



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 01:51 PM BST

PDB ID : 3J7H
EMDB ID: : EMD-5995
Title : Structure of beta-galactosidase at 3.2-A resolution obtained by cryo-electron microscopy
Authors : Bartesaghi, A.; Matthies, D.; Banerjee, S.; Merk, A.; Subramaniam, S.
Deposited on : 2014-06-30
Resolution : 3.20 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

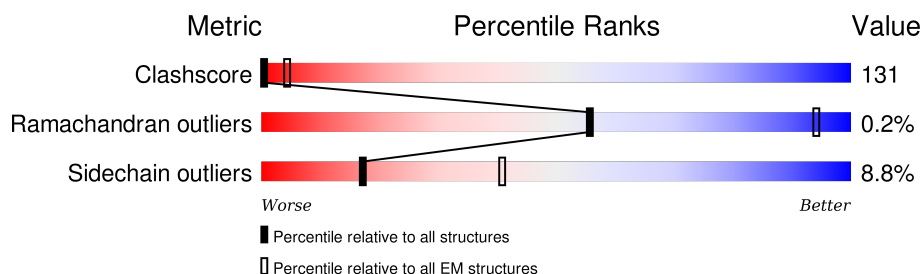
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	1024	22% 71% 7%
1	B	1024	22% 71% 7%
1	C	1024	22% 71% 7%
1	D	1024	22% 71% 7%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 32828 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 Beta-galactosidase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1022	Total	C	N	O	S	0	0
			8206	5190	1452	1525	39		
1	B	1022	Total	C	N	O	S	0	0
			8206	5190	1452	1525	39		
1	C	1022	Total	C	N	O	S	0	0
			8206	5190	1452	1525	39		
1	D	1022	Total	C	N	O	S	0	0
			8206	5190	1452	1525	39		

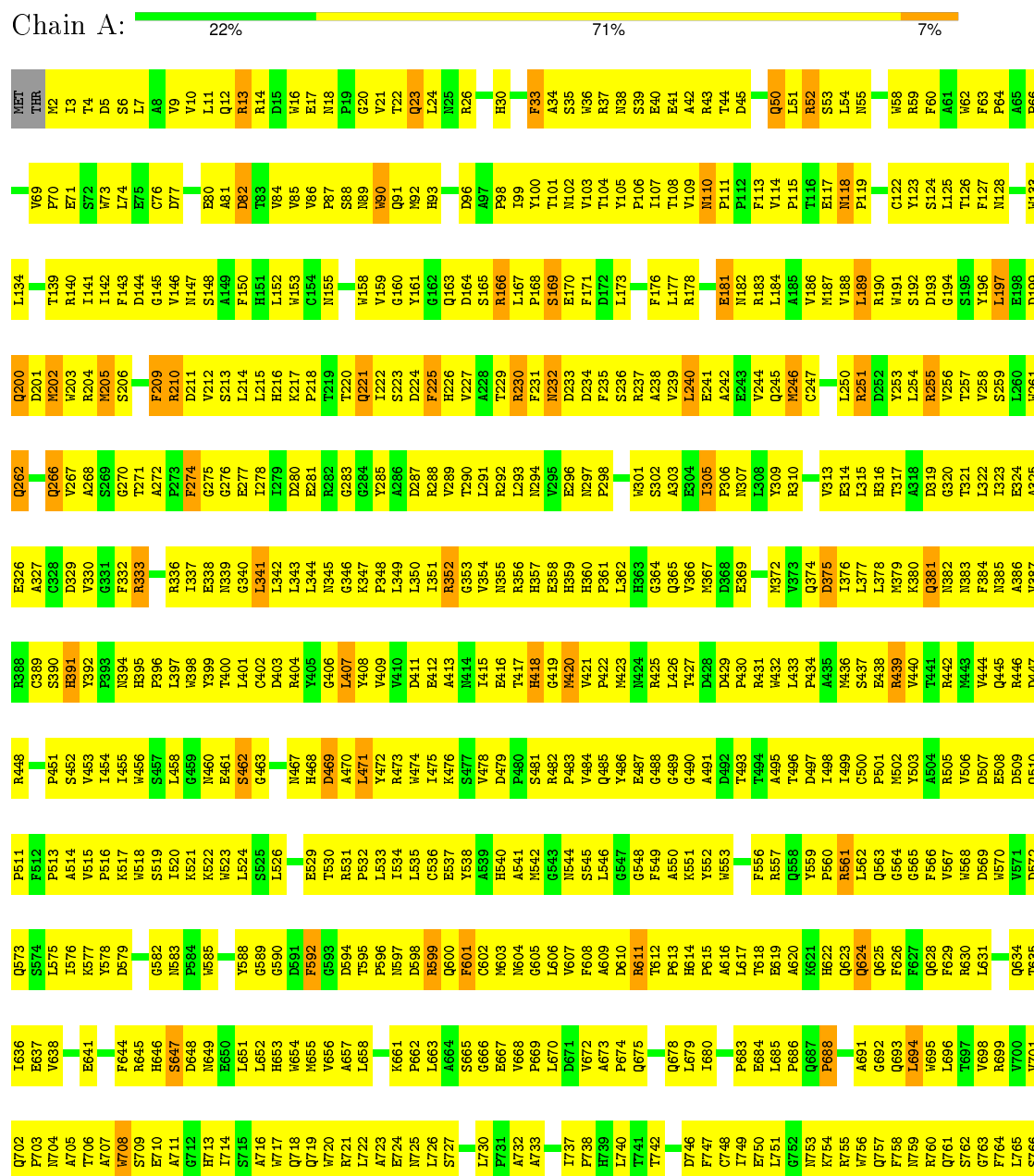
- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
2	B	1	Total	Mg	0
			1	1	
2	A	1	Total	Mg	0
			1	1	
2	D	1	Total	Mg	0
			1	1	
2	C	1	Total	Mg	0
			1	1	

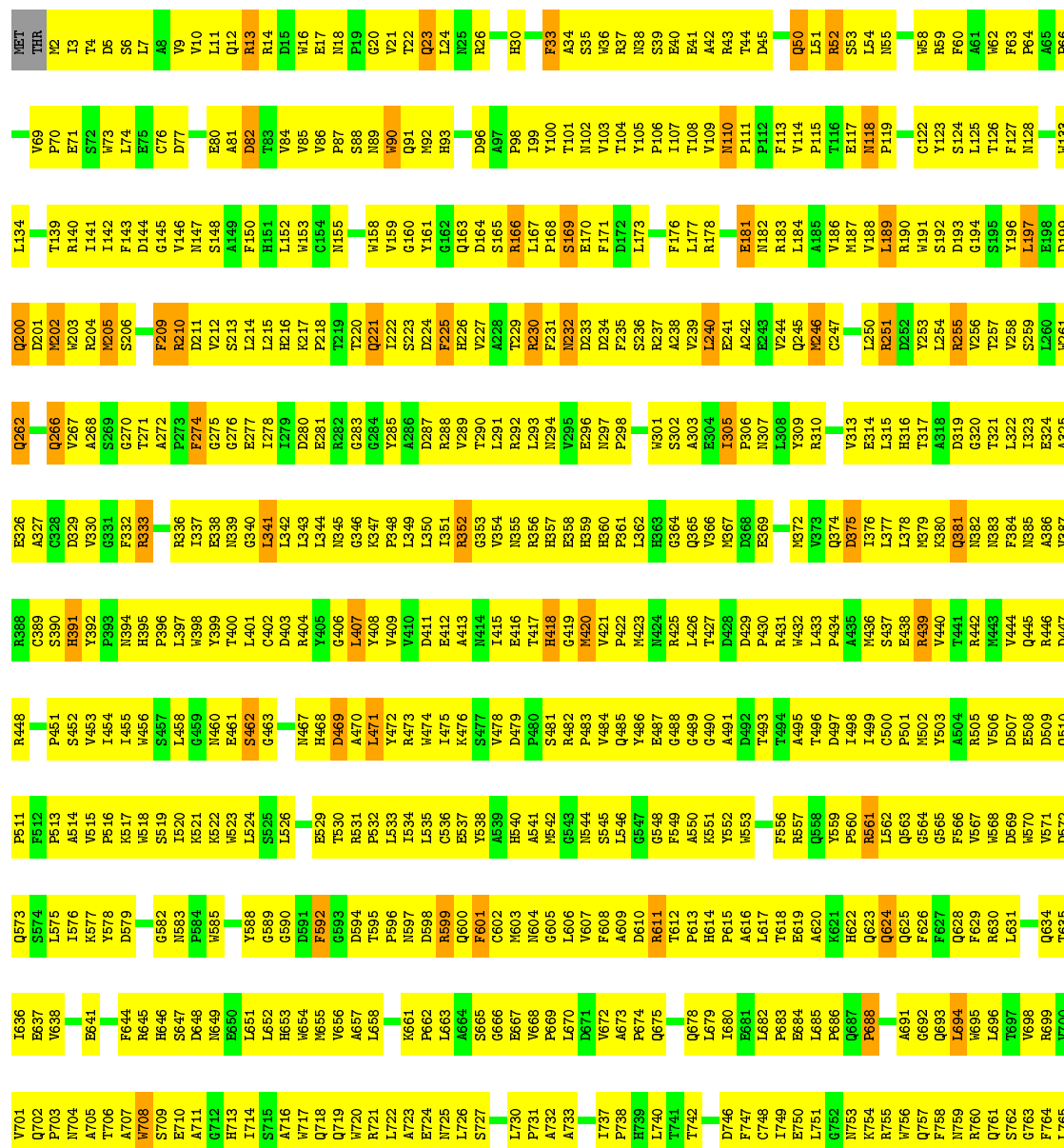
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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: Beta-galactosidase







Q966	Q967	Q968	Q969	Q970	Q971	Q972	Q973	Q974	Q975	Q976	Q977	Q978	Q979	Q980	Q981	Q982	Q983	Q984	Q985	Q986	Q987	Q988	Q989	Q990	Q991	Q992	Q993	Q994	Q995	Q996	Q997	Q998	Q999	P000	P001	P002	P003	P004	P005	P006	P007	P008	P009	P010	P011	P012	P013	P014	P015	P016	P017	P018	P019	P020	P021	P022	P023	P024	P025	P026	P027	P028	P029	P030	P031	P032	P033	P034	P035	P036	P037	P038	P039	P040	P041	P042	P043	P044	P045	P046	P047	P048	P049	P050	P051	P052	P053	P054	P055	P056	P057	P058	P059	P060	P061	P062	P063	P064	P065	P066	P067	P068	P069	P070	P071	P072	P073	P074	P075	P076	P077	P078	P079	P080	P081	P082	P083	P084	P085	P086	P087	P088	P089	P090	P091	P092	P093	P094	P095	P096	P097	P098	P099	P100	P101	P102	P103	P104	P105	P106	P107	P108	P109	P110	P111	P112	P113	P114	P115	P116	P117	P118	P119	P120	P121	P122	P123	P124	P125	P126	P127	P128	P129	P130	P131	P132	P133	P134	P135	P136	P137	P138	P139	P140	P141	P142	P143	P144	P145	P146	P147	P148	P149	P150	P151	P152	P153	P154	P155	P156	P157	P158	P159	P160	P161	P162	P163	P164	P165	P166	P167	P168	P169	P170	P171	P172	P173	P174	P175	P176	P177	P178	P179	P180	P181	P182	P183	P184	P185	P186	P187	P188	P189	P190	P191	P192	P193	P194	P195	P196	P197	P198	P199	P200	P201	P202	P203	P204	P205	P206	P207	P208	P209	P210	P211	P212	P213	P214	P215	P216	P217	P218	P219	P220	P221	P222	P223	P224	P225	P226	P227	P228	P229	P230	P231	P232	P233	P234	P235	P236	P237	P238	P239	P240	P241	P242	P243	P244	P245	P246	P247	P248	P249	P250	P251	P252	P253	P254	P255	P256	P257	P258	P259	P260	P261	P262	P263	P264	P265	P266	P267	P268	P269	P270	P271	P272	P273	P274	P275	P276	P277	P278	P279	P280	P281	P282	P283	P284	P285	P286	P287	P288	P289	P290	P291	P292	P293	P294	P295	P296	P297	P298	P299	P300	P301	P302	P303	P304	P305	P306	P307	P308	P309	P310	P311	P312	P313	P314	P315	P316	P317	P318	P319	P320	P321	P322	P323	P324	P325	P326	P327	P328	P329	P330	P331	P332	P333	P334	P335	P336	P337	P338	P339	P340	P341	P342	P343	P344	P345	P346	P347	P348	P349	P350	P351	P352	P353	P354	P355	P356	P357	P358	P359	P360	P361	P362	P363	P364	P365	P366	P367	P368	P369	P370	P371	P372	P373	P374	P375	P376	P377	P378	P379	P380	P381	P382	P383	P384	P385	P386	P387	P388	P389	P390	P391	P392	P393	P394	P395	P396	P397	P398	P399	P400	P401	P402	P403	P404	P405	P406	P407	P408	P409	P410	P411	P412	P413	P414	P415	P416	P417	P418	P419	P420	P421	P422	P423	P424	P425	P426	P427	P428	P429	P430	P431	P432	P433	P434	P435	P436	P437	P438	P439	P440	P441	P442	P443	P444	P445	P446	P447	P448	P449	P450	P451	P452	P453	P454	P455	P456	P457	P458	P459	P460	P461	P462	P463	P464	P465	P466	P467	P468	P469	P470	P471	P472	P473	P474	P475	P476	P477	P478	P479	P480	P481	P482	P483	P484	P485	P486	P487	P488	P489	P490	P491	P492	P493	P494	P495	P496	P497	P498	P499	P500	P501	P502	P503	P504	P505	P506	P507	P508	P509	P510	P511	P512	P513	P514	P515	P516	P517	P518	P519	P520	P521	P522	P523	P524	P525	P526	P527	P528	P529	P530	P531	P532	P533	P534	P535	P536	P537	P538	P539	P540	P541	P542	P543	P544	P545	P546	P547	P548	P549	P550	P551	P552	P553	P554	P555	P556	P557	P558	P559	P560	P561	P562	P563	P564	P565	P566	P567	P568	P569	P570	P571	P572	P573	P574	P575	P576	P577	P578	P579	P580	P581	P582	P583	P584	P585	P586	P587	P588	P589	P590	P591	P592	P593	P594	P595	P596	P597	P598	P599	P600	P601	P602	P603	P604	P605	P606	P607	P608	P609	P610	P611	P612	P613	P614	P615	P616	P617	P618	P619	P620	P621	P622	P623	P624	P625	P626	P627	P628	P629	P630	P631	P632	P633	P634	P635	P636	P637	P638	P639	P640	P641	P642	P643	P644	P645	P646	P647	P648	P649	P650	P651	P652	P653	P654	P655	P656	P657	P658	P659	P660	P661	P662	P663	P664	P665	P666	P667	P668	P669	P670	P671	P672	P673	P674	P675	P676	P677	P678	P679	P680	P681	P682	P683	P684	P685	P686	P687	P688	P689	P690	P691	P692	P693	P694	P695	P696	P697	P698	P699	P700	P701	P702	P703	P704	P705	P706	P707	P708	P709	P710	P711	P712	P713	P714	P715	P716	P717	P718	P719	P720	P721	P722	P723	P724	P725	P726	P727	P728	P729	P730	P731	P732	P733	P734	P735	P736	P737	P738	P739	P740	P741	P742	P743	P744	P745	P746	P747	P748	P749	P750	P751	P752	P753	P754	P755	P756	P757	P758	P759	P760	P761	P762	P763	P764	P765	P766	P767	P768	P769	P770	P771	P772	P773	P774	P775	P776	P777	P778	P779	P780	P781	P782	P783	P784	P785	P786	P787	P788	P789	P790	P791	P792	P793	P794	P795	P796	P797	P798	P799	P800	P801	P802	P803	P804	P805	P806	P807	P808	P809	P810	P811	P812	P813	P814	P815	P816	P817	P818	P819	P820	P821	P822	P823	P824	P825	P826	P827	P828	P829	P830	P831	P832	P833	P834	P835	P836	P837	P838	P839	P840	P841	P842	P843	P844	P845	P846	P847	P848	P849	P850	P851	P852	P853	P854	P855	P856	P857	P858	P859	P860	P861	P862	P863	P864	P865	P866	P867	P868	P869	P870	P871	P872	P873	P874	P875	P876	P877	P878	P879	P880	P881	P882	P883	P884	P885	P886	P887	P888	P889	P890	P891	P892	P893	P894	P895	P896	P897	P898	P899	P900	P901	P902	P903	P904	P905	P906	P907	P908	P909	P910	P911	P912	P913	P914	P915	P916	P917	P918	P919	P920	P921	P922	P923	P924	P925	P926	P927	P928	P929	P930	P931	P932	P933	P934	P935	P936	P937	P938	P939	P940	P941	P942	P943	P944	P945	P946	P947	P948	P949	P950	P951	P952	P953	P954	P955	P956	P957	P958	P959	P960	P961	P962	P963	P964	P965	P966	P967	P968	P969	P970	P971	P972	P973	P974	P975	P976	P977	P978	P979	P980	P981	P982	P983	P984	P985	P986	P987	P988	P989	P990	P991	P992	P993	P994	P995	P996	P997	P998	P999	P1000	P1001	P1002	P1003	P1004	P1005	P1006	P1007	P1008	P1009	P1010	P1011	P1012	P1013	P1014	P1015	P1016	P1017	P1018	P1019	P1020	P1021	P1022	P1023	P1024	P1025	P1026	P1027	P1028	P1029	P1030	P1031	P1032	P1033	P1034	P1035	P1036	P1037	P1038	P1039	P1040	P1041	P1042	P1043	P1044	P1045	P1046	P1047	P1048	P1049	P1050	P1051	P1052	P1053	P1054	P1055	P1056	P1057	P1058	P1059	P1060	P1061	P1062	P1063	P1064	P1065	P1066	P1067	P1068	P1069	P1070	P1071	P1072	P1073	P1074	P1075	P1076	P1077	P1078	P1079	P1080	P1081	P1082	P1083	P1084	P1085	P1086	P1087	P1088	P1089	P1090	P1091	P1092	P1093	P1094	P1095	P1096	P1097	P1098	P1099	P1100	P1101	P1102	P1103	P1104	P1105	P1106	P1107	P1108	P1109	P1110	P1111	P1112	P1113	P1114	P1115	P1116	P1117	P1118	P1119	P1120	P1121	P1122	P1123	P1124	P1125	P1126	P1127	P1128	P1129	P1130	P1131	P1132	P1133	P1134	P1135	P1136	P1137	P1138	P1139	P1140	P1141	P1142	P1143	P1144	P1145	P1146	P1147	P1148	P1149	P1150	P1151	P1152	P1153	P1154	P1155	P1156	P1157	P1158	P1159	P1160	P1161	P1162	P1163	P1164	P1165	P1166	P1167	P1168	P1169	P1170	P1171	P1172	P1173	P1174	P1175	P1176	P1177	P1178	P1179	P1180	P1181	P1182	P1183	P1184	P1185	P1186	P1187	P1188	P1189	P1190	P1191	P1192	P1193	P1194	P1195	P1196	P1197	P1198	P1199	P1200	P1201	P1202	P1203	P1204	P1205	P1206	P1207	P1208	P1209	P1210	P1211	P1212	P1213	P1214	P1215	P1216	P1217	P1218	P1219	P1220	P1221	P1222	P1223	P1224	P1225	P1226	P1227	P1228	P1229	P1230	P1231	P1232	P1233	P1234	P1235	P1236	P1237	P1238	P1239	P1240	P1241	P1242	P1243	P1244	P1245	P1246	P1247	P1248	P1249	P1250	P1251	P1252	P1253	P1254	P1255	P1256	P1257	P1258	P1259	P1260	P1261	P1262	P1263	P1264	P1265	P1266	P1267	P1268	P1269	P1270	P1271	P1272	P1273	P1274	P1275	P1276	P1277	P1278	P1279	P1280	P1281	P1282	P1283	P1284	P1285	P1286	P1287	P1288	P1289	P1290	P1291	P1292	P1293	P1294	P1295	P1296	P1297	P1298	P1299	P1300	P1301	P1302	P1303	P1304	P1305	P1306	P1307	P1308	P1309	P1310	P1311	P1312	P1313	P1314	P1315	P1316	P1317	P1318	P1319	P1320	P1321	P1322	P1323	P1324	P1325	P1326	P1327	P1328	P1329	P1330	P1331	P1332	P1333	P1334	P1335	P1336	P1337	P1338	P1339	P1340	P1341	P1342	P1343	P1344	P1345	P1346	P1347	P1348	P1349	P1350	P1351	P1352	P1353	P1354	P1355	P1356	P1357	P1358	P1359	P1360	P1361	P1362	P1363	P1364	P1365	P1366	P1367	P1368	P1369	P1370	P1371	P1372	P1373	P1374	P1375	P1376	P1377	P1378	P1379	P1380	P1381	P1382	P1383	P1384	P1385	P1386	P1387	P1388	P1389	P1390	P1391	P1392	P1393	P1394	P1395	P1396	P1397	P1398	P1399	P1400	P1401	P1402	P1403	P1404	P1405	P1406	P1407	P1408	P1409	P1410	P1411	P1412	P1413	P1414	P1415	P1416	P1417	P1418	P1419	P1420	P1421	P1422	P1423	P1424	P1425	P1426	P1427	P1428	P1429	P1430	P1431	P1432	P1433	P1434	P1435	P1436	P1437
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S766	A833	P902	Q966
Q767	V834	Q903	L967
W768	L835	E904	W968
W769	I836	I905	E969
T770	T837	Y906	T970
G771	T838	P907	S971
D772	A839	D908	H972
K773	H840	R909	R973
K774	A841	I910	H974
Q775	W842	T911	L975
L776	Q843	A912	L976
L777	H844	A913	H977
T778	Q845	C914	A978
F779		F915	E979
L780	T848	D916	E980
R781	L849	R917	G981
D782	F850	W918	T982
Q783	I851	D919	W983
F784	S852	L920	L984
T785	R853	P921	W985
R786	K854	L922	L986
A787	T855	S923	D987
P788	Y856	D924	G988
L789	R857		F989
D790	I858	T927	H990
W791		P928	W991
D792	Q863	Y929	G992
L793	W864	Y930	L993
G794	A865	F931	G994
W795	I866		G995
S796	T867	E934	D996
E797	W868	W935	D997
A798	D869	G936	S998
T799	W870	L937	W999
R800	E871	R938	S1000
L801	W872	C939	P1001
D802	A873	G940	S1002
P803	S874	T941	
	D875	R942	A1005
W806	T876	E943	E1006
W807	P877	L944	F1007
E808	H878	W945	Q1008
R809	P879	Y946	L1009
W810	A880	G947	S1010
W811	R881	P948	A1011
	I882	H949	G1012
H815	G883	Q950	R1013
Y816	L884	W951	Y1014
		R952	H1015
		G953	Y1016
			Q1017
L822	Q887		L1018
L823	L888	Q956	Y1019
Q824	A889	F957	W1020
C825	Q890	W958	C1021
T826	W891	L959	Q1022
A827	A892	S960	K1023
D828			
T829	L898	R961	
L830	G899	W962	
A831	L900	S963	
D832	G901		

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	11726	Depositor
Resolution determination method	FSC 0.143	Depositor
CTF correction method	Individual frames of each movie were aligned by cross-correlation using the cumulative average of previously aligned frames as a reference to align the remaining frames. Parameters of the contrast transfer function for each micrograph were estimated from power spectra obtained using periodogram averaging with tiles of size 512x512 pixels extracted from all frames of each movie. These power spectra were then radially averaged and used to estimate the defocus for each image using frequencies in the 15.0-3.0 Angstrom range. CTF correction was done for each particle as implemented in FREALIGN's reconstruction protocol.	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 (4k x 4k)	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: MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 2$	RMSZ	# $ Z > 2$
1	A	0.26	0/8448	0.47	2/11526 (0.0%)
1	B	0.26	1/8448 (0.0%)	0.47	2/11526 (0.0%)
1	C	0.26	0/8448	0.47	2/11526 (0.0%)
1	D	0.26	0/8448	0.47	2/11526 (0.0%)
All	All	0.26	1/33792 (0.0%)	0.47	8/46104 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	306	PRO	N-CD	5.03	1.54	1.47

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	305	ILE	C-N-CD	5.72	140.41	128.40
1	C	305	ILE	C-N-CD	5.72	140.41	128.40
1	D	305	ILE	C-N-CD	5.71	140.39	128.40
1	B	305	ILE	C-N-CD	5.71	140.39	128.40
1	B	110	ASN	C-N-CD	5.11	139.14	128.40

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	8206	0	7791	2164	0
1	B	8206	0	7791	2165	0
1	C	8206	0	7791	2156	0
1	D	8206	0	7791	2161	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
All	All	32828	0	31164	8379	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 131.

The worst 5 of 8379 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:C:427:THR:HA	1:C:436:MET:CE	1.21	1.67
1:D:427:THR:HA	1:D:436:MET:CE	1.21	1.67
1:C:159:VAL:HG22	1:C:176:PHE:CE1	1.25	1.64
1:D:159:VAL:HG22	1:D:176:PHE:CE1	1.25	1.64
1:A:159:VAL:HG22	1:A:176:PHE:CE1	1.25	1.63

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	1020/1024 (100%)	993 (97%)	25 (2%)	2 (0%)	52	88
1	B	1020/1024 (100%)	993 (97%)	25 (2%)	2 (0%)	52	88
1	C	1020/1024 (100%)	993 (97%)	25 (2%)	2 (0%)	52	88
1	D	1020/1024 (100%)	993 (97%)	25 (2%)	2 (0%)	52	88

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	4080/4096 (100%)	3972 (97%)	100 (2%)	8 (0%)	56	88

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	511	PRO
1	B	511	PRO
1	C	511	PRO
1	D	511	PRO
1	A	688	PRO

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	874/876 (100%)	797 (91%)	77 (9%)	12	45
1	B	874/876 (100%)	797 (91%)	77 (9%)	12	45
1	C	874/876 (100%)	797 (91%)	77 (9%)	12	45
1	D	874/876 (100%)	797 (91%)	77 (9%)	12	45
All	All	3496/3504 (100%)	3188 (91%)	308 (9%)	17	45

5 of 308 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	836	ILE
1	C	221	GLN
1	D	624	GLN
1	B	881	ARG
1	C	33	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 160 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	843	GLN
1	C	266	GLN
1	D	713	HIS
1	B	890	GLN
1	C	23	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.