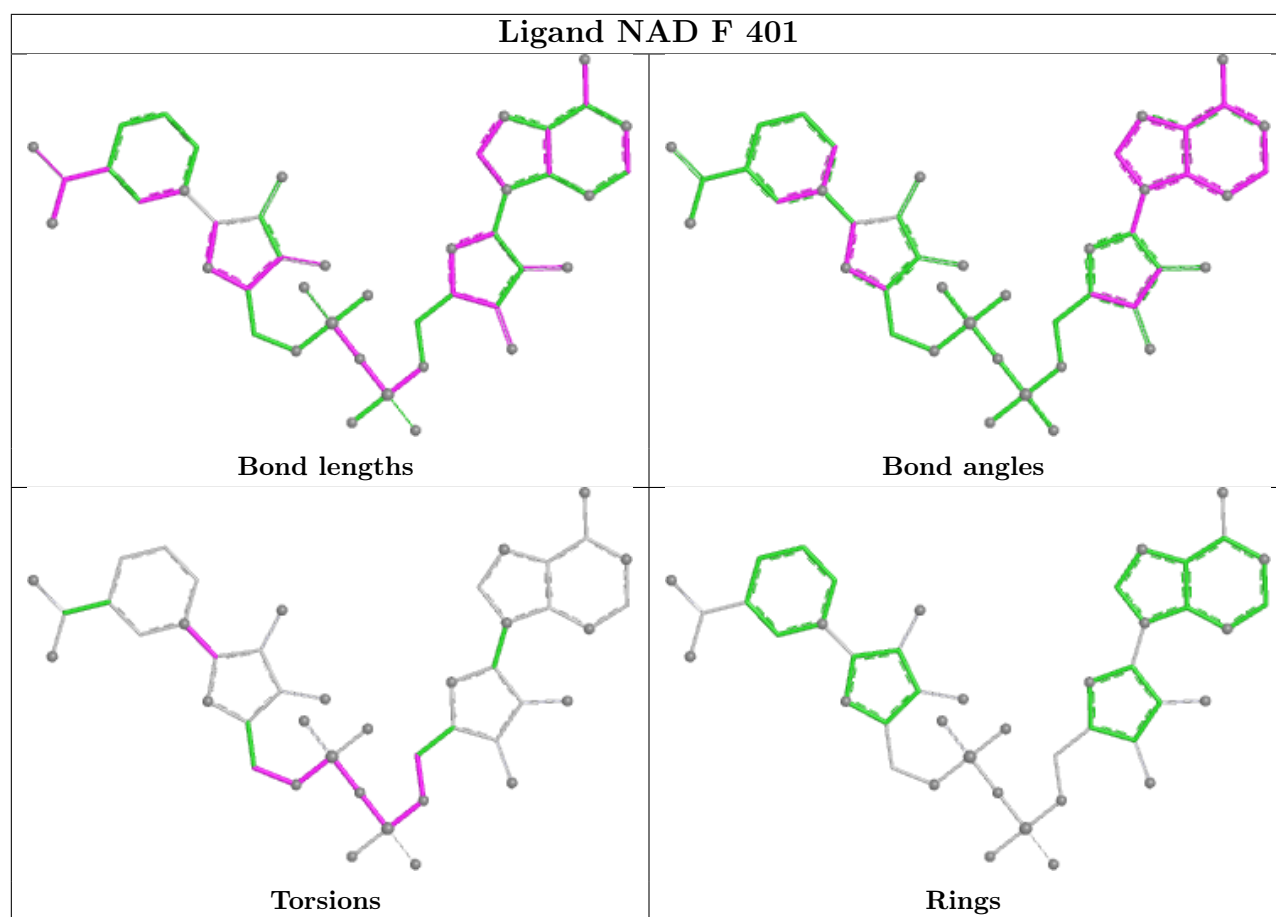


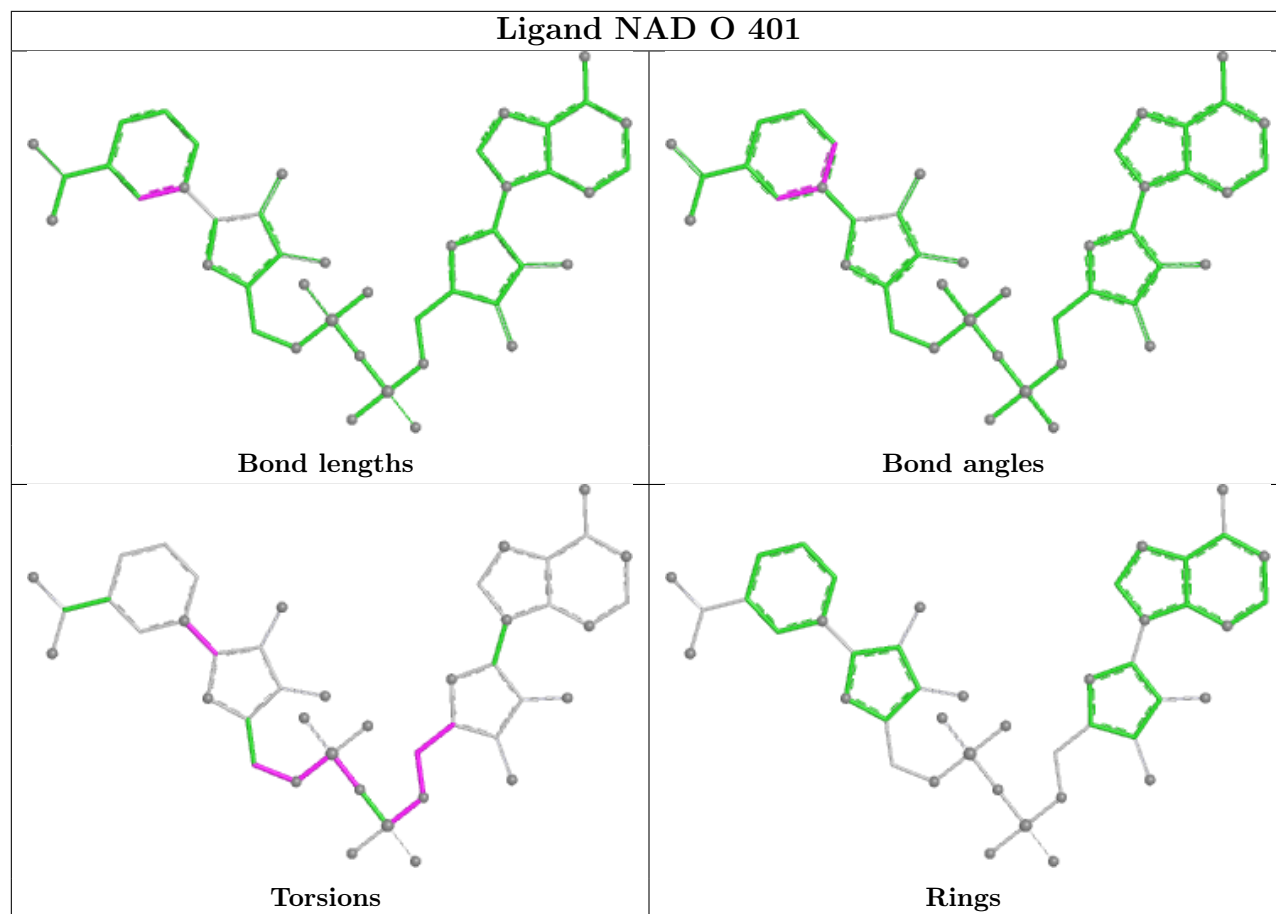


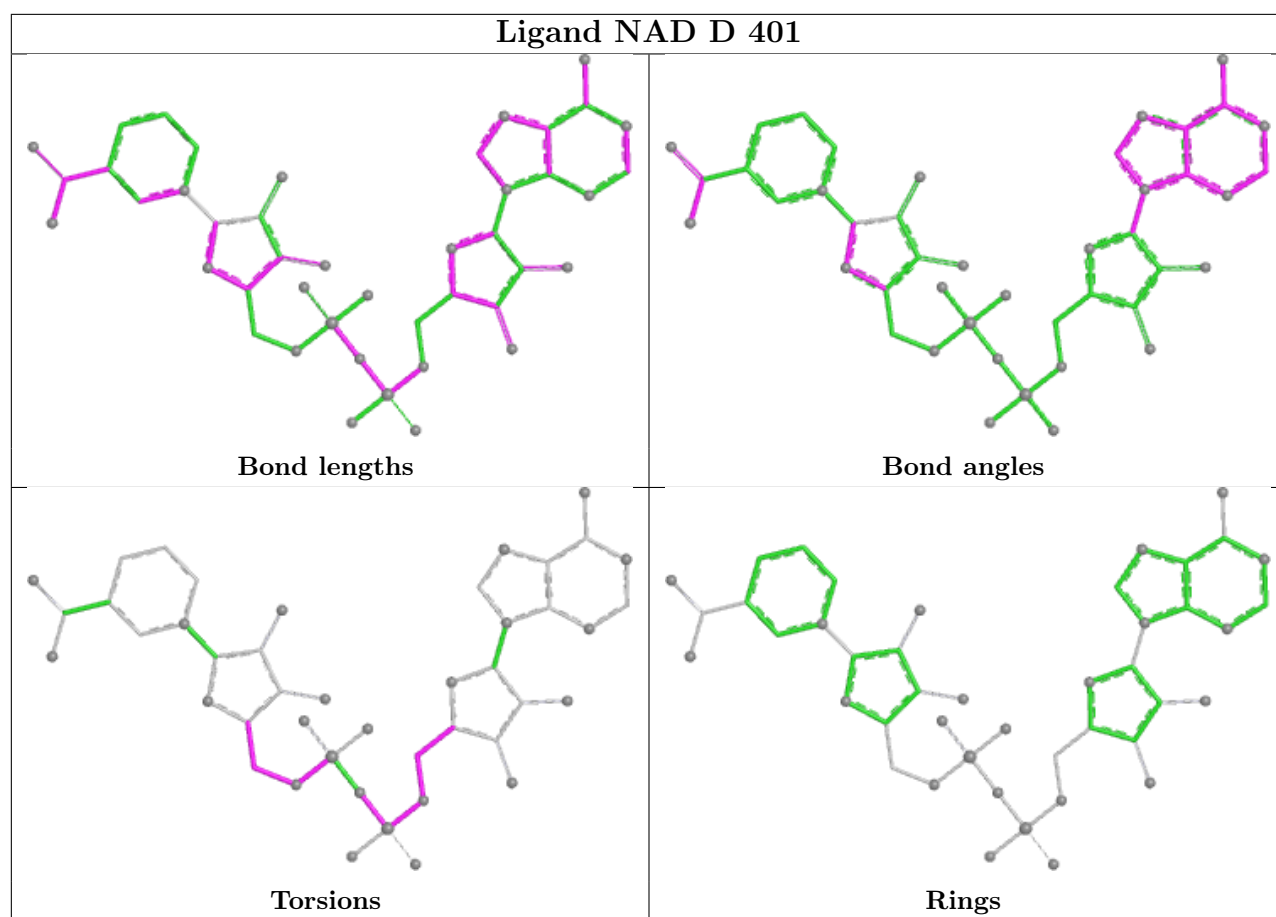


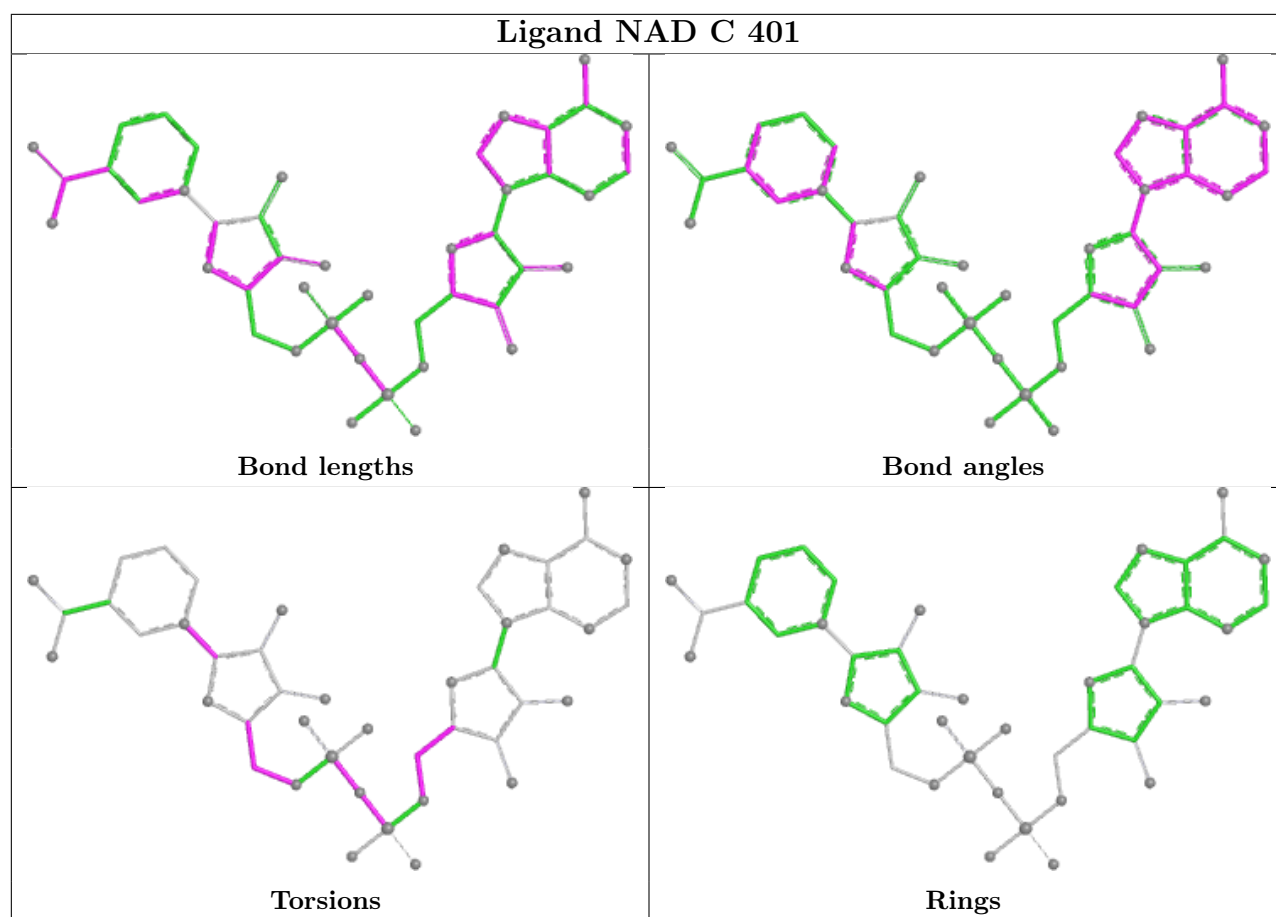


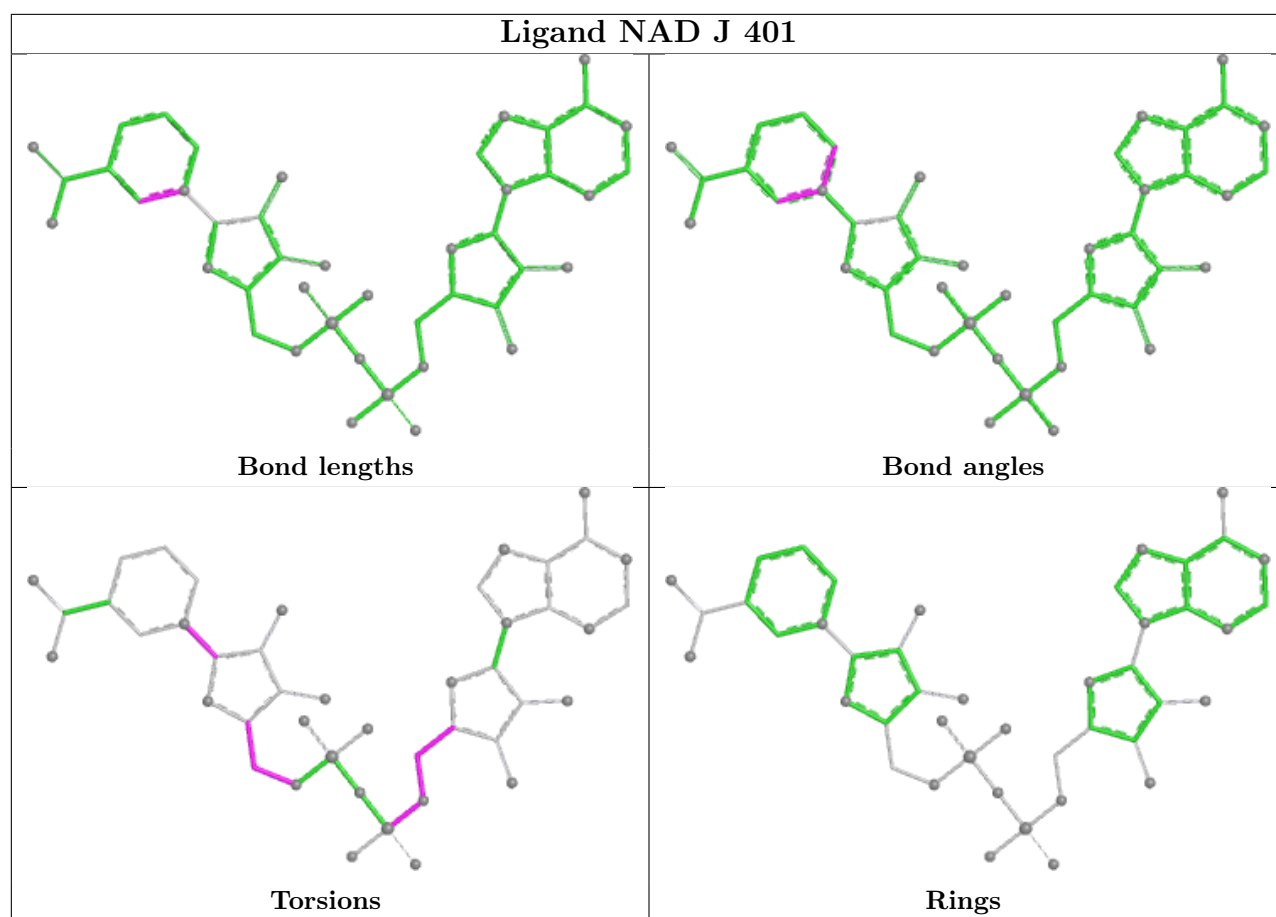


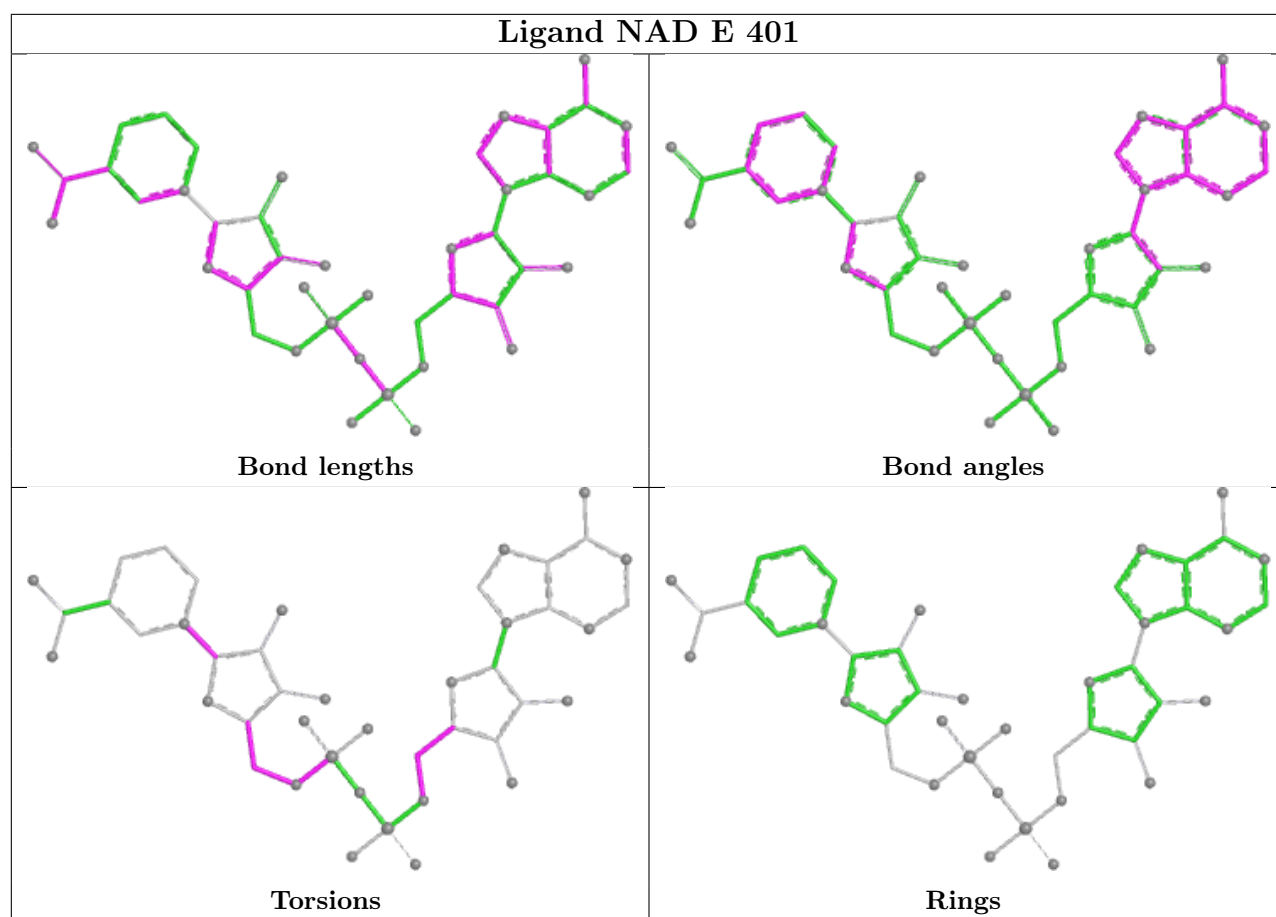


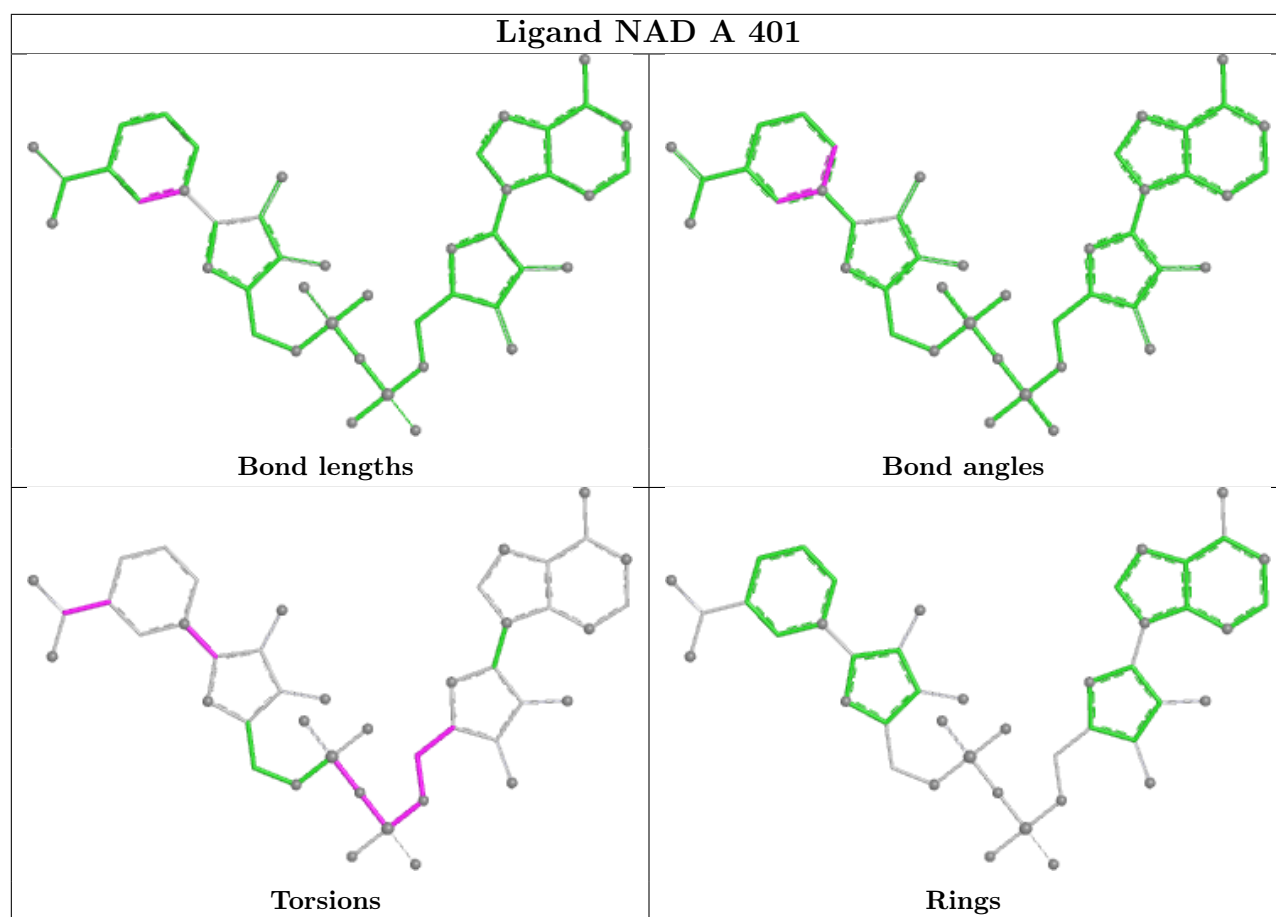












5.7 Other polymers [i](#)

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-13826. These allow visual inspection of the internal detail of the map and identification of artifacts.

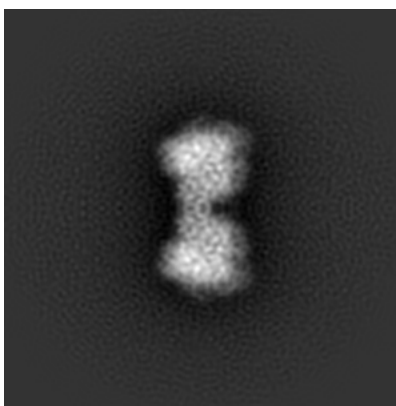
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

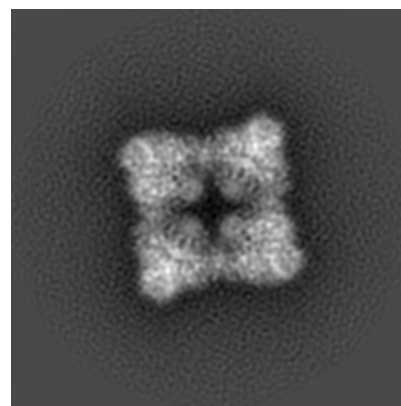
6.1.1 Primary map



X

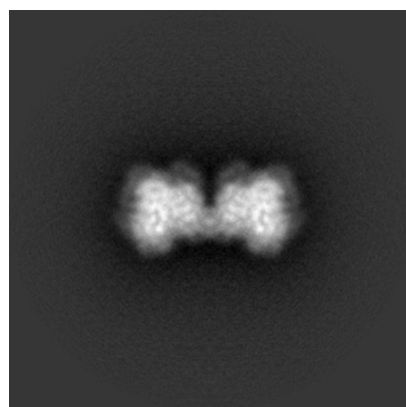


Y

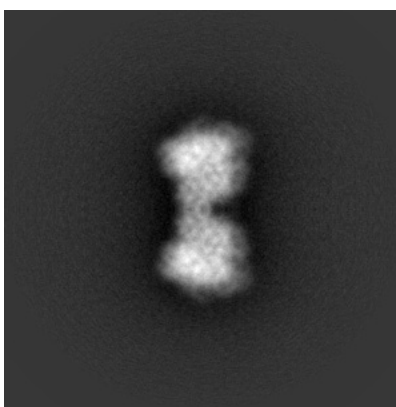


Z

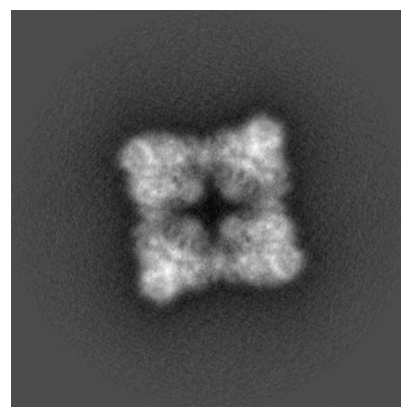
6.1.2 Raw map



X



Y

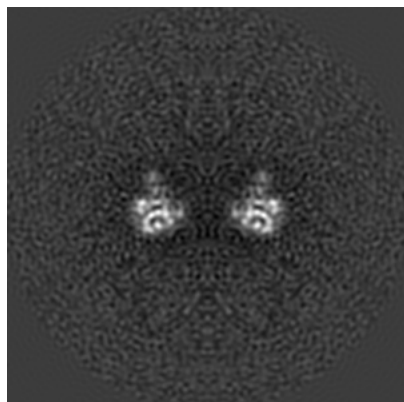


Z

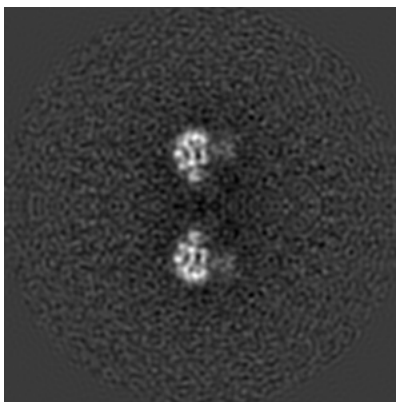
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

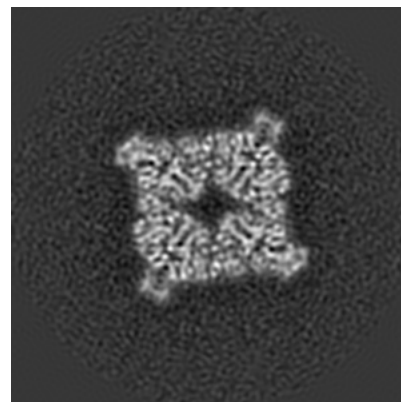
6.2.1 Primary map



X Index: 150

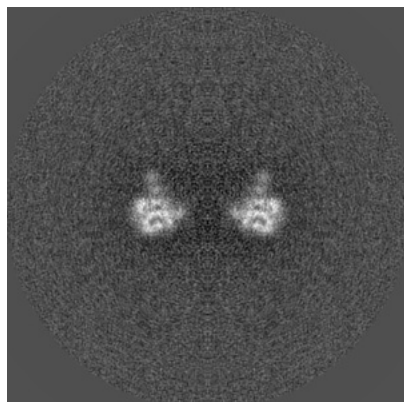


Y Index: 150

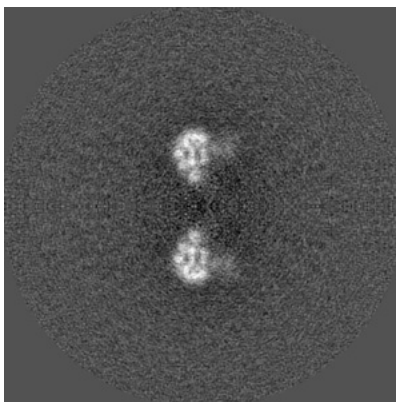


Z Index: 150

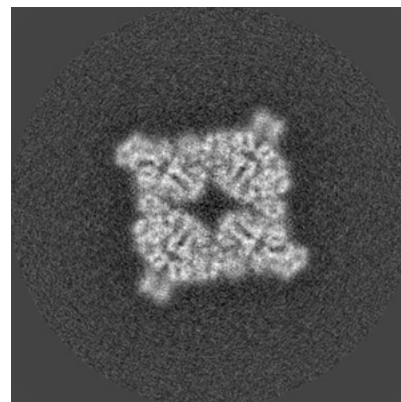
6.2.2 Raw map



X Index: 150



Y Index: 150

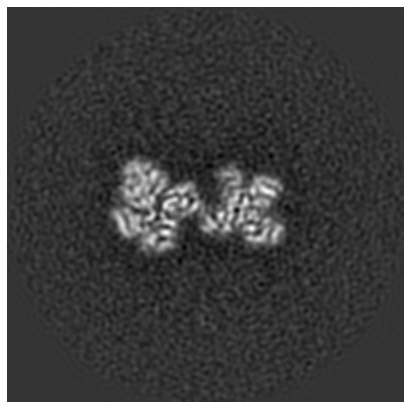


Z Index: 150

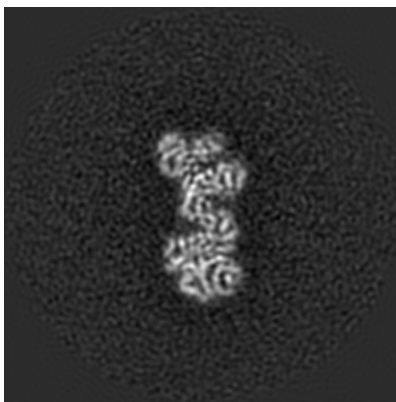
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

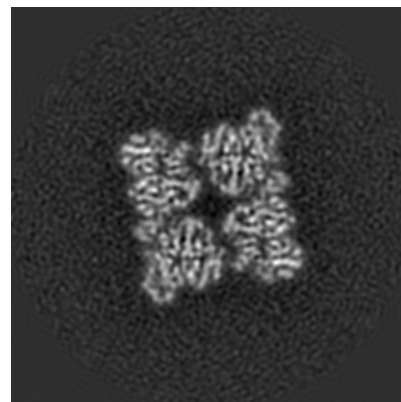
6.3.1 Primary map



X Index: 119

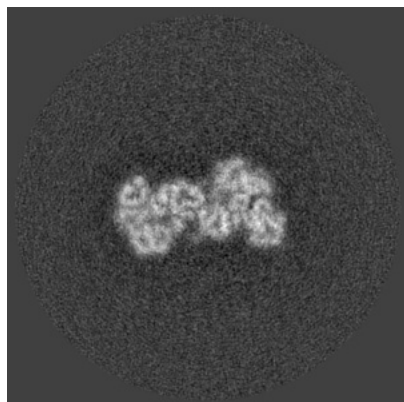


Y Index: 186

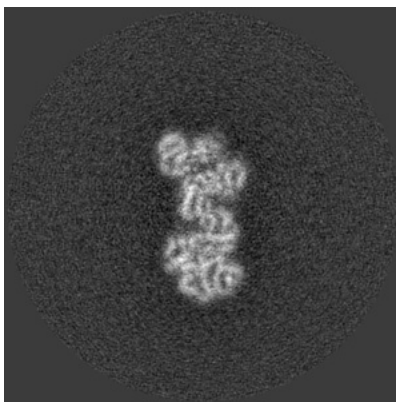


Z Index: 143

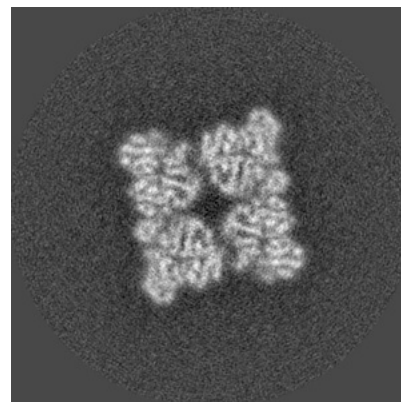
6.3.2 Raw map



X Index: 105



Y Index: 187

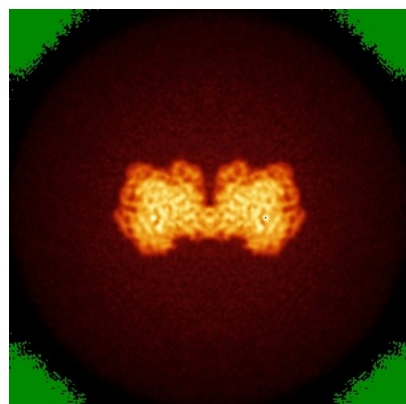


Z Index: 144

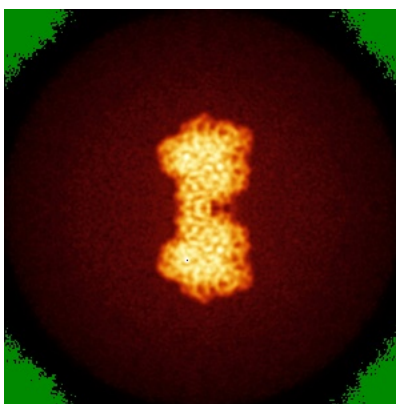
The images above show the largest variance slices of the map in three orthogonal directions.

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

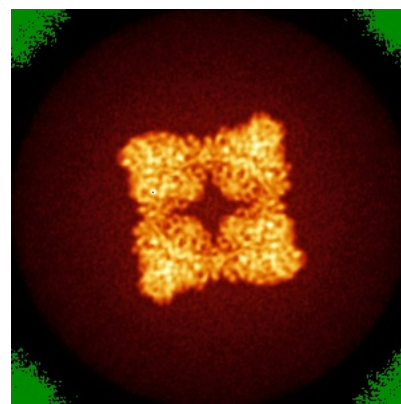
6.4.1 Primary map



X

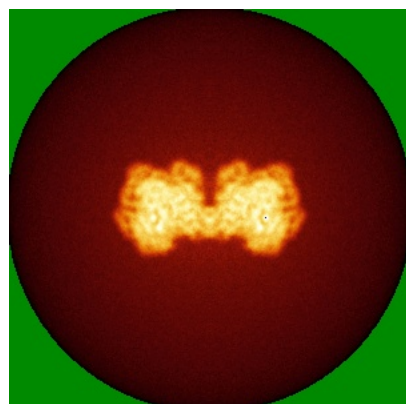


Y

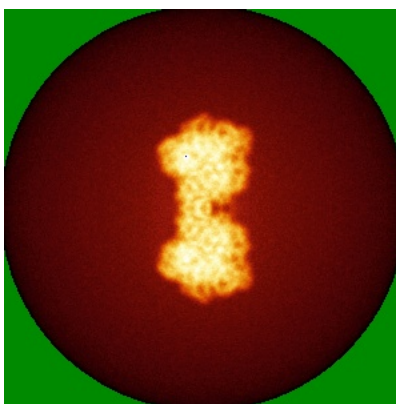


Z

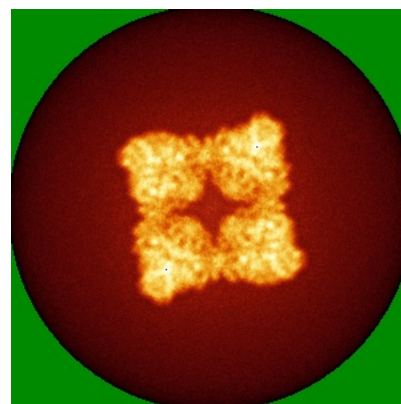
6.4.2 Raw map



X



Y

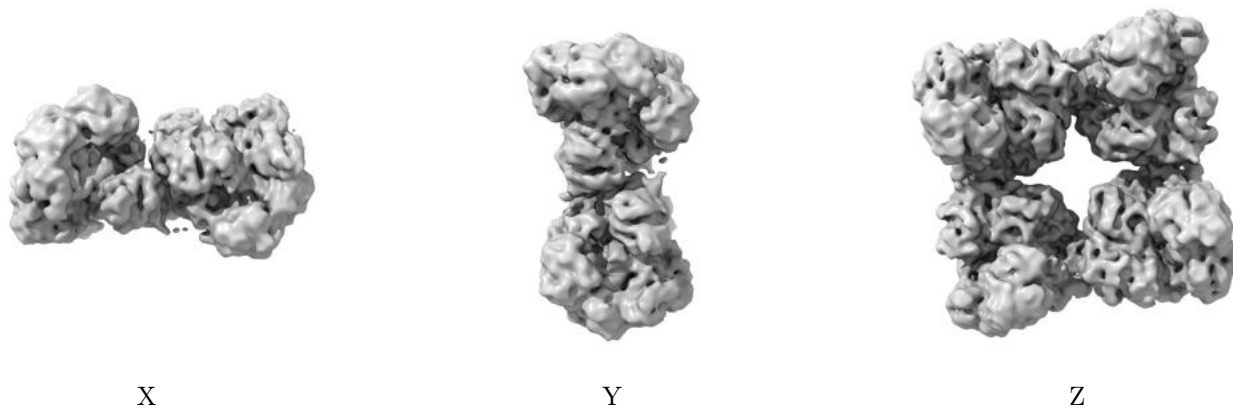


Z

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.

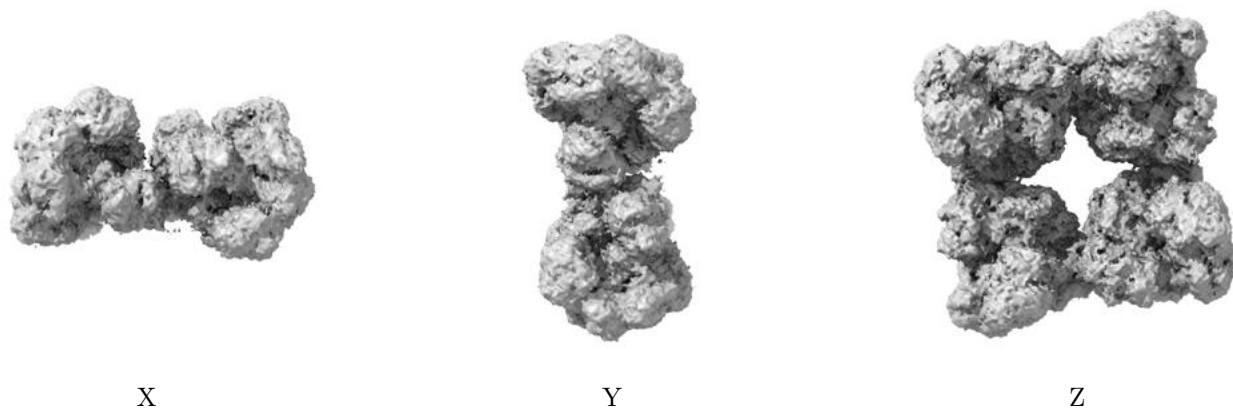
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.012. 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



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.

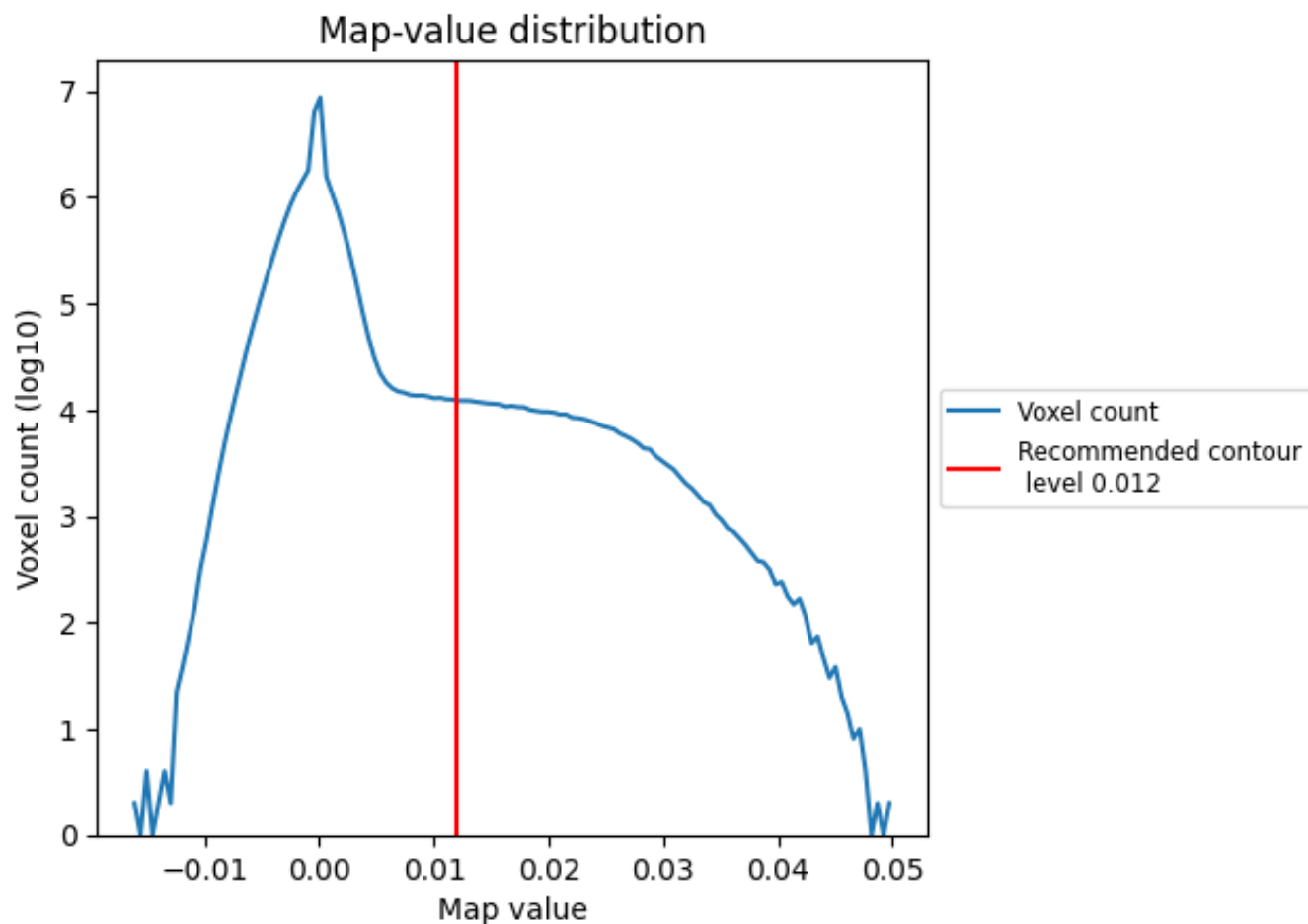
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

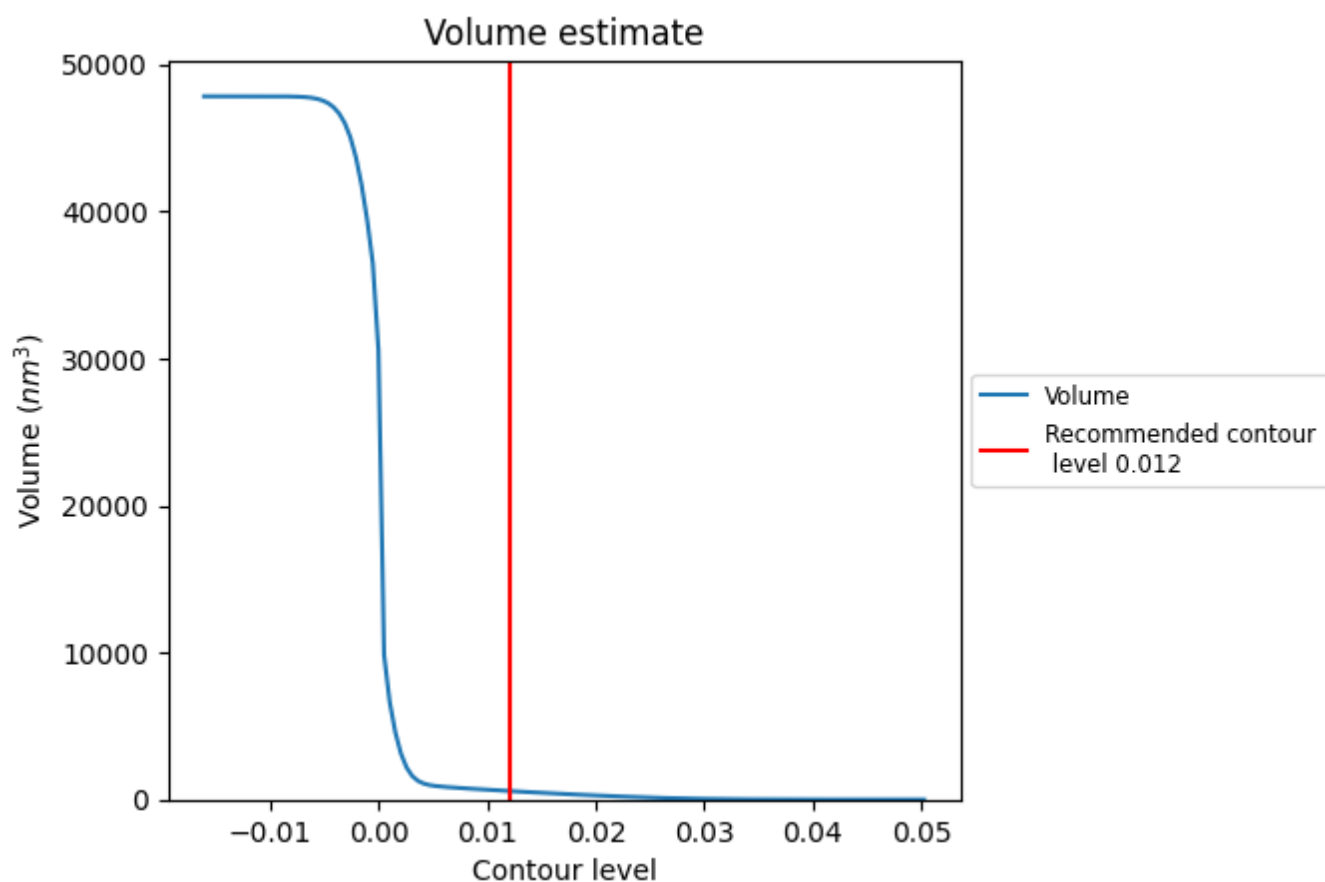
This section contains the results of statistical analysis of the map.

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.

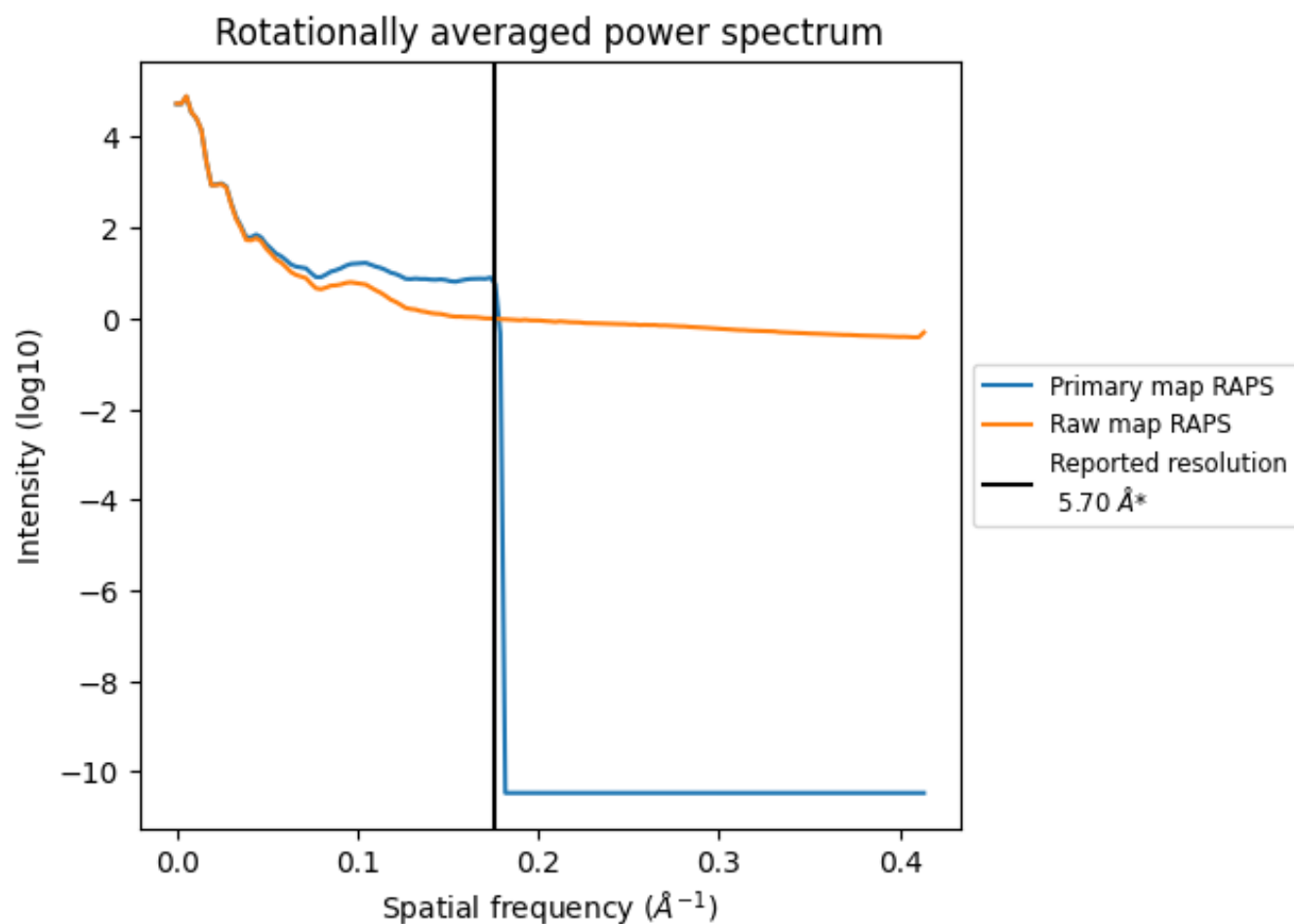
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 581 nm³; this corresponds to an approximate mass of 525 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 ⓘ

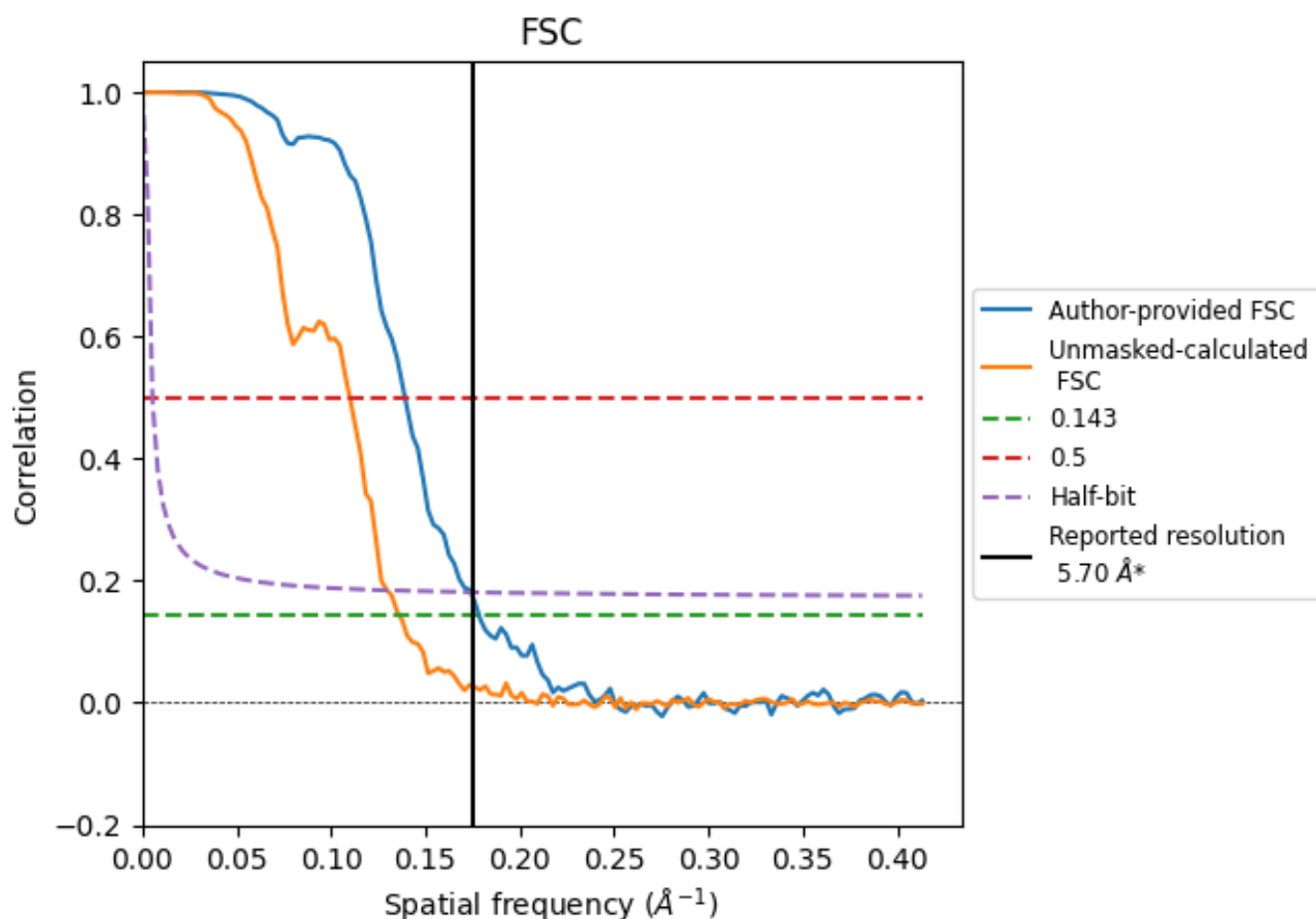


*Reported resolution corresponds to spatial frequency of $0.175 \text{ \AA}^{-1}$

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 $0.175 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

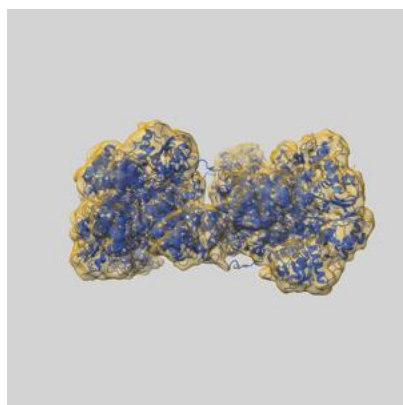
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.70	-	-
Author-provided FSC curve	5.61	7.18	5.74
Unmasked-calculated*	7.34	9.09	7.70

*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 7.34 differs from the reported value 5.7 by more than 10 %

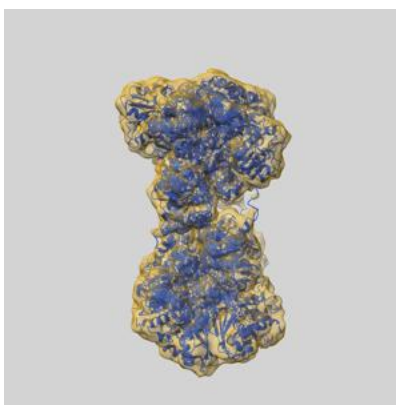
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13826 and PDB model 7Q55. Per-residue inclusion information can be found in section [3](#) on page [7](#).

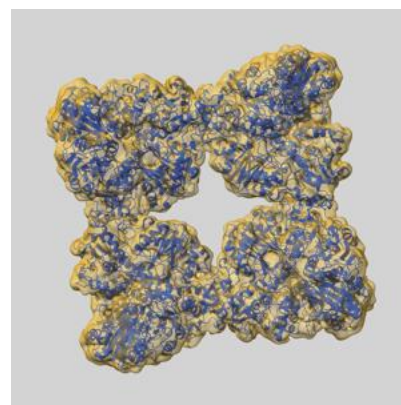
9.1 Map-model overlay [i](#)



X



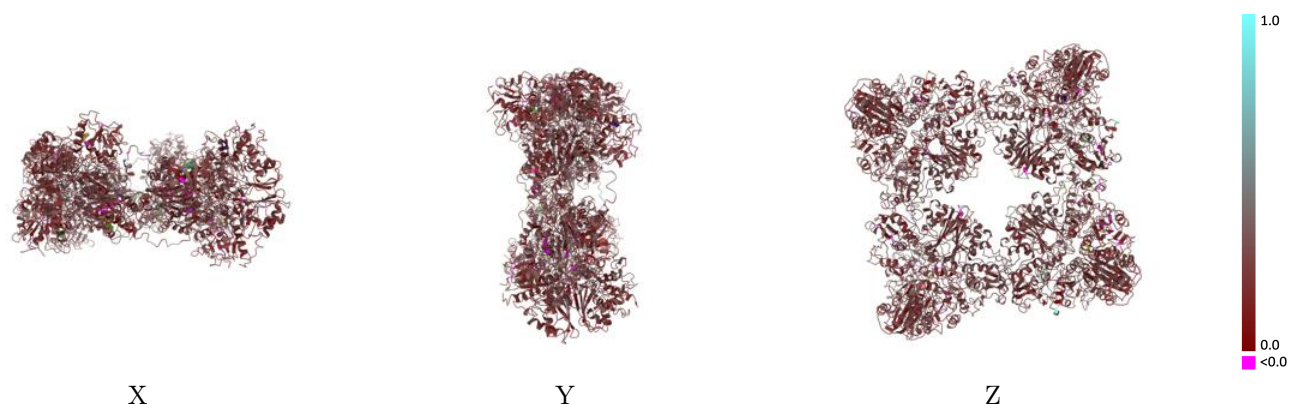
Y



Z

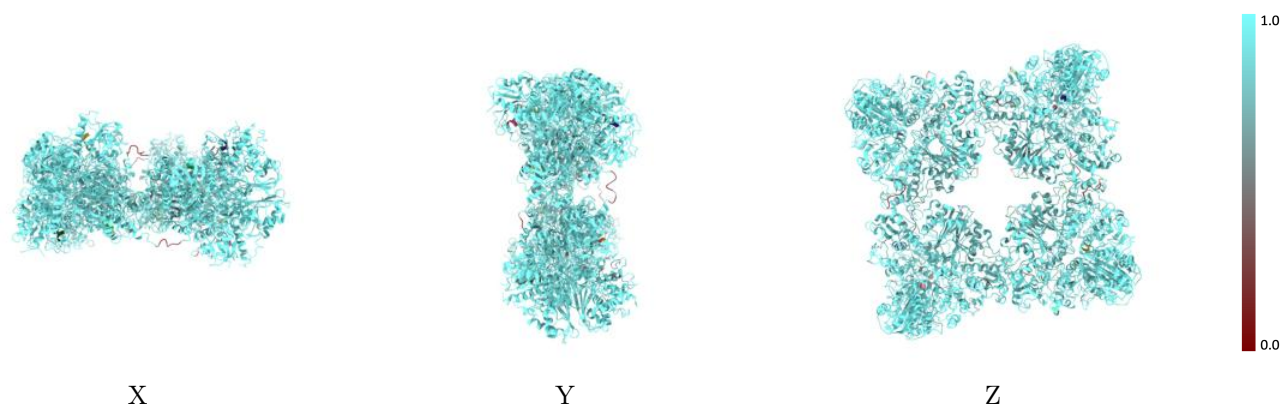
The images above show the 3D surface view of the map at the recommended contour level 0.012 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



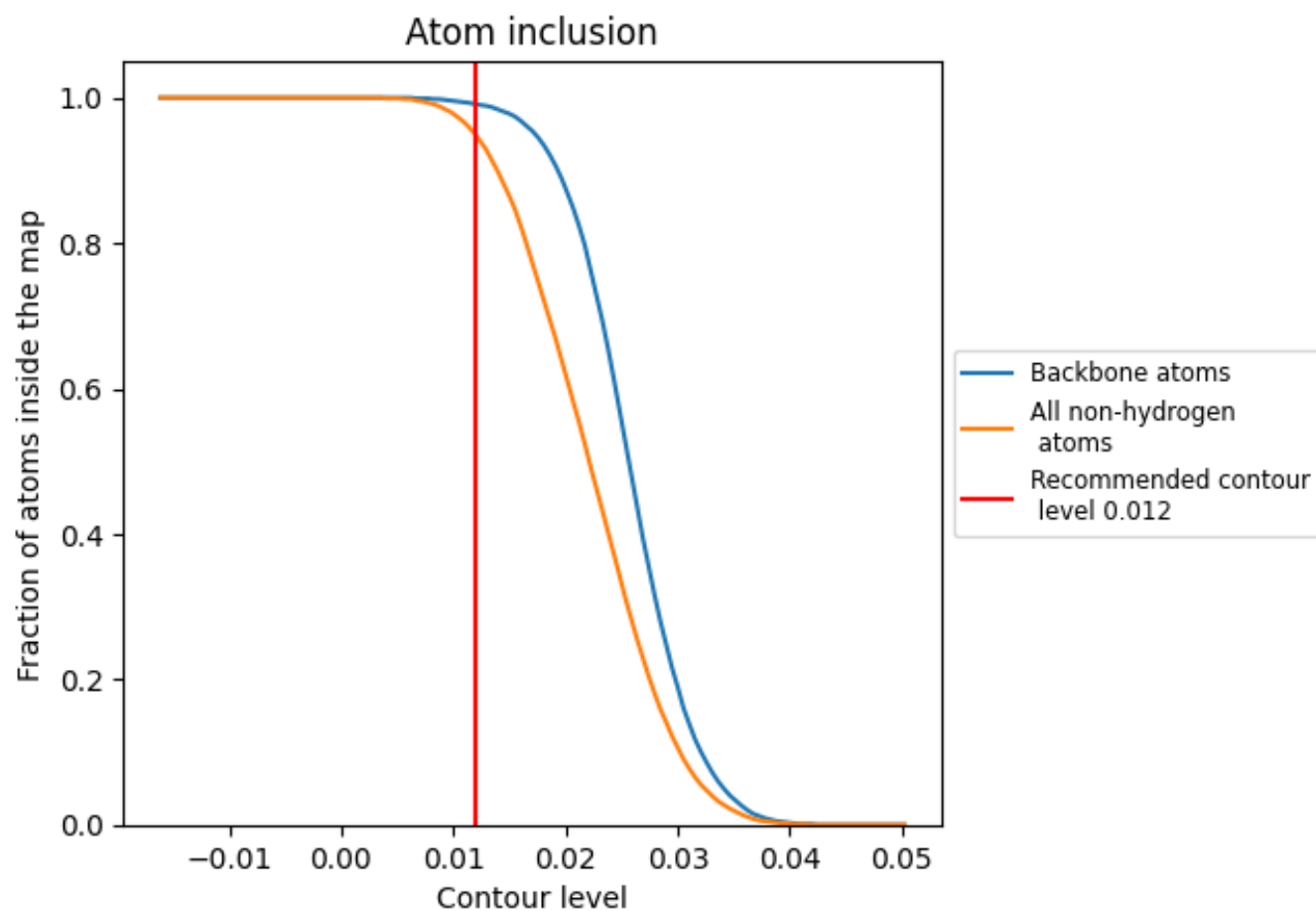
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.012).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 95% 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 (0.012) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9490	0.2620
A	0.9370	0.2700
B	0.9660	0.2560
C	0.9330	0.2690
D	0.9670	0.2510
E	0.9310	0.2700
F	0.9620	0.2550
G	0.9380	0.2690
H	0.9630	0.2600
I	0.9300	0.2680
J	0.9680	0.2540
K	0.9360	0.2710
L	0.9680	0.2520
O	0.9320	0.2680
P	0.9650	0.2520
Q	0.9300	0.2670
R	0.9650	0.2610

1.0

0.0

<0.0