



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 03:51 AM UTC

PDB ID : 6R9G / pdb_00006r9g
EMDB ID : EMD-4770
Title : Structural basis of transcription inhibition by the DNA mimic Ocr protein of bacteriophage T7
Authors : Ye, F.Z.; Zhang, X.D.
Deposited on : 2019-04-03
Resolution : 3.70 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:

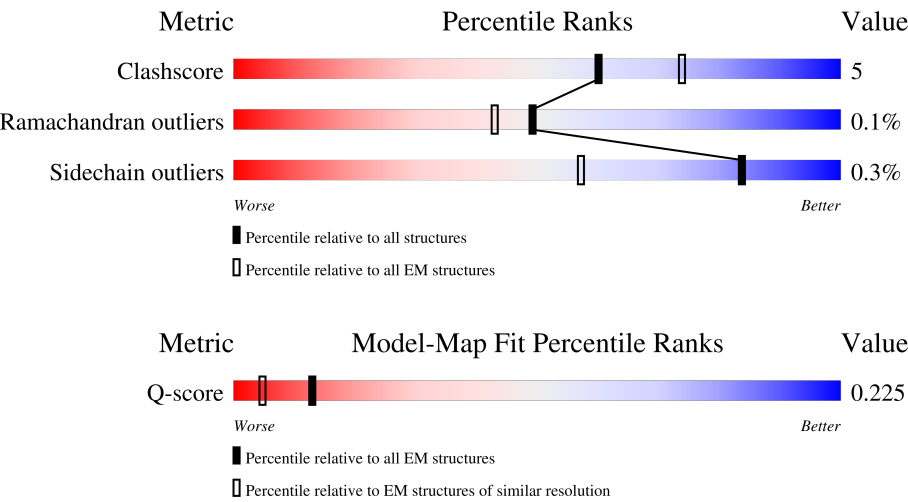
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.70 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	11569 (3.20 - 4.20)

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	329	
1	B	329	
2	C	1342	
3	D	1407	

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Mol	Chain	Length	Quality of chain
4	E	80	94% 88% 6% 6%
5	F	117	91% 79% 11% 9%
5	G	117	89% 79% 10% 11%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 25944 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 DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	230	Total	C	N	O	S	0	0
			1765	1100	308	351	6		
1	B	231	Total	C	N	O	S	0	0
			1743	1090	301	346	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	1341	Total	C	N	O	S	0	0
			10112	6334	1735	2006	37		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	1334	Total	C	N	O	S	0	0
			10051	6297	1777	1934	43		

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

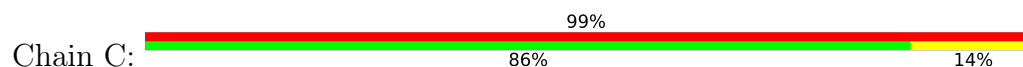
Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	75	Total	C	N	O	S	0	0
			572	351	110	109	2		

- Molecule 5 is a protein called Overcome classical restriction gp0.3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	104	Total	C	N	O	S	0	0
			849	534	131	179	5		
5	F	106	Total	C	N	O	S	0	0
			852	530	136	182	4		

GLU	THR
VAL	GLU
ILE	ILE
LYS	LYS
GLY	ASP
GLY	VAL
LYS	LEU
PRO	ALA
GLU	SER
PHE	SER
ASP	ARG
PRO	GLY
ILE	LEU
LEU	SER
LEU	LEU
ARG	GLY
VAL	PRO
VAL	ARG
ASP	LEU
ASP	GLU
LEU	ASP
LEU	ASN
TRP	PRO
PRO	THR
LEU	VAL
LEU	ALA
LEU	VAL
LEU	ARG
LEU	SER
LEU	SER
LEU	ILE
LEU	ASP
LEU	ASP
LEU	GLU

• Molecule 2: DNA-directed RNA polymerase subunit beta



E541	L481	S421	S361	Y301	L241	G181	E121	S61	V2
R542	G482	K422	A362	I302	V242	S182	V122	Y62	V2
A543	D483	D423	L363	D303	P243	W183	Y123	S63	Y3
G544	L484	D424	V364	E304	E244	L184	M124	G64	S4
F545	D485	I425	E365	S305	R245	D185	G125	N65	Y5
E546	T486	I426	L366	T306	L246	F186	E126	S66	T6
V547	L487	D427	Y367	G307	R247	E187	I127	E67	E7
R548	M488	V428	R368	E308	G248	F188	P128	L68	K9
D549	P489	M429	K369	L309	E249	D189	L129	Q69	R10
V550	Q490	K430	M370	I310	T250	P190	M130	Y70	I11
H551	D491	K431	R371	C311	A251	K191	T131	V71	I12
P552	M492	L432	P372	A312	S252	D192	D132	S72	K13
T553	I493	I433	G373	A313	F253	N193	M133	Y73	D14
H554	M494	D434	E374	N314	D254	L194	G134	R74	F15
Y555	A495	I435	P375	M315	I255	F195	T135	L75	G16
G556	K496	R436	P376	E316	E256	V196	F136	G76	K17
R557	P497	M437	T377	L317	A257	R197	V137	E77	R18
V558	L498	G438	R378	S318	N258	I198	I138	P78	P19
C559	S499	K439	E379	L319	G259	D199	M139	V79	Q20
P560	A500	G440	A380	D320	K260	R200	G140	F80	V21
I561	E501	E441	A381	L321	V261	R201	T141	D81	L22
E562	V502	V442	E382	L322	V262	R202	E142	V82	D23
T563	K503	D443	S383	A323	V263	K203	R143	Q83	V24
P564	E504	D444	L384	K324	E264	L204	V144	E84	P25
E565	F505	I445	F385	L325	K265	P205	I145	C85	Y26
G566	F506	D446	E386	S326	G266	A206	V146	Q86	L27
P567	G507	H447	N387	Q327	R267	T207	S147	I87	L28
N568	S508	L448	L388	S328	K268	I208	Q148	R88	S29
I569	S509	G449	F389	G329	L269	L209	L149	C89	I30
G570	Q510	N450	F390	H330	T270	L210	H150	V90	Q31
L571	L511	R451	S391	K331	A271	R211	R151	T91	L32
I572	S512	R452	E392	R332	R272	A212	S152	Y92	D33
N573	Q513	I453	D393	I333	H273	L213	P153	S93	S34
S574	F514	R454	K394	E334	L274	N214	G154	A94	P35
L575	M515	S455	Y395	T335	R275	Y215	V155	P95	Q36
S576	D516	V456	D396	L336	Q276	T216	F156	L96	K37
Y577	G517	G457	L397	F337	L277	T217	F157	R97	F38
E578	N518	E458	S398	T338	E278	E218	D158	V98	I39
A579	N519	M459	A399	N339	K279	Q219	S159	K99	E40
Q580	P520	A460	V400	D340	D280	T220	D160	L100	Q41
T581	L521	E461	G401	L341	D281	L221	R161	R101	D42
N582	S522	N462	R402	D342	V282	D222	G162	L102	P43
E583	E523	Q463	M403	H343	K283	L223	K163	V103	E44
Y584	I524	F464	K404	G344	L284	F224	T164	I104	G45
G585	T525	R465	F405	P345	I285	F225	H165	Y105	Q46
F586	H526	V466	M406	Y346	E286	E226	S166	E106	V47
L587	K527	G467	R407	T347	V287	K227	S167	R107	G48
E588	R528	L468	S408	S348	P288	V228	G168	E108	L49
T589	R529	V469	L409	E349	V289	I229	K169	A109	E50
P590	I530	R470	L410	T350	E290	F230	V170	P110	A51
Y591	S531	V471	R411	L351	Y291	E231	L171	E111	A52
R592	A532	E472	E412	R352	I292	L232	V172	G112	F53
K593	R473	R472	E413	V353	A293	R233	M173	T113	R54
V594	G534	A474	I414	D354	G294	D234	A174	V114	S55
T595	P535	V475	E415	P355	K295	N235	R175	K115	V56
D596	G536	K476	G416	T356	V296	K236	I176	D116	F57
G597	G537	R477	S417	N357	V297	L237	I177	T117	P58
V598	L538	R478	G418	D358	A298	Q238	P178	K118	I59
F599	T539	L479	I419	R359	K299	M239	Y179	E119	G60
E600	R540	G480	L420	L360	K300	T240	S120	V62	

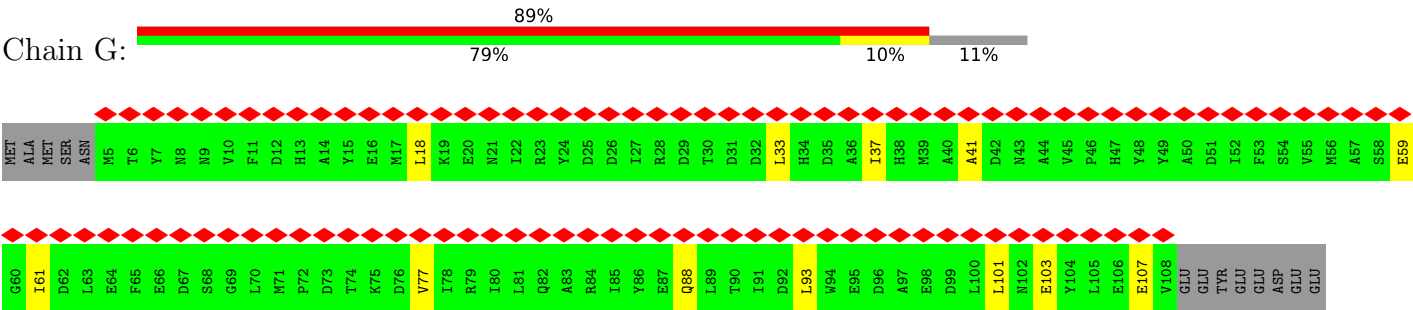
F1323	A1263	D1203	E1083	L1021	S961	L901	R941	D781	G721	V661	D601
N1324	Q1264	L1204	D1084	K1022	E962	L902	D842	V782	G722	S662	E602
V1325	F1265	L1205	M1085	H1023	E963	R903	T943	L783	V723	I603	I604
L1326	G1266	T1206	Y1086	E1024	L964	A904	K944	A784	V724	G664	H604
L1327	G1267	S1207	Y1087	F1025	Q965	I905	L945	D785	Q725	A665	Y605
K1328	G1268	G1208	D1088	E1026	I966	F906	G946	F786	V726	S666	L606
E1329	A1269	Q1209	E1089	K1027	L967	G907	P947	P787	L667	S607	S607
I1330	F1270	I1210	M1090	K1028	E968	E908	E948	S788	D728	I668	A608
L1331	G1271	L1211	G1091	L1029	A969	K909	E949	A729	P669	P669	I609
S1332	E1272	L1212	T1092	E1030	G970	A910	I950	D790	S730	F670	E610
L1333	M1273	Y1213	P1093	A1031	L971	S911	T951	L791	R731	L671	E611
E1334	E1274	D1214	V1094	K1032	F972	D912	A952	G792	I732	E672	G612
I1335	V1275	G1215	D1095	R1033	R973	V913	D953	E793	V733	H673	N613
N1336	W1276	R1216	I1096	R1034	R974	K914	I954	L794	I734	D674	Y614
I1337	Q1157	T1217	V1097	K1035	I975	D915	P955	A795	K735	D675	V615
E1338	K1158	G1218	L1098	I1036	R976	S916	N956	L796	V736	A676	I616
L1339	V1159	E1219	M1099	T1037	A977	S917	V957	G797	N737	N677	A617
E1340	Q1220	D1220	P1100	Q1038	V978	L918	G958	Q798	E738	R678	Q618
D1341	F1221	L1161	L1101	G1039	L979	R919	E959	N799	D739	A679	A619
G1282	G1282	S1162	G1102	D1040	V960	V920	A860	M800	E740	L680	M620
A1283	T1163	F1164	V1103	D1041	A961	P921	A861	R801	M741	M681	S621
A1284	F1164	P1104	P1104	L1042	G962	N922	L962	V902	I742	G682	N622
Y1285	S1165	S1105	S1105	A1043	G963	G923	S963	A803	P743	A683	L623
T1286	D1166	R1106	R1106	P1044	V964	V924	K964	F904	G744	N684	D624
V1227	E1167	M1107	M1107	G1045	E965	S925	L965	M905	E745	M685	E625
Q1288	E1168	M1108	M1108	V1046	A966	G926	D966	P906	A746	Q686	E626
E1289	V1169	I1109	I1109	L1047	E967	T927	E967	W907	G747	R687	G627
M1290	M1170	Q1110	Q1110	K1048	K968	V928	S968	N908	I748	Q688	H628
L1291	R1171	G1111	G1111	I1049	L969	I929	G969	G909	D749	A689	F629
M1232	L1172	I1112	I1112	V1050	D990	D930	I970	Y810	I750	V690	V630
L1233	A1173	L1113	L1113	K1051	K991	V931	V971	N811	Y751	P691	E631
E1174	E1174	E1114	E1114	V1052	L992	Q932	Y972	F812	N752	T692	D632
L1235	M1175	T1115	T1115	Y1053	P993	V933	I973	E913	L753	L693	L633
N1236	L1176	H1116	H1116	L1054	R994	F934	G974	D814	T754	R694	V634
H1237	L1177	L1117	L1117	A1055	D995	T935	A975	S815	K755	A695	T635
V1238	K1178	G1118	G1118	V1056	R996	R936	E976	I816	Y756	D696	C636
M1299	G1179	M1119	M1119	K1057	W997	D937	V977	L817	K697	K697	R637
G1300	M1180	A1120	A1120	R1058	L998	G938	T978	V818	R758	P698	S638
D1241	P1181	A1121	A1121	R1059	E999	V939	G979	S819	S759	L699	K639
K1242	T1182	K1122	K1122	I1060	L1000	E940	G880	E920	N760	V700	G640
M1243	A1183	G1123	G1123	Q1061	G1001	K941	D881	R821	Q761	G701	E641
H1244	T1184	I1124	I1124	P1062	L1002	D942	I882	V922	T762	T702	S642
A1245	F1185	G1125	G1125	G1063	T1003	K943	L983	V923	T763	G703	S643
R1246	V1186	D1126	D1126	D1064	R944	R944	V984	Q924	C764	M704	L644
S1247	F1187	K1127	K1127	K1065	E1005	A945	G885	E925	I765	E705	F645
T1248	D1188	I1128	I1128	M1066	E1006	L946	K886	D926	N766	R706	S646
G1249	G1189	M1129	M1129	M1066	K1007	E947	V887	R827	Q767	A707	R647
S1250	A1190	A1130	A1130	R1069	Q1008	I948	T988	F928	M768	V708	D648
Y1251	K1191	M1131	M1131	H1070	N1009	E949	P989	T929	P769	A709	Q649
S1252	E1192	L1132	L1132	G1071	Q1010	E950	K990	T930	C770	V710	V650
L1253	A1193	K1133	K1133	N1072	L1011	M951	G991	I831	V771	D711	D651
V1254	E1194	Q1134	Q1134	K1073	E1012	Q952	E992	H832	S772	S712	Y652
T1255	I1195	Q1135	Q1135	I1076	Q1013	L953	T993	I833	L773	G713	M653
Q1256	K1196	Q1136	Q1136	S1077	L1014	K954	Q994	Q834	G774	V714	D654
Q1257	E1197	E1137	E1137	K1078	A1015	Q955	L995	E835	E775	T715	V655
P1317	L1198	V1138	V1138	I1079	E1016	A956	T996	L836	P776	A716	S656
G1318	L1259	A1139	A1139	N1080	Q1017	K957	P997	A837	V777	V717	T657
M1319	G1260	K1140	K1140	N1081	Y1018	K958	E998	C838	E778	A718	Q658
E1321	S1322	L1201	L1141	I1082	D1019	D959	E999	V839	R779	K719	Q659
		G1202	R1142	I1082	E1020	L960	K900	S940	G780	R720	V660

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

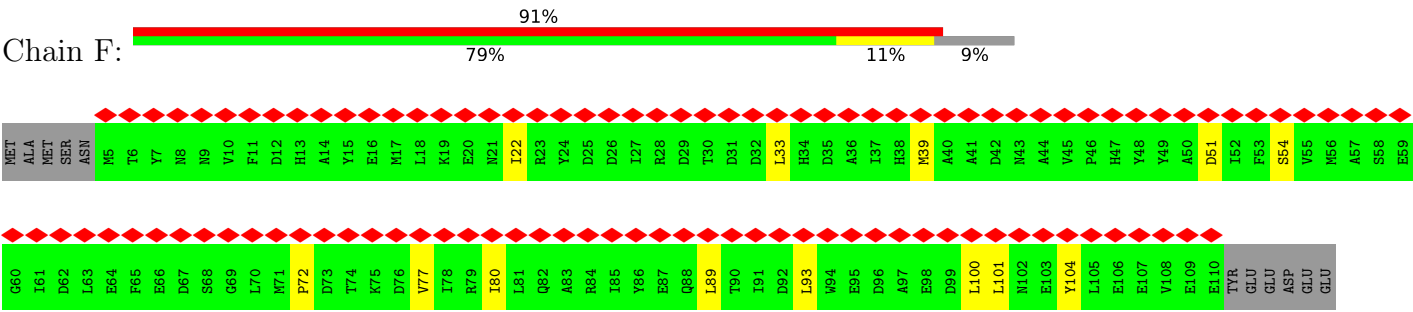
Response	Percentage
Yes	94%
No	85%
Don't know	10%
No answer	5%



● Molecule 5: Overcome classical restriction gp0.3



● Molecule 5: Overcome classical restriction gp0.3



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	33646	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	49.53	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.220	Depositor
Minimum map value	-0.151	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.1	Depositor
Map size ($\text{\AA}$)	270.08, 270.08, 270.08	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.055, 1.055, 1.055	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.19	0/1786	0.51	0/2424
1	B	0.21	0/1764	0.57	1/2398 (0.0%)
2	C	0.19	0/10263	0.52	0/13922
3	D	0.21	1/10187 (0.0%)	0.55	1/13803 (0.0%)
4	E	0.20	0/574	0.48	0/775
5	F	0.18	0/866	0.47	0/1177
5	G	0.16	0/866	0.38	0/1178
All	All	0.20	1/26306 (0.0%)	0.53	2/35677 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	925	GLU	C-N	5.02	1.40	1.33

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	885	VAL	N-CA-C	6.40	122.65	109.34
1	B	29	GLU	N-CA-C	5.49	121.95	109.81

There are no chirality outliers.

There are no planarity outliers.

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	1765	0	1775	22	0
1	B	1743	0	1741	14	0
2	C	10112	0	9785	118	0
3	D	10051	0	10034	85	0
4	E	572	0	574	3	0
5	F	852	0	772	8	0
5	G	849	0	768	7	0
All	All	25944	0	25449	229	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 5.

All (229) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:121:PRO:HD2	5:G:59:GLU:HG3	1.66	0.75
5:F:100:LEU:O	5:F:104:TYR:HB2	1.87	0.74
3:D:189:LEU:HD21	3:D:234:PRO:HB2	1.76	0.67
3:D:707:ILE:H	3:D:716:GLN:HG2	1.60	0.65
2:C:205:PRO:HG2	2:C:208:ILE:HG12	1.79	0.65
2:C:1209:GLN:HB3	2:C:1224:PRO:HB2	1.79	0.64
2:C:340:ASP:HB3	2:C:437:ASN:HD21	1.66	0.60
2:C:153:PRO:HD2	2:C:452:ARG:HH12	1.66	0.60
3:D:288:PRO:HD2	3:D:291:ILE:HD12	1.82	0.60
3:D:422:LEU:HB2	3:D:469:HIS:HB2	1.83	0.60
2:C:803:ALA:HB3	2:C:1097:VAL:HG22	1.84	0.60
3:D:124:ILE:HD12	3:D:1334:GLU:HG2	1.84	0.59
2:C:1269:ARG:NH2	5:F:39:MET:SD	2.75	0.59
3:D:1237:VAL:HG11	3:D:1253:ILE:HG12	1.84	0.59
2:C:29:SER:O	2:C:33:ASP:HB2	2.03	0.58
2:C:673:HIS:HB3	2:C:1109:ILE:HB	1.86	0.58
2:C:528:ARG:NH1	2:C:576:SER:O	2.36	0.58
3:D:21:LYS:HE2	3:D:23:ALA:HB2	1.85	0.58
3:D:749:LYS:HE3	3:D:751:ASP:HB2	1.85	0.57
3:D:491:LEU:HA	3:D:498:PRO:HA	1.86	0.57
3:D:799:ARG:NH1	3:D:1146:GLU:OE2	2.35	0.57
2:C:1254:VAL:HG22	2:C:1255:THR:HG23	1.86	0.57
1:B:91:ARG:HD2	1:B:122:GLU:HB3	1.87	0.56
3:D:1288:ALA:O	3:D:1292:LEU:HB2	2.04	0.56
1:A:11:PRO:HA	1:A:30:PRO:HG2	1.88	0.56
2:C:782:VAL:HG21	2:C:792:GLY:HA3	1.86	0.56
2:C:622:ASN:HD21	2:C:631:GLU:HB2	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:226:ALA:O	3:D:230:SER:HB3	2.06	0.56
1:B:182:ARG:HG3	3:D:581:MET:HE1	1.87	0.56
2:C:9:LYS:NZ	2:C:770:CYS:SG	2.78	0.56
3:D:806:ASP:OD1	3:D:1259:GLN:NE2	2.38	0.56
3:D:702:GLN:NE2	3:D:714:GLU:O	2.38	0.56
3:D:806:ASP:HA	3:D:1346:GLY:HA2	1.87	0.56
2:C:519:ASN:HB2	2:C:796:LEU:HD22	1.88	0.55
3:D:647:PRO:HB2	3:D:650:LYS:HB2	1.88	0.55
2:C:811:ASN:HA	2:C:815:SER:HB2	1.86	0.55
2:C:1287:LEU:HD23	3:D:1357:ILE:HG12	1.87	0.55
2:C:104:ILE:HB	2:C:115:LYS:HB2	1.89	0.55
3:D:17:PHE:O	3:D:1355:ARG:NH1	2.39	0.55
2:C:854:ILE:HD11	2:C:887:VAL:HG22	1.88	0.55
2:C:68:LEU:HD11	2:C:100:LEU:HD23	1.88	0.54
1:A:83:LEU:HD13	2:C:694:ARG:HE	1.71	0.54
2:C:179:TYR:HB3	2:C:396:ASP:HB3	1.89	0.54
2:C:519:ASN:ND2	2:C:686:GLN:O	2.40	0.54
2:C:877:VAL:HG13	2:C:881:ASP:HB2	1.89	0.54
2:C:1269:ARG:HH11	3:D:426:ALA:HB1	1.71	0.54
3:D:517:CYS:SG	3:D:716:GLN:NE2	2.80	0.54
1:A:82:LEU:HD11	1:A:171:LEU:HD13	1.90	0.54
1:A:58:GLU:HG2	1:A:172:LEU:HG	1.89	0.54
2:C:41:GLN:NE2	2:C:73:TYR:O	2.41	0.54
3:D:1256:ILE:HG22	3:D:1260:MET:HE2	1.90	0.54
2:C:805:MET:HE2	2:C:1225:VAL:HG21	1.90	0.54
1:A:60:GLU:OE1	1:A:143:ARG:NH2	2.41	0.54
2:C:636:CYS:SG	2:C:637:ARG:N	2.81	0.54
2:C:1108:ASN:ND2	2:C:1111:GLN:OE1	2.40	0.54
2:C:471:VAL:HG22	2:C:493:ILE:HG21	1.90	0.53
3:D:528:THR:OG1	3:D:551:ARG:NH1	2.42	0.53
2:C:1295:SER:O	2:C:1301:ARG:NH1	2.41	0.53
3:D:1368:ASP:OD1	3:D:1371:ARG:NH2	2.40	0.53
2:C:560:PRO:O	3:D:780:ARG:NH1	2.41	0.53
2:C:314:ASN:ND2	2:C:348:SER:O	2.42	0.53
2:C:798:GLN:HB3	2:C:827:ARG:HH21	1.74	0.53
3:D:976:THR:HG22	3:D:1026:PRO:HB2	1.91	0.53
2:C:138:ILE:HD13	2:C:143:ARG:HD2	1.91	0.52
2:C:560:PRO:HB2	3:D:776:THR:HG21	1.90	0.52
2:C:932:GLN:HB2	2:C:1051:LYS:HB2	1.90	0.52
2:C:836:LEU:HB3	2:C:1052:VAL:HB	1.92	0.52
2:C:694:ARG:HB2	2:C:798:GLN:HE22	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:45:ARG:HH12	2:C:1084:ASP:HB3	1.74	0.52
2:C:849:GLU:HG3	2:C:941:LYS:HE2	1.92	0.52
3:D:744:ARG:HH21	3:D:747:MET:HE1	1.75	0.52
5:G:103:GLU:O	5:G:107:GLU:HB2	2.10	0.52
1:A:43:LEU:HA	1:A:46:ILE:HG22	1.92	0.51
3:D:576:ARG:NH1	3:D:593:ASN:OD1	2.43	0.51
1:B:191:ARG:NH1	3:D:413:ASP:OD2	2.43	0.51
2:C:1101:LEU:HD21	3:D:508:LEU:HD22	1.91	0.51
2:C:1065:LYS:HG3	2:C:1235:LEU:HD12	1.91	0.51
3:D:354:VAL:HG13	3:D:463:GLY:HA2	1.92	0.51
1:B:27:THR:HG22	1:B:202:VAL:HG22	1.93	0.51
1:A:70:THR:HG22	1:A:78:ILE:HG12	1.93	0.51
2:C:903:ARG:HA	2:C:907:GLY:HA2	1.93	0.51
2:C:59:ILE:HD12	2:C:59:ILE:O	2.11	0.51
3:D:810:THR:HG23	3:D:811:GLU:HG2	1.93	0.51
3:D:422:LEU:HD13	3:D:434:ILE:HD11	1.93	0.51
3:D:742:GLY:H	3:D:762:ASN:HD22	1.58	0.51
1:B:29:GLU:HB3	1:B:30:PRO:HD3	1.92	0.50
2:C:1085:MET:HE2	2:C:1094:VAL:HG23	1.92	0.50
1:A:103:ASN:ND2	1:A:140:ILE:O	2.43	0.50
2:C:1223:ARG:NH1	3:D:719:PHE:O	2.43	0.50
2:C:1297:ASP:O	2:C:1301:ARG:NH2	2.44	0.50
2:C:411:ARG:NH2	2:C:427:ASP:OD2	2.44	0.50
3:D:1000:GLY:HA3	3:D:1026:PRO:HG3	1.92	0.50
3:D:341:ASN:HD22	3:D:1351:VAL:HG13	1.76	0.50
1:B:51:MET:SD	1:B:219:ARG:NH1	2.79	0.50
2:C:734:ILE:HD11	2:C:783:LEU:HD11	1.94	0.50
4:E:10:VAL:HG21	4:E:16:ARG:HE	1.77	0.49
1:A:183:ILE:HG12	1:A:205:MET:HG3	1.95	0.49
2:C:187:GLU:HB2	2:C:195:PHE:HB2	1.95	0.49
3:D:1152:GLU:HB3	3:D:1214:PRO:HD2	1.94	0.49
2:C:148:GLN:NE2	2:C:533:LEU:O	2.46	0.49
3:D:1134:ILE:O	3:D:1140:ARG:NE	2.44	0.49
2:C:148:GLN:OE1	2:C:531:SER:OG	2.31	0.49
2:C:204:LEU:HG	2:C:369:MET:HG2	1.95	0.49
2:C:719:LYS:HA	2:C:779:ARG:HG3	1.94	0.49
2:C:838:CYS:HB3	2:C:1050:VAL:HB	1.93	0.49
3:D:510:LEU:HD11	3:D:624:ILE:HG23	1.95	0.48
2:C:530:ILE:HD11	2:C:575:LEU:HD12	1.95	0.48
2:C:731:ARG:NH1	2:C:958:LYS:O	2.47	0.48
2:C:933:VAL:HG22	2:C:1050:VAL:HG22	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:122:SER:HB3	3:D:132:LEU:HD22	1.94	0.48
2:C:592:ARG:NH2	2:C:601:ASP:OD1	2.47	0.48
3:D:732:GLY:HA2	3:D:736:GLN:HE21	1.79	0.47
2:C:563:THR:HG21	3:D:780:ARG:HH22	1.79	0.47
1:A:75:GLN:HB3	1:A:132:HIS:HB3	1.97	0.47
2:C:801:ARG:HD2	2:C:1094:VAL:HA	1.95	0.47
5:G:61:ILE:HG13	5:G:88:GLN:HG3	1.97	0.47
1:A:46:ILE:HG23	1:A:220:ALA:HB1	1.97	0.47
2:C:699:LEU:HD13	2:C:799:ASN:HD21	1.79	0.47
5:F:33:LEU:HD13	5:F:101:LEU:HD11	1.95	0.47
1:A:59:VAL:HG21	1:A:85:LEU:HD13	1.96	0.47
1:A:99:ILE:HD11	1:A:143:ARG:HB3	1.96	0.47
3:D:502:PRO:HB3	3:D:506:VAL:HB	1.95	0.47
3:D:755:ILE:HD13	3:D:774:ILE:HD13	1.97	0.47
3:D:755:ILE:HG21	3:D:774:ILE:HD13	1.96	0.47
1:A:57:THR:HG22	1:A:58:GLU:HG3	1.97	0.47
3:D:57:PHE:H	3:D:61:ILE:HD12	1.80	0.47
3:D:555:TYR:HB2	3:D:586:GLY:HA3	1.96	0.47
2:C:123:TYR:OH	2:C:126:GLU:OE2	2.33	0.47
2:C:800:MET:O	2:C:1229:TYR:HA	2.15	0.47
3:D:1302:TYR:HE2	3:D:1304:ARG:HE	1.63	0.47
1:A:75:GLN:HE21	2:C:769:PRO:HB2	1.79	0.46
2:C:145:ILE:HG23	2:C:511:LEU:HB3	1.98	0.46
2:C:578:TYR:HE2	2:C:656:SER:HB2	1.80	0.46
2:C:1117:LEU:HD12	2:C:1195:ILE:HG12	1.98	0.46
1:B:188:GLU:HB2	1:B:200:LYS:HB2	1.97	0.46
2:C:256:GLU:HA	2:C:261:VAL:HA	1.98	0.46
2:C:1101:LEU:HD13	3:D:504:GLN:HG3	1.97	0.46
1:B:55:ALA:HB3	1:B:175:ALA:HB1	1.98	0.46
2:C:521:LEU:HD11	2:C:664:GLY:HA2	1.98	0.46
2:C:1073:LYS:HD2	3:D:462:ASP:HB3	1.97	0.46
2:C:1246:ARG:HB2	2:C:1261:GLY:H	1.81	0.46
1:A:166:ARG:NH1	2:C:876:GLU:OE1	2.41	0.45
2:C:421:SER:OG	2:C:423:ASP:OD1	2.34	0.45
3:D:371:LYS:NZ	3:D:404:GLU:OE2	2.49	0.45
1:B:188:GLU:O	1:B:199:ASP:HA	2.17	0.45
2:C:706:ARG:NH2	2:C:793:GLU:OE2	2.46	0.45
3:D:755:ILE:HD13	3:D:774:ILE:HG21	1.99	0.45
2:C:725:GLN:HB2	2:C:733:VAL:HG23	1.97	0.45
1:B:25:LYS:HA	1:B:203:ILE:O	2.16	0.45
4:E:9:ALA:HB1	4:E:54:ILE:HG22	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:77:VAL:HG13	5:F:77:VAL:HB	2.00	0.44
5:F:22:ILE:HD12	5:F:100:LEU:HD11	1.99	0.44
2:C:701:GLY:O	2:C:1184:THR:N	2.45	0.44
1:A:104:LYS:HD3	1:A:110:VAL:HG22	1.99	0.44
1:B:193:GLU:HB3	3:D:406:ALA:HB1	1.98	0.44
2:C:346:TYR:OH	2:C:436:ARG:NH2	2.50	0.44
2:C:366:ILE:HG12	2:C:370:MET:HE3	2.00	0.44
3:D:535:ARG:HH21	3:D:541:LEU:HD13	1.83	0.44
2:C:732:ILE:HB	2:C:751:TYR:HB2	1.99	0.44
2:C:756:TYR:HD1	2:C:764:CYS:HB2	1.83	0.44
2:C:14:ASP:N	2:C:1157:GLN:OE1	2.46	0.44
2:C:876:GLU:HA	2:C:927:THR:HA	1.99	0.44
2:C:802:VAL:HA	2:C:1096:ILE:O	2.18	0.44
2:C:1244:HIS:CD2	2:C:1245:ALA:H	2.36	0.44
3:D:826:ILE:HA	3:D:1242:ARG:HH22	1.82	0.44
3:D:841:GLY:HA2	3:D:901:ARG:HB2	2.00	0.44
3:D:1146:GLU:OE1	3:D:1148:ARG:NE	2.41	0.44
5:G:33:LEU:HD11	5:G:101:LEU:HD11	2.00	0.44
2:C:1274:GLU:HG2	3:D:424:ASN:HD21	1.83	0.44
2:C:1279:GLU:HB3	3:D:1347:LEU:HD21	1.98	0.44
3:D:242:LEU:HD12	3:D:243:PRO:HD2	1.99	0.44
2:C:122:VAL:HG11	2:C:492:MET:HE2	2.00	0.43
1:A:45:ARG:NH1	2:C:1215:GLY:O	2.47	0.43
1:A:60:GLU:HB3	1:A:143:ARG:HB2	1.99	0.43
2:C:633:LEU:HB3	2:C:644:LEU:HD11	2.00	0.43
2:C:617:ALA:HB2	2:C:650:VAL:HG21	2.00	0.43
2:C:945:ALA:HB1	2:C:948:ILE:HD11	2.01	0.43
1:B:161:SER:OG	1:B:162:GLU:N	2.51	0.43
2:C:459:MET:HB3	2:C:505:PHE:HZ	1.82	0.43
2:C:522:SER:HA	2:C:525:THR:HG22	2.00	0.43
2:C:691:PRO:HG3	2:C:787:PRO:HB3	1.99	0.43
3:D:885:VAL:O	3:D:887:SER:N	2.51	0.43
3:D:615:LYS:NZ	4:E:8:ASP:OD2	2.51	0.43
5:F:89:LEU:O	5:F:93:LEU:HB2	2.18	0.43
3:D:1350:ASN:HD22	3:D:1358:PRO:HD3	1.82	0.43
3:D:959:LYS:HB2	3:D:983:LYS:HB2	2.01	0.43
3:D:507:VAL:HG11	3:D:730:ALA:HB2	1.99	0.42
5:G:18:LEU:HD22	5:G:93:LEU:HD22	2.00	0.42
2:C:1065:LYS:HG2	2:C:1237:HIS:HB2	2.01	0.42
2:C:519:ASN:HB3	2:C:689:ALA:HB3	2.01	0.42
2:C:805:MET:HB2	3:D:636:GLY:HA2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:647:PRO:HA	3:D:700:ASN:HD22	1.84	0.42
5:F:51:ASP:HA	5:F:54:SER:HB3	2.01	0.42
2:C:12:ARG:NH2	2:C:793:GLU:OE1	2.51	0.42
2:C:582:ASN:ND2	2:C:588:GLU:OE2	2.52	0.42
1:A:84:ASN:HB3	1:A:130:ILE:HG23	2.01	0.42
3:D:491:LEU:HB2	3:D:904:ALA:HA	2.01	0.42
2:C:715:THR:HG22	2:C:786:GLY:H	1.84	0.42
1:A:76:GLU:HG2	2:C:768:MET:HE3	2.00	0.42
2:C:732:ILE:HG21	2:C:783:LEU:HD13	2.01	0.42
1:B:207:THR:HG22	1:B:209:GLY:H	1.84	0.42
2:C:518:ASN:HB3	2:C:689:ALA:H	1.85	0.42
2:C:1281:TYR:HE2	3:D:434:ILE:HG23	1.83	0.42
1:B:90:VAL:HG13	1:B:121:VAL:HG13	2.00	0.41
2:C:18:ARG:HH12	2:C:622:ASN:HA	1.85	0.41
2:C:807:TRP:CG	2:C:808:ASN:H	2.38	0.41
2:C:1275:VAL:HG21	3:D:341:ASN:HB3	2.01	0.41
2:C:13:LYS:HE3	2:C:15:PHE:HE1	1.84	0.41
2:C:339:ASN:HD22	2:C:340:ASP:H	1.69	0.41
2:C:803:ALA:HB2	2:C:1094:VAL:HG11	2.01	0.41
2:C:1062:PRO:HA	2:C:1076:ILE:HB	2.02	0.41
3:D:838:ARG:NH2	3:D:1250:ASP:OD2	2.53	0.41
3:D:954:ASN:HB2	3:D:984:LEU:HD21	2.02	0.41
3:D:743:MET:HE3	3:D:760:THR:HA	2.03	0.41
2:C:979:LEU:HD21	2:C:989:LEU:HD11	2.03	0.41
3:D:535:ARG:HE	3:D:541:LEU:HD22	1.86	0.41
3:D:1135:THR:HA	3:D:1140:ARG:HE	1.85	0.41
2:C:196:VAL:HB	2:C:204:LEU:HB2	2.02	0.41
2:C:608:ALA:HA	2:C:611:GLU:HG2	2.03	0.41
3:D:1060:VAL:HA	3:D:1107:VAL:HB	2.03	0.41
3:D:694:SER:HB2	3:D:738:ARG:HE	1.86	0.40
3:D:826:ILE:HD11	3:D:993:GLU:HA	2.01	0.40
3:D:973:LEU:HD12	3:D:1007:ASP:H	1.86	0.40
3:D:226:ALA:O	3:D:230:SER:CB	2.69	0.40
2:C:803:ALA:HA	2:C:1227:VAL:HG12	2.02	0.40
5:G:37:ILE:O	5:G:41:ALA:N	2.54	0.40
2:C:1269:ARG:H	3:D:344:GLY:HA3	1.87	0.40
3:D:1136:GLY:H	3:D:1240:VAL:HG22	1.85	0.40
5:F:72:PRO:HG2	5:F:80:ILE:HG12	2.03	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	228/329 (69%)	220 (96%)	8 (4%)	0	100	100
1	B	229/329 (70%)	214 (93%)	13 (6%)	2 (1%)	14	45
2	C	1339/1342 (100%)	1226 (92%)	113 (8%)	0	100	100
3	D	1324/1407 (94%)	1198 (90%)	124 (9%)	2 (0%)	43	72
4	E	73/80 (91%)	66 (90%)	7 (10%)	0	100	100
5	F	104/117 (89%)	100 (96%)	4 (4%)	0	100	100
5	G	102/117 (87%)	100 (98%)	2 (2%)	0	100	100
All	All	3399/3721 (91%)	3124 (92%)	271 (8%)	4 (0%)	49	78

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	30	PRO
3	D	886	VAL
3	D	1183	SER
1	B	29	GLU

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	194/286 (68%)	194 (100%)	0	100	100
1	B	189/286 (66%)	189 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	C	1057/1157 (91%)	1052 (100%)	5 (0%)	81	80
3	D	1048/1168 (90%)	1044 (100%)	4 (0%)	84	81
4	E	58/68 (85%)	58 (100%)	0	100	100
5	F	91/105 (87%)	91 (100%)	0	100	100
5	G	91/105 (87%)	91 (100%)	0	100	100
All	All	2728/3175 (86%)	2719 (100%)	9 (0%)	84	83

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	59	ILE
2	C	569	ILE
2	C	1175	ASN
2	C	1176	LEU
2	C	1335	ILE
3	D	119	SER
3	D	126	LEU
3	D	128	LEU
3	D	324	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	GLN
1	A	75	GLN
1	A	84	ASN
1	A	128	HIS
1	B	66	HIS
1	B	103	ASN
2	C	31	GLN
2	C	69	GLN
2	C	165	HIS
2	C	339	ASN
2	C	437	ASN
2	C	580	GLN
2	C	628	HIS
2	C	686	GLN
2	C	767	GLN
2	C	922	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	C	965	GLN
2	C	1136	GLN
2	C	1175	ASN
2	C	1209	GLN
2	C	1244	HIS
2	C	1299	ASN
3	D	276	ASN
3	D	277	ASN
3	D	320	ASN
3	D	341	ASN
3	D	424	ASN
3	D	458	ASN
3	D	495	ASN
3	D	504	GLN
3	D	623	GLN
3	D	651	HIS
3	D	716	GLN
3	D	736	GLN
3	D	792	ASN
3	D	817	HIS
3	D	1023	HIS
3	D	1195	GLN
3	D	1227	HIS
3	D	1238	GLN
3	D	1252	HIS
3	D	1268	ASN
4	E	31	GLN
5	G	34	HIS
5	G	38	HIS
5	F	38	HIS

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

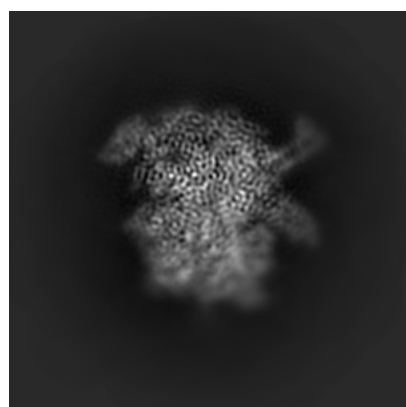
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4770. These allow visual inspection of the internal detail of the map and identification of artifacts.

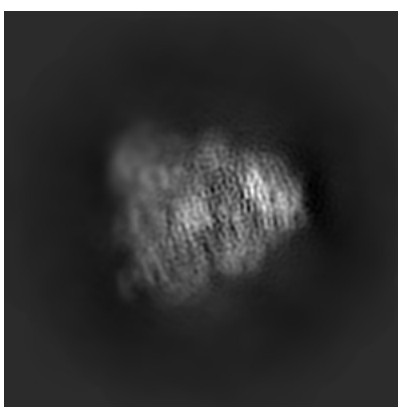
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

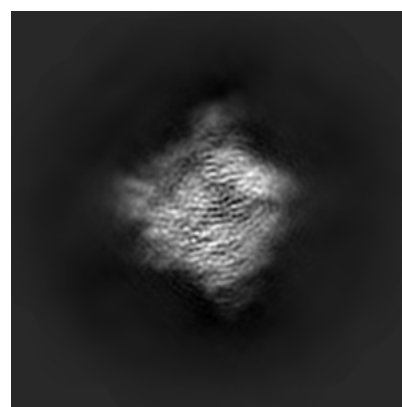
6.1.1 Primary map



X



Y

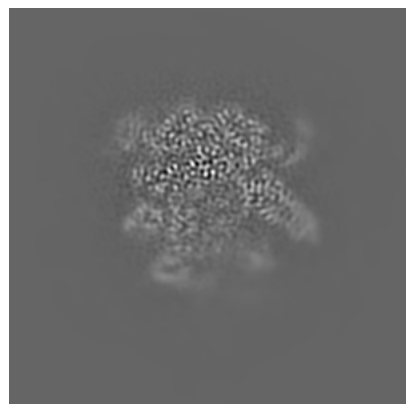


Z

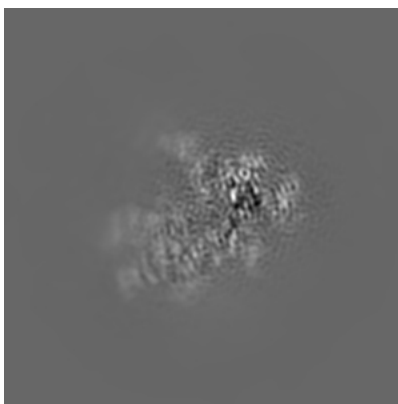
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

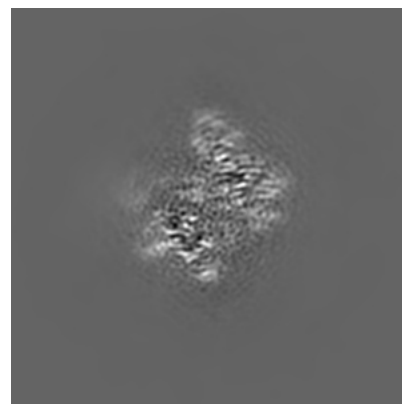
6.2.1 Primary map



X Index: 128



Y Index: 128

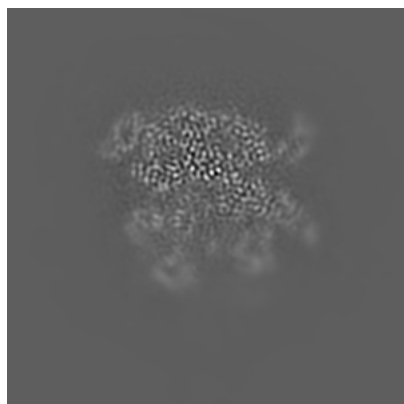


Z Index: 128

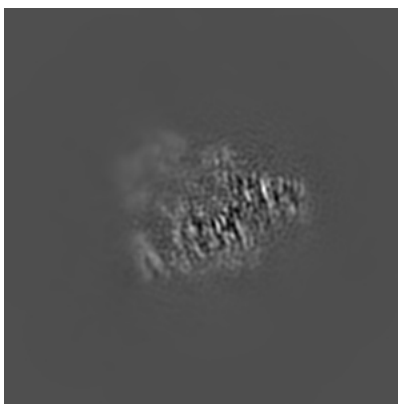
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

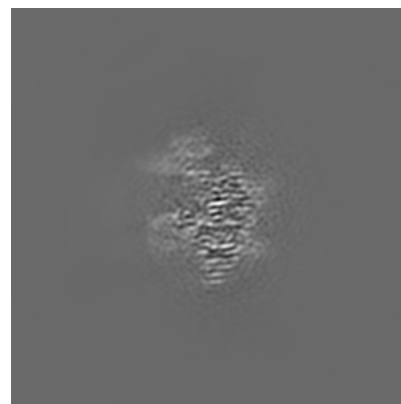
6.3.1 Primary map



X Index: 133



Y Index: 115

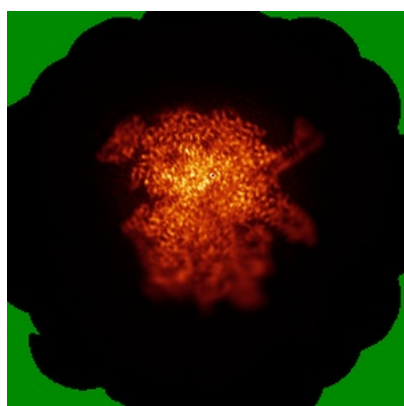


Z Index: 150

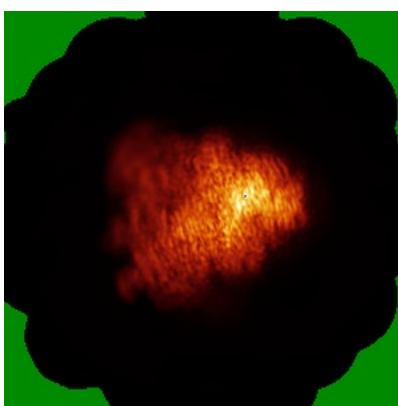
The images above show the largest variance slices of the map in three orthogonal directions.

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

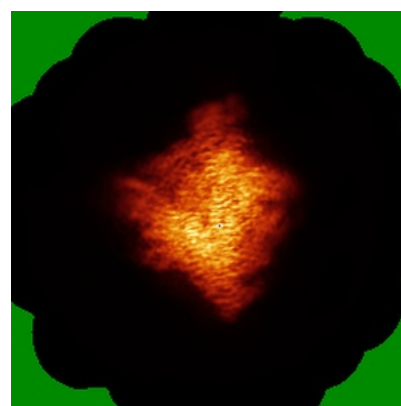
6.4.1 Primary map



X



Y

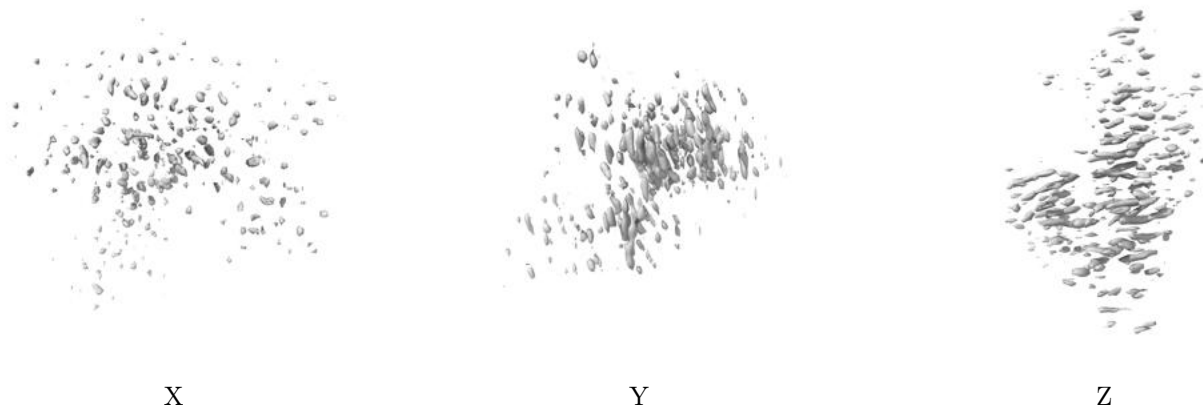


Z

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 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

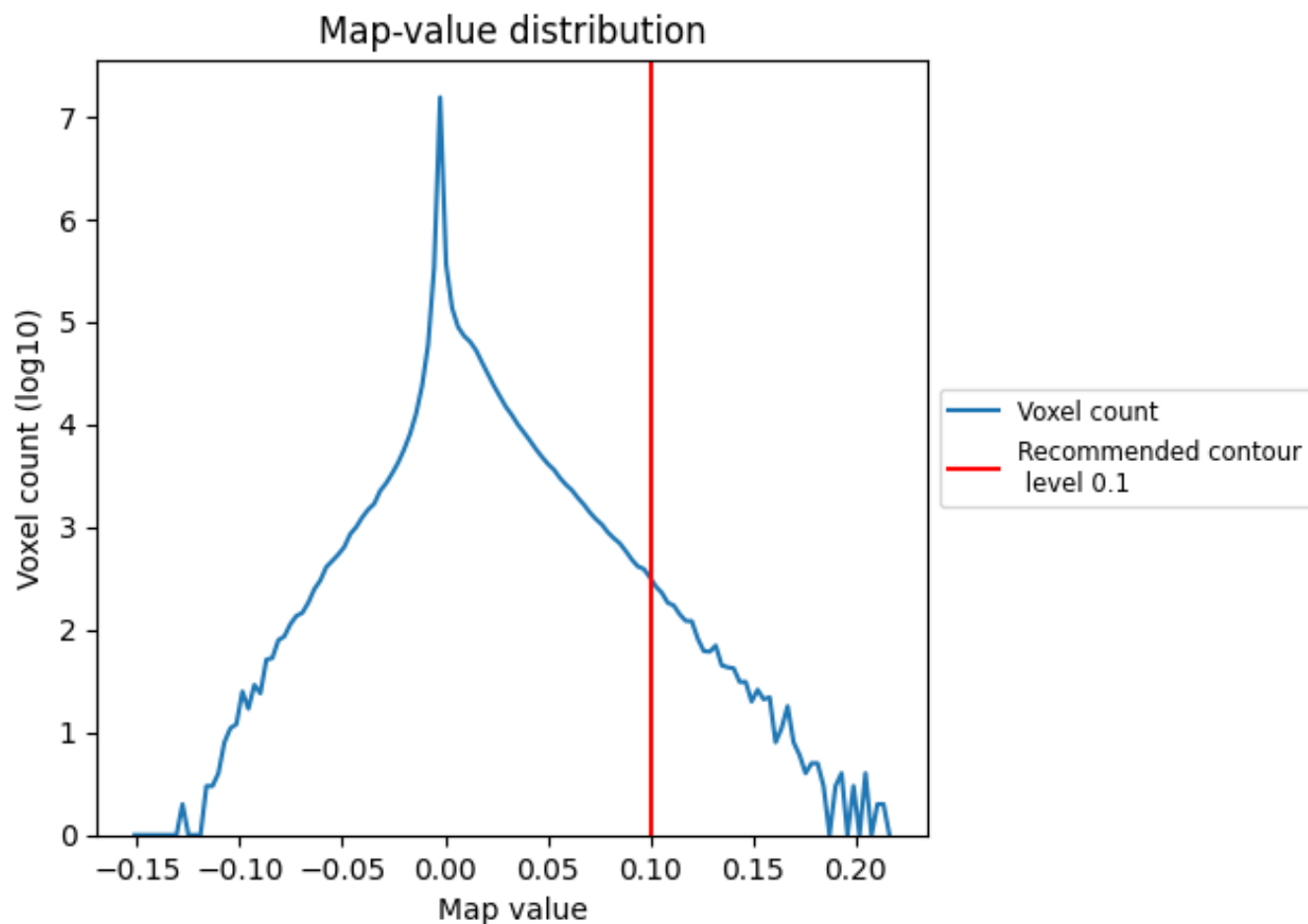
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

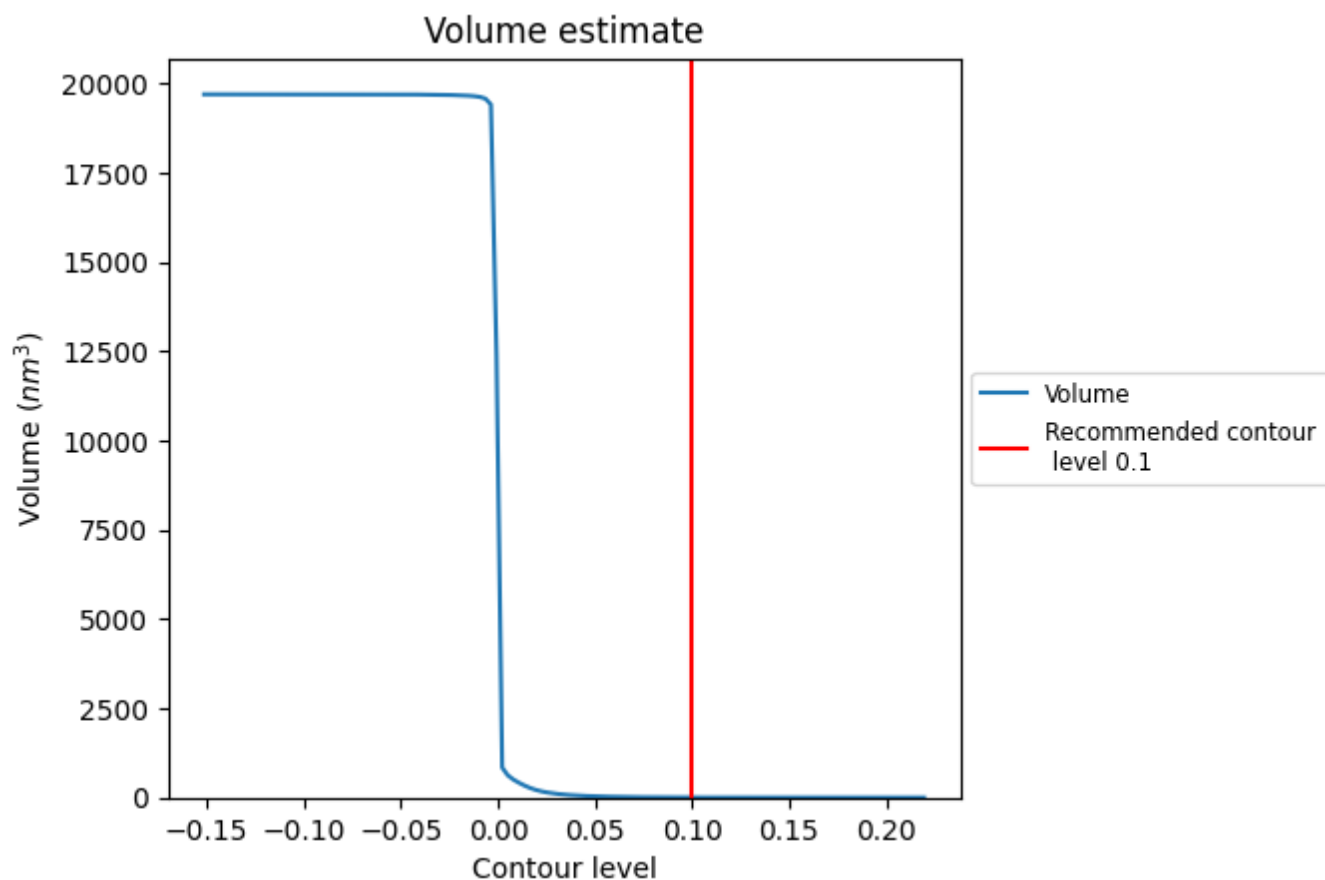
This section contains the results of statistical analysis of the map.

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.

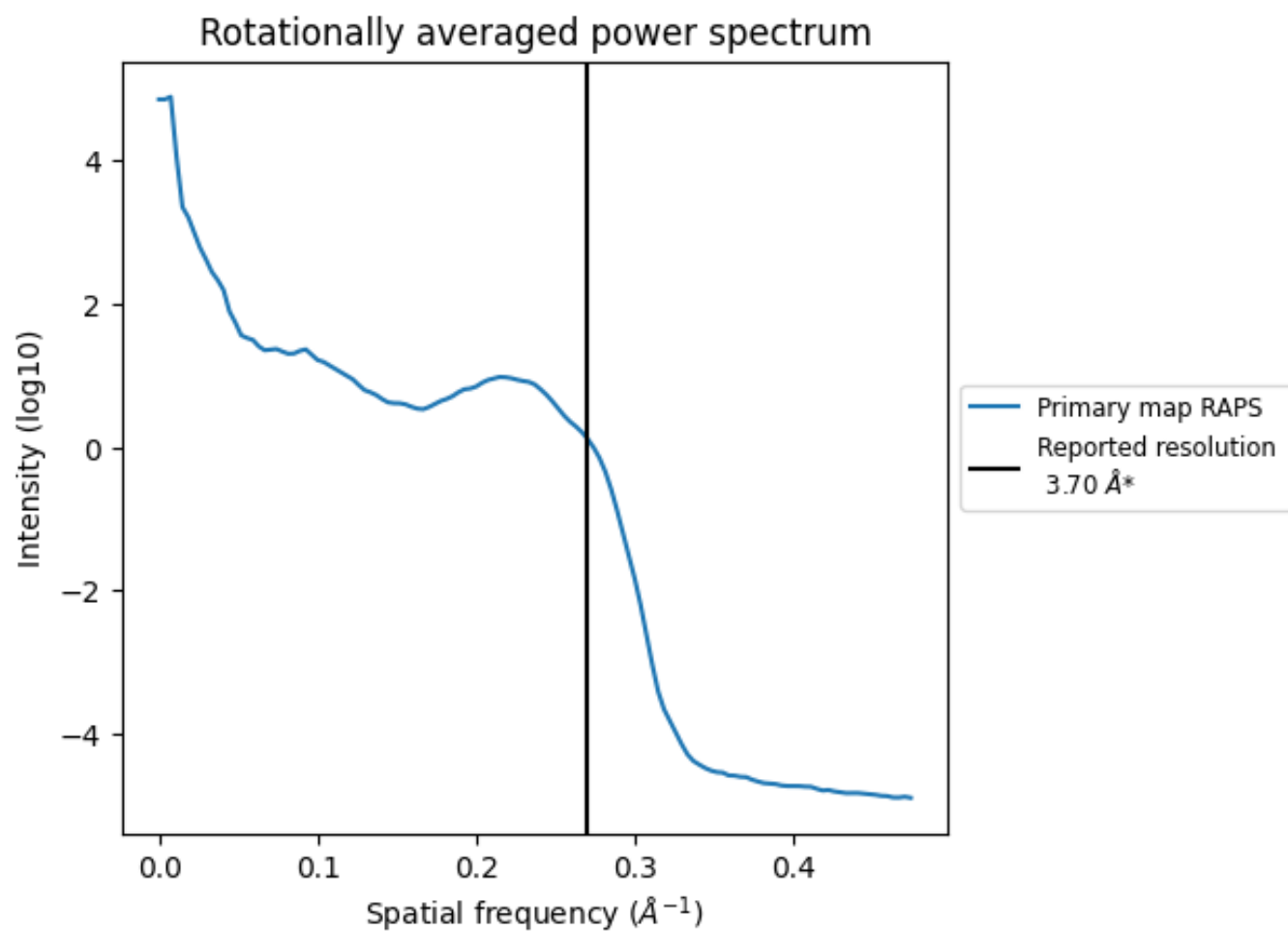
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3 nm³; this corresponds to an approximate mass of 2 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 0.270 Å⁻¹

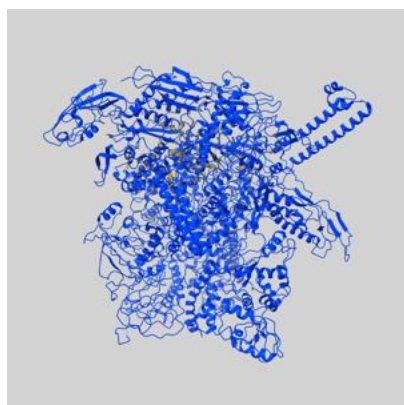
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

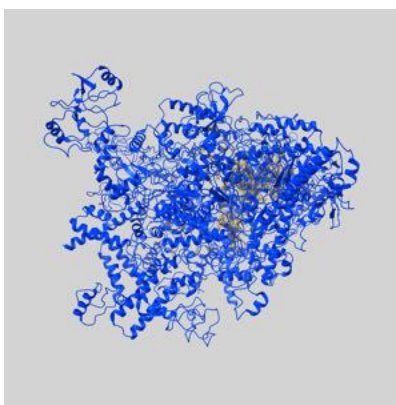
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4770 and PDB model 6R9G. Per-residue inclusion information can be found in section [3](#) on page [5](#).

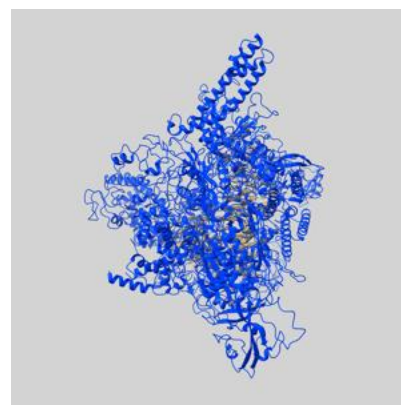
9.1 Map-model overlay [i](#)



X



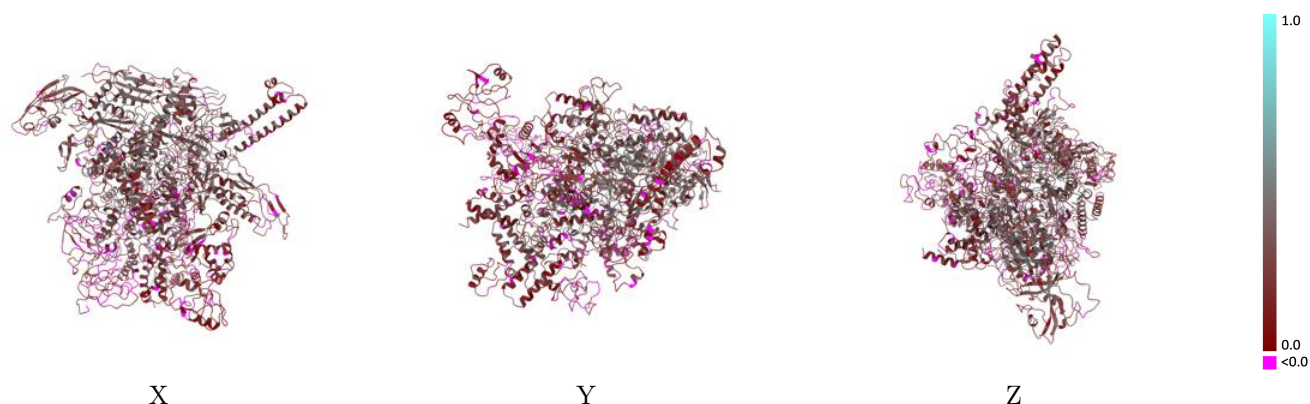
Y



Z

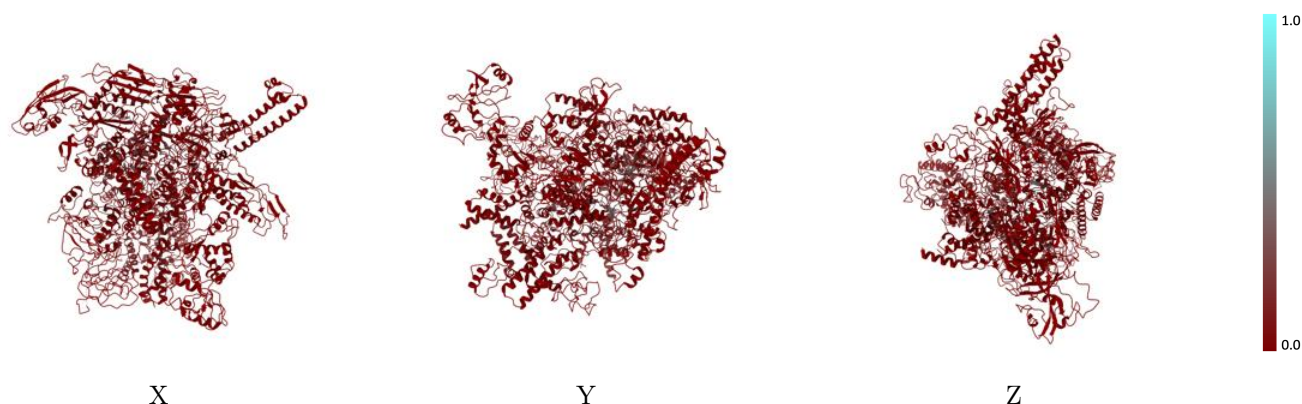
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



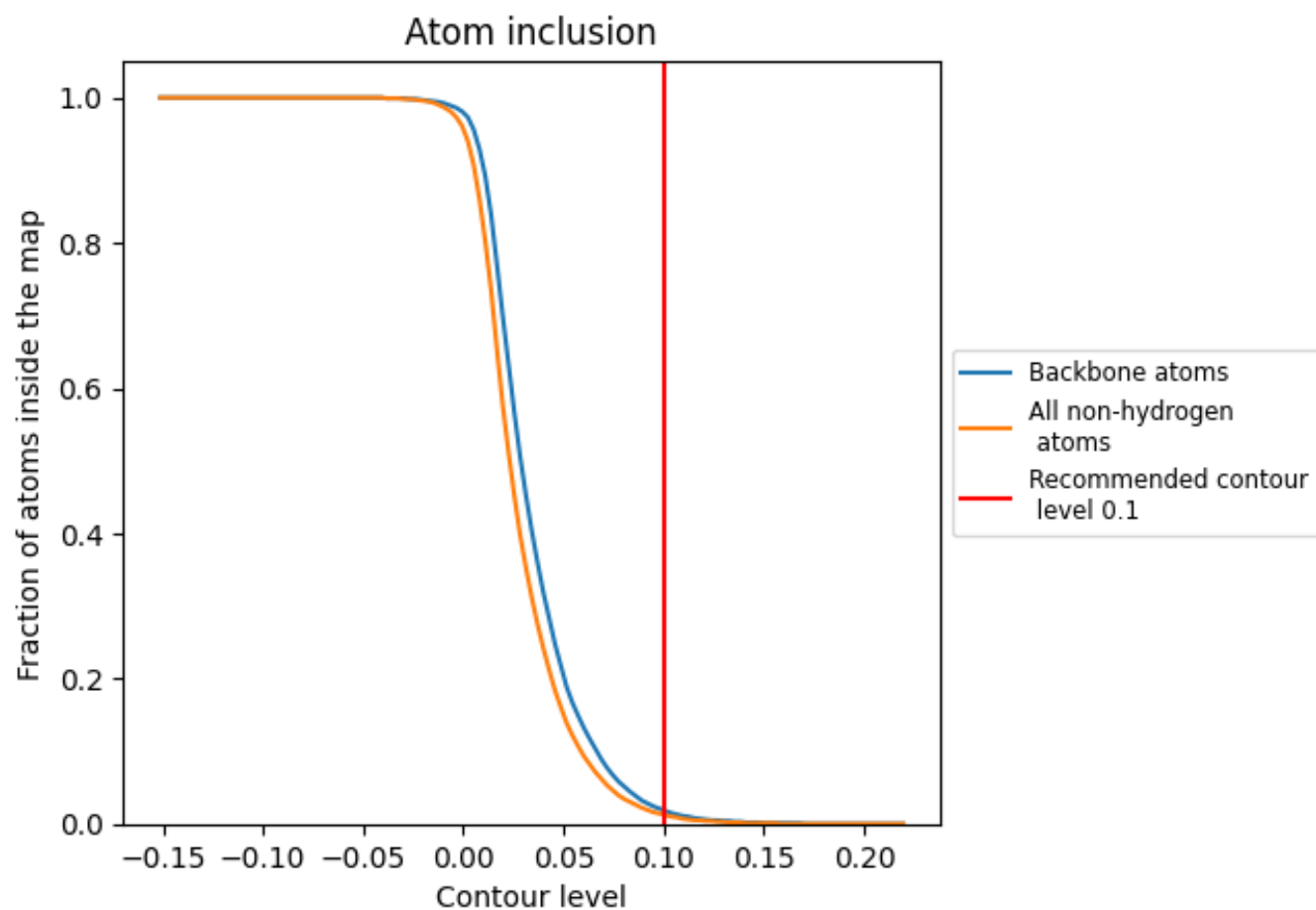
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 2% of all backbone atoms, 1% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.0130	0.2250
A	0.0060	0.3070
B	0.0030	0.2760
C	0.0170	0.2340
D	0.0140	0.2030
E	0.0000	0.1290
F	0.0000	0.2230
G	0.0000	0.1720

1.0

0.0

<0.0