



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:14 PM UTC

PDB ID : 1ZOT / pdb_00001zot
Title : crystal structure analysis of the CyaA/C-Cam with PMEAPP
Authors : Guo, Q.; Tang, W.J.
Deposited on : 2005-05-13
Resolution : 2.20 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

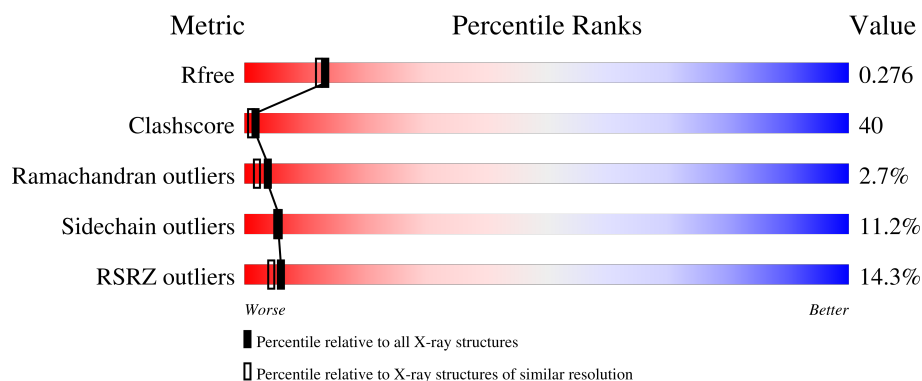
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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

Mol	Chain	Length	Quality of chain
1	A	358	15% 47% 39% 9% ••
2	B	69	10% 52% 33% 10% •

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 3427 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called CyaA with C-terminal Calmodulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	351	Total	C	N	O	S	0	0	0
			2684	1664	495	519	6			

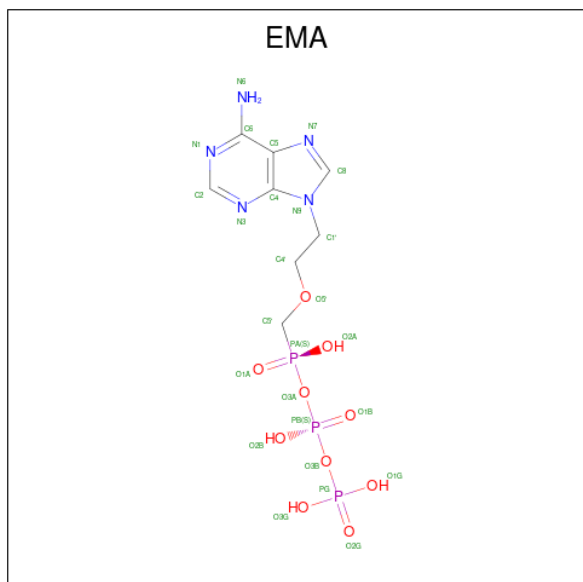
- Molecule 2 is a protein called Calmodulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	69	Total	C	N	O	S	0	0	0
			551	335	90	122	4			

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	Mg	0	0
			3	3		

- Molecule 4 is (ADENIN-9-YL-ETHOXYMETHYL)-HYDROXYPHOSPHINYLDIPHOSPHATE (CCD ID: EMA) (formula: C₈H₁₄N₅O₁₀P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			26	8	5	10	3		

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	2	Total	Ca	0	0
			2	2		

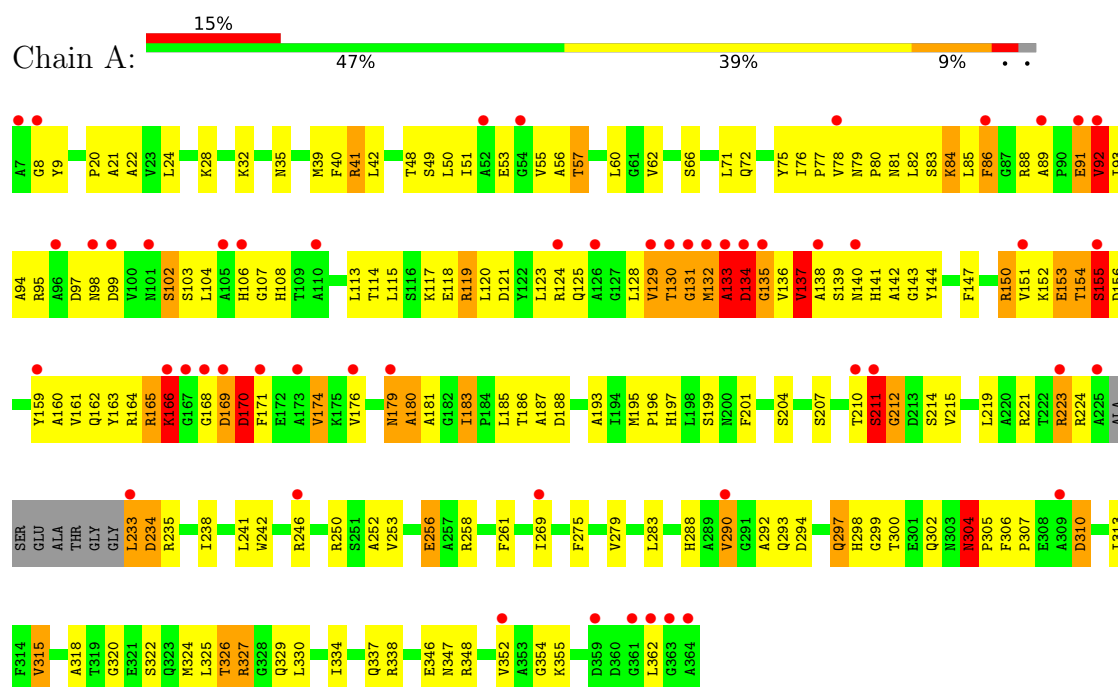
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	128	Total	O	0	0
			128	128		
6	B	33	Total	O	0	0
			33	33		

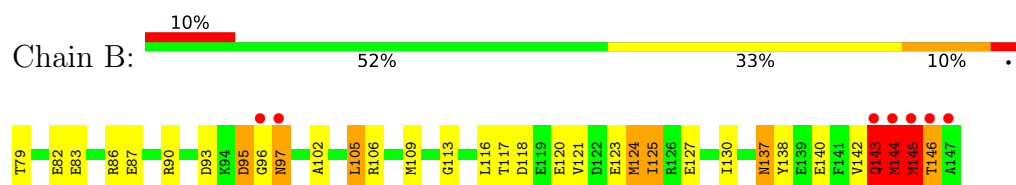
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: CyaA with C-terminal Calmodulin



• Molecule 2: Calmodulin



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	79.67Å 79.67Å 139.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.52 – 2.20 34.52 – 2.20	Depositor EDS
% Data completeness (in resolution range)	92.2 (34.52-2.20) 99.8 (34.52-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.36 (at 2.10Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.252 , 0.291 0.279 , 0.276	Depositor DCC
R_{free} test set	1361 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	24.2	Xtriage
Anisotropy	0.339	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 31.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	3427	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.75% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, EMA, 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	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.19	11/2728 (0.4%)	1.55	41/3682 (1.1%)
2	B	1.00	2/556 (0.4%)	1.34	10/746 (1.3%)
All	All	1.16	13/3284 (0.4%)	1.52	51/4428 (1.2%)

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	A	0	3
2	B	1	0
All	All	1	3

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	134	ASP	C-N	-22.81	1.00	1.33
1	A	233	LEU	C-N	-20.71	1.04	1.33
1	A	212	GLY	N-CA	17.80	1.73	1.44
1	A	89	ALA	N-CA	7.62	1.56	1.45
2	B	124	MET	SD-CE	-7.22	1.61	1.79
2	B	146	THR	CA-CB	6.82	1.64	1.53
1	A	132	MET	C-N	-6.45	1.24	1.33
1	A	133	ALA	C-N	-6.27	1.23	1.34
1	A	170	ASP	C-N	5.91	1.41	1.33
1	A	304	ASN	CG-OD1	5.49	1.33	1.23
1	A	169	ASP	N-CA	5.13	1.52	1.46
1	A	130	THR	CA-CB	5.11	1.59	1.52
1	A	315	VAL	CA-CB	-5.09	1.48	1.54

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	134	ASP	O-C-N	-25.44	87.55	122.15
1	A	134	ASP	N-CA-C	-17.39	86.28	112.54
1	A	211	SER	CA-C-N	-15.21	100.65	122.86
1	A	211	SER	C-N-CA	-15.21	100.65	122.86
2	B	144	MET	N-CA-CB	-13.00	89.20	110.40
1	A	133	ALA	O-C-N	-12.55	105.89	122.59
1	A	9	TYR	N-CA-CB	-12.54	89.92	110.23
1	A	89	ALA	N-CA-C	12.49	127.20	109.84
1	A	169	ASP	N-CA-C	12.21	136.82	110.80
1	A	180	ALA	N-CA-C	-11.84	98.08	111.82
1	A	234	ASP	N-CA-CB	-10.75	92.32	110.49
1	A	233	LEU	N-CA-C	-10.60	81.33	111.00
1	A	168	GLY	CA-C-N	9.96	140.57	121.54
1	A	168	GLY	C-N-CA	9.96	140.57	121.54
1	A	310	ASP	N-CA-C	-9.66	98.07	110.53
1	A	169	ASP	CA-C-N	-9.20	106.13	121.39
1	A	169	ASP	C-N-CA	-9.20	106.13	121.39
1	A	134	ASP	CA-C-N	8.48	138.03	121.41
1	A	134	ASP	C-N-CA	8.48	138.03	121.41
1	A	183	ILE	N-CA-C	-7.82	101.90	108.63
1	A	315	VAL	N-CA-C	7.79	119.02	108.11
1	A	106	HIS	N-CA-C	7.55	119.19	108.54
2	B	143	GLN	N-CA-C	7.43	126.64	110.80
1	A	132	MET	CA-C-N	-7.35	107.50	121.54
1	A	132	MET	C-N-CA	-7.35	107.50	121.54
1	A	134	ASP	CA-CB-CG	7.25	119.84	112.60
1	A	89	ALA	N-CA-CB	-7.02	99.44	110.03
1	A	169	ASP	O-C-N	-6.92	113.39	122.59
1	A	76	ILE	CA-C-N	6.47	126.23	119.76
1	A	76	ILE	C-N-CA	6.47	126.23	119.76
2	B	143	GLN	CB-CA-C	6.45	123.26	110.42
2	B	144	MET	N-CA-C	6.41	120.83	112.89
1	A	221	ARG	N-CA-C	6.35	117.87	111.07
1	A	166	LYS	N-CA-C	6.28	119.94	110.64
1	A	137	VAL	N-CA-C	6.19	119.38	110.09
2	B	97	ASN	N-CA-C	6.16	118.25	110.24
1	A	326	THR	N-CA-C	-6.12	102.28	110.55
2	B	96	GLY	CA-C-N	5.89	129.47	120.82
2	B	96	GLY	C-N-CA	5.89	129.47	120.82
1	A	214	SER	N-CA-C	-5.73	102.94	110.33
2	B	130	ILE	N-CA-C	5.45	116.08	110.36
1	A	53	GLU	N-CA-C	-5.42	106.70	113.15

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	41	ARG	N-CA-C	-5.36	101.80	110.32
1	A	169	ASP	N-CA-CB	-5.28	101.57	110.49
1	A	234	ASP	N-CA-C	5.27	122.02	110.80
1	A	21	ALA	N-CA-C	5.26	116.70	111.07
2	B	113	GLY	N-CA-C	5.22	122.55	115.30
2	B	118	ASP	N-CA-C	-5.19	105.62	111.28
1	A	92	VAL	N-CA-C	-5.12	107.41	111.81
1	A	261	PHE	N-CA-C	-5.08	102.55	110.42
1	A	48	THR	N-CA-C	5.04	117.43	111.33

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	143	GLN	CA

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	133	ALA	Mainchain
1	A	134	ASP	Mainchain
1	A	211	SER	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2684	0	2622	217	0
2	B	551	0	503	54	0
3	A	3	0	0	0	0
4	A	26	0	8	1	0
5	B	2	0	0	0	0
6	A	128	0	0	14	0
6	B	33	0	0	4	0
All	All	3427	0	3133	255	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 40.

All (255) 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:A:212:GLY:N	1:A:212:GLY:CA	1.73	1.51
1:A:362:LEU:HD12	2:B:90:ARG:HH22	1.05	1.16
1:A:362:LEU:HD12	2:B:90:ARG:NH2	1.65	1.12
2:B:144:MET:HE2	2:B:145:MET:HG2	1.32	1.07
1:A:57:THR:HG23	1:A:188:ASP:HB3	1.32	1.07
1:A:152:LYS:HD2	1:A:162:GLN:HE22	1.14	1.07
1:A:124:ARG:NH2	1:A:131:GLY:HA2	1.71	1.05
1:A:124:ARG:HH21	1:A:131:GLY:HA2	0.86	1.02
1:A:42:LEU:HD21	1:A:324:MET:HE1	1.39	1.01
1:A:211:SER:C	1:A:212:GLY:CA	2.33	1.01
1:A:223:ARG:HA	1:A:223:ARG:NE	1.76	1.01
1:A:327:ARG:HH11	1:A:327:ARG:HG3	1.29	0.98
1:A:151:VAL:HG21	1:A:159:TYR:HB3	1.46	0.97
1:A:8:GLY:O	6:A:983:HOH:O	1.83	0.95
1:A:147:PHE:HB3	6:A:965:HOH:O	1.73	0.89
1:A:151:VAL:CG2	1:A:159:TYR:HB3	2.03	0.87
1:A:103:SER:O	1:A:108:HIS:HB2	1.74	0.87
1:A:233:LEU:O	1:A:233:LEU:HD12	1.76	0.86
1:A:304:ASN:ND2	1:A:306:PHE:H	1.72	0.86
2:B:86:ARG:HH11	2:B:86:ARG:HG2	1.39	0.86
1:A:39:MET:HG2	1:A:315:VAL:HG22	1.59	0.85
1:A:57:THR:HG23	1:A:188:ASP:CB	2.07	0.84
1:A:300:THR:HG22	1:A:302:GLN:H	1.42	0.84
2:B:144:MET:CE	2:B:145:MET:HG2	2.08	0.83
2:B:144:MET:C	2:B:146:THR:H	1.82	0.83
1:A:169:ASP:C	1:A:169:ASP:OD2	2.21	0.82
1:A:223:ARG:HA	1:A:223:ARG:HE	1.43	0.81
1:A:246:ARG:HG3	2:B:145:MET:SD	2.20	0.81
1:A:113:LEU:HB3	1:A:174:VAL:HG23	1.60	0.81
2:B:137:ASN:ND2	2:B:140:GLU:H	1.78	0.81
1:A:327:ARG:HG3	1:A:327:ARG:NH1	1.90	0.81
1:A:152:LYS:HD2	1:A:162:GLN:NE2	1.95	0.81
1:A:124:ARG:HH21	1:A:131:GLY:CA	1.83	0.81
1:A:24:LEU:HD11	1:A:28:LYS:HE3	1.63	0.80
1:A:85:LEU:HD22	1:A:88:ARG:HG3	1.64	0.79
1:A:154:THR:C	1:A:156:ASP:H	1.91	0.78
1:A:152:LYS:CD	1:A:162:GLN:HE22	1.95	0.78
1:A:304:ASN:HD22	1:A:306:PHE:H	1.32	0.78
2:B:143:GLN:HG3	6:B:247:HOH:O	1.84	0.77
1:A:86:PHE:CZ	1:A:143:GLY:HA2	2.19	0.76

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:137:ASN:C	2:B:137:ASN:HD22	1.93	0.75
1:A:124:ARG:HG2	1:A:129:VAL:CG1	2.18	0.74
4:A:900:EMA:H1'1	6:A:1031:HOH:O	1.86	0.74
2:B:137:ASN:HD21	2:B:140:GLU:H	1.36	0.73
1:A:246:ARG:HA	2:B:145:MET:HE1	1.70	0.73
1:A:132:MET:HG3	1:A:135:GLY:HA2	1.69	0.72
1:A:197:HIS:HD2	1:A:199:SER:OG	1.72	0.72
1:A:298:HIS:HD2	1:A:299:GLY:O	1.73	0.71
1:A:169:ASP:OD2	1:A:170:ASP:N	2.23	0.70
1:A:66:SER:O	1:A:84:LYS:HG2	1.91	0.70
2:B:109:MET:HG3	2:B:124:MET:HE1	1.71	0.70
1:A:132:MET:HB2	1:A:136:VAL:C	2.17	0.69
1:A:24:LEU:HD13	1:A:24:LEU:O	1.93	0.69
1:A:327:ARG:HH11	1:A:327:ARG:CG	2.04	0.69
2:B:105:LEU:HD12	2:B:125:ILE:HD12	1.75	0.69
1:A:326:THR:OG1	1:A:329:GLN:HG3	1.93	0.68
1:A:151:VAL:HG23	1:A:160:ALA:O	1.93	0.68
2:B:105:LEU:HD12	2:B:125:ILE:CD1	2.23	0.68
1:A:117:LYS:HD3	1:A:159:TYR:HE1	1.59	0.68
1:A:41:ARG:NE	1:A:310:ASP:OD2	2.27	0.68
2:B:93:ASP:OD1	2:B:97:ASN:O	2.12	0.68
1:A:24:LEU:CD1	1:A:28:LYS:HE3	2.23	0.67
2:B:117:THR:O	2:B:121:VAL:HG23	1.94	0.66
1:A:233:LEU:HD12	1:A:233:LEU:C	2.20	0.66
1:A:362:LEU:CD1	2:B:90:ARG:HH22	1.95	0.65
1:A:22:ALA:HB1	1:A:290:VAL:HG21	1.78	0.65
1:A:304:ASN:HD22	1:A:304:ASN:C	2.05	0.65
1:A:304:ASN:ND2	1:A:306:PHE:N	2.43	0.65
1:A:124:ARG:HD2	1:A:132:MET:HE1	1.78	0.65
1:A:166:LYS:O	1:A:166:LYS:HG2	1.96	0.65
1:A:246:ARG:HB2	2:B:145:MET:HE2	1.78	0.65
1:A:246:ARG:CG	2:B:145:MET:SD	2.85	0.64
1:A:125:GLN:HG2	1:A:125:GLN:O	1.96	0.64
1:A:183:ILE:HD13	1:A:293:GLN:HE22	1.62	0.64
1:A:304:ASN:HD22	1:A:306:PHE:N	1.95	0.64
2:B:116:LEU:HD13	2:B:124:MET:HE2	1.79	0.64
1:A:75:TYR:HB3	1:A:176:VAL:HG21	1.78	0.63
2:B:144:MET:C	2:B:146:THR:N	2.52	0.63
1:A:300:THR:HG21	6:A:934:HOH:O	1.98	0.63
2:B:86:ARG:HH11	2:B:86:ARG:CG	2.09	0.63
1:A:297:GLN:HE21	1:A:297:GLN:HA	1.63	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:22:ALA:HB1	1:A:290:VAL:CG2	2.30	0.62
1:A:313:ILE:HD12	1:A:330:LEU:HD22	1.80	0.62
1:A:211:SER:O	1:A:212:GLY:HA3	2.00	0.61
1:A:300:THR:HG22	1:A:302:GLN:N	2.15	0.61
2:B:116:LEU:CD1	2:B:124:MET:HE2	2.31	0.61
2:B:117:THR:OG1	2:B:120:GLU:HG3	2.01	0.61
2:B:138:TYR:O	2:B:142:VAL:HG23	1.99	0.61
1:A:91:GLU:O	1:A:91:GLU:HG2	2.00	0.60
1:A:120:LEU:O	1:A:124:ARG:HG3	2.02	0.60
1:A:50:LEU:HB3	1:A:55:VAL:HG21	1.84	0.59
1:A:71:LEU:HD11	1:A:137:VAL:HG11	1.84	0.59
1:A:86:PHE:CE2	1:A:143:GLY:HA2	2.36	0.59
1:A:211:SER:O	1:A:212:GLY:CA	2.50	0.59
1:A:133:ALA:HB3	1:A:136:VAL:CG2	2.33	0.58
1:A:164:ARG:HD3	1:A:171:PHE:CZ	2.37	0.58
1:A:153:GLU:CG	1:A:154:THR:N	2.66	0.58
1:A:165:ARG:HG2	1:A:165:ARG:HH11	1.68	0.58
1:A:104:LEU:HA	1:A:108:HIS:O	2.03	0.57
1:A:113:LEU:HG	1:A:161:VAL:CG2	2.34	0.57
1:A:57:THR:HG22	1:A:297:GLN:CG	2.35	0.57
1:A:133:ALA:HB3	1:A:136:VAL:HG23	1.85	0.57
1:A:201:PHE:CZ	1:A:252:ALA:HA	2.40	0.57
1:A:302:GLN:O	1:A:347:ASN:HA	2.04	0.57
1:A:300:THR:CG2	1:A:302:GLN:H	2.14	0.57
1:A:233:LEU:HD11	1:A:235:ARG:HD2	1.88	0.56
1:A:57:THR:CG2	1:A:188:ASP:HB3	2.22	0.56
1:A:324:MET:O	1:A:325:LEU:HD23	2.05	0.56
1:A:85:LEU:O	1:A:88:ARG:HG2	2.06	0.56
1:A:153:GLU:HG2	1:A:154:THR:N	2.21	0.56
1:A:304:ASN:ND2	6:A:1031:HOH:O	2.39	0.56
1:A:325:LEU:HA	1:A:329:GLN:OE1	2.04	0.56
1:A:238:ILE:CD1	2:B:123:GLU:HB3	2.36	0.56
1:A:113:LEU:HD11	1:A:115:LEU:CD2	2.37	0.55
1:A:300:THR:HB	6:A:949:HOH:O	2.05	0.55
1:A:20:PRO:HG2	1:A:51:ILE:HG22	1.89	0.55
1:A:113:LEU:HG	1:A:161:VAL:HG21	1.88	0.55
1:A:57:THR:HB	1:A:294:ASP:O	2.07	0.55
1:A:250:ARG:HH12	1:A:256:GLU:HG3	1.71	0.55
1:A:151:VAL:HG23	1:A:160:ALA:C	2.32	0.54
1:A:305:PRO:O	1:A:307:PRO:HD3	2.07	0.54
1:A:57:THR:CG2	1:A:188:ASP:CB	2.84	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:139:SER:HB3	1:A:144:TYR:CD1	2.43	0.54
1:A:246:ARG:HB2	2:B:145:MET:CE	2.37	0.54
1:A:195:MET:HE1	1:A:337:GLN:CB	2.37	0.54
1:A:95:ARG:HE	1:A:95:ARG:HA	1.71	0.54
1:A:164:ARG:HD3	1:A:171:PHE:CE2	2.44	0.53
1:A:238:ILE:HD11	2:B:123:GLU:OE1	2.09	0.53
2:B:144:MET:O	2:B:146:THR:N	2.41	0.53
1:A:354:GLY:O	1:A:355:LYS:HD3	2.09	0.53
1:A:24:LEU:HD13	1:A:24:LEU:C	2.34	0.53
1:A:129:VAL:HG22	1:A:137:VAL:HB	1.91	0.53
1:A:246:ARG:CA	2:B:145:MET:HE1	2.36	0.53
1:A:302:GLN:NE2	1:A:347:ASN:H	2.07	0.53
2:B:86:ARG:CG	2:B:86:ARG:NH1	2.69	0.52
1:A:348:ARG:HD3	2:B:83:GLU:OE2	2.09	0.52
1:A:183:ILE:CD1	1:A:293:GLN:HE22	2.22	0.52
1:A:238:ILE:HD13	2:B:123:GLU:HB3	1.91	0.52
1:A:129:VAL:CG2	1:A:137:VAL:HB	2.40	0.52
1:A:113:LEU:HD12	1:A:114:THR:N	2.25	0.51
1:A:179:ASN:HB3	1:A:181:ALA:H	1.76	0.51
1:A:132:MET:HB2	1:A:136:VAL:N	2.25	0.51
1:A:246:ARG:HG2	6:A:909:HOH:O	2.10	0.50
2:B:86:ARG:HG2	2:B:86:ARG:NH1	2.15	0.50
2:B:137:ASN:ND2	2:B:137:ASN:C	2.63	0.50
1:A:77:PRO:HG2	1:A:83:SER:HB3	1.93	0.50
1:A:85:LEU:CD2	1:A:88:ARG:HG3	2.37	0.50
1:A:119:ARG:HD3	6:A:920:HOH:O	2.11	0.50
1:A:195:MET:HE1	1:A:337:GLN:HB2	1.94	0.50
2:B:82:GLU:OE2	2:B:138:TYR:HE2	1.94	0.50
1:A:164:ARG:HG2	1:A:171:PHE:CE1	2.46	0.50
1:A:78:VAL:O	1:A:80:PRO:HD3	2.12	0.49
1:A:50:LEU:HD21	1:A:119:ARG:HD2	1.95	0.49
1:A:152:LYS:NZ	6:A:980:HOH:O	2.40	0.49
1:A:297:GLN:HE21	1:A:297:GLN:CA	2.26	0.49
2:B:93:ASP:CG	2:B:97:ASN:O	2.56	0.49
1:A:193:ALA:HA	1:A:300:THR:CG2	2.42	0.49
1:A:42:LEU:HD21	1:A:324:MET:CE	2.28	0.49
1:A:32:LYS:NZ	1:A:320:GLY:HA3	2.28	0.48
1:A:348:ARG:HD3	2:B:83:GLU:CD	2.38	0.48
2:B:116:LEU:CD1	2:B:124:MET:CE	2.91	0.48
1:A:150:ARG:NH1	1:A:150:ARG:HG2	2.28	0.48
1:A:179:ASN:N	1:A:183:ILE:O	2.37	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:ILE:O	1:A:269:ILE:CG2	2.61	0.48
1:A:352:VAL:O	1:A:352:VAL:CG1	2.61	0.48
1:A:151:VAL:HG22	1:A:159:TYR:HB3	1.90	0.48
1:A:246:ARG:CB	2:B:145:MET:CE	2.92	0.48
1:A:71:LEU:HB3	1:A:115:LEU:HD11	1.96	0.48
1:A:304:ASN:HD22	1:A:305:PRO:N	2.12	0.47
1:A:124:ARG:CD	1:A:132:MET:HE1	2.44	0.47
1:A:75:TYR:HB3	1:A:176:VAL:CG2	2.45	0.47
1:A:102:SER:HA	6:A:1020:HOH:O	2.13	0.47
1:A:141:HIS:O	1:A:142:ALA:C	2.57	0.47
1:A:302:GLN:HE21	1:A:347:ASN:H	1.62	0.47
1:A:81:ASN:OD1	1:A:93:ILE:HG12	2.14	0.47
1:A:215:VAL:HG21	1:A:241:LEU:HD23	1.97	0.47
1:A:103:SER:OG	1:A:108:HIS:CD2	2.68	0.47
1:A:107:GLY:O	1:A:180:ALA:HA	2.14	0.47
1:A:154:THR:C	1:A:156:ASP:N	2.63	0.47
1:A:133:ALA:N	1:A:136:VAL:H	2.12	0.47
1:A:306:PHE:HD1	6:A:1031:HOH:O	1.97	0.47
1:A:57:THR:HG22	1:A:297:GLN:HG3	1.97	0.46
2:B:82:GLU:OE2	2:B:138:TYR:CE2	2.68	0.46
2:B:83:GLU:O	2:B:87:GLU:HG3	2.15	0.46
1:A:35:ASN:HD22	1:A:318:ALA:HB1	1.79	0.46
1:A:139:SER:HB3	1:A:144:TYR:CE1	2.50	0.46
1:A:154:THR:HB	1:A:156:ASP:HB3	1.97	0.46
2:B:95:ASP:HB3	6:B:302:HOH:O	2.15	0.46
2:B:144:MET:HE3	2:B:145:MET:HA	1.96	0.46
1:A:153:GLU:CG	1:A:154:THR:H	2.28	0.46
2:B:106:ARG:NH2	6:B:229:HOH:O	2.39	0.46
1:A:94:ALA:O	1:A:95:ARG:C	2.58	0.46
1:A:141:HIS:C	1:A:143:GLY:N	2.71	0.45
1:A:338:ARG:HD2	6:B:177:HOH:O	2.15	0.45
2:B:144:MET:HG3	2:B:145:MET:N	2.31	0.45
1:A:62:VAL:HG22	1:A:108:HIS:CD2	2.51	0.45
1:A:72:GLN:NE2	1:A:82:LEU:O	2.47	0.45
1:A:85:LEU:HD13	1:A:92:VAL:HG13	1.97	0.45
1:A:330:LEU:O	1:A:334:ILE:HG13	2.17	0.45
2:B:102:ALA:HA	2:B:125:ILE:CD1	2.46	0.45
1:A:195:MET:HE1	1:A:337:GLN:HB3	1.98	0.45
1:A:55:VAL:HG12	1:A:56:ALA:N	2.32	0.45
1:A:98:ASN:O	1:A:99:ASP:C	2.58	0.45
1:A:186:THR:HG23	1:A:187:ALA:O	2.17	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:102:ALA:HA	2:B:125:ILE:HD11	1.99	0.45
1:A:113:LEU:HD11	1:A:115:LEU:HD21	1.97	0.44
2:B:116:LEU:HB3	2:B:120:GLU:HB2	1.97	0.44
1:A:196:PRO:HB3	1:A:275:PHE:CE2	2.51	0.44
1:A:141:HIS:O	1:A:143:GLY:N	2.50	0.44
1:A:279:VAL:O	1:A:283:LEU:HG	2.17	0.44
1:A:20:PRO:HG2	1:A:51:ILE:CG2	2.47	0.44
1:A:163:TYR:HB2	6:A:965:HOH:O	2.18	0.44
1:A:79:ASN:HB3	1:A:82:LEU:HG	1.99	0.44
1:A:129:VAL:O	1:A:129:VAL:HG13	2.18	0.44
1:A:155:SER:O	1:A:155:SER:OG	2.32	0.44
1:A:117:LYS:CD	1:A:159:TYR:HE1	2.29	0.43
1:A:152:LYS:CD	1:A:162:GLN:NE2	2.69	0.43
1:A:40:PHE:N	1:A:40:PHE:CD1	2.87	0.43
1:A:288:HIS:HA	1:A:292:ALA:O	2.17	0.43
1:A:132:MET:HG3	1:A:135:GLY:CA	2.45	0.43
1:A:179:ASN:HB2	1:A:183:ILE:H	1.84	0.43
1:A:193:ALA:HA	1:A:300:THR:HG21	2.00	0.43
1:A:269:ILE:HD13	1:A:269:ILE:HA	1.80	0.43
1:A:56:ALA:C	1:A:185:LEU:HD23	2.43	0.43
1:A:165:ARG:HG2	1:A:165:ARG:NH1	2.31	0.43
1:A:219:LEU:HA	1:A:219:LEU:HD23	1.82	0.43
1:A:315:VAL:O	1:A:322:SER:HA	2.19	0.43
1:A:118:GLU:O	1:A:121:ASP:HB2	2.19	0.43
1:A:133:ALA:H	1:A:136:VAL:H	1.67	0.43
1:A:161:VAL:HB	1:A:174:VAL:CG2	2.49	0.43
1:A:165:ARG:NE	6:A:1028:HOH:O	2.48	0.42
1:A:242:TRP:NE1	2:B:124:MET:HB3	2.33	0.42
1:A:117:LYS:O	1:A:120:LEU:HB3	2.19	0.42
1:A:233:LEU:C	1:A:233:LEU:CD1	2.91	0.42
1:A:8:GLY:C	6:A:983:HOH:O	2.50	0.42
1:A:150:ARG:HG2	1:A:150:ARG:HH11	1.84	0.42
1:A:113:LEU:HD11	1:A:115:LEU:HD23	2.01	0.42
2:B:95:ASP:C	2:B:95:ASP:OD1	2.62	0.42
1:A:124:ARG:HG2	1:A:129:VAL:HG13	1.96	0.42
1:A:117:LYS:NZ	1:A:153:GLU:OE2	2.48	0.42
1:A:129:VAL:CG1	1:A:129:VAL:O	2.68	0.41
1:A:346:GLU:O	1:A:347:ASN:C	2.63	0.41
1:A:352:VAL:O	1:A:352:VAL:HG12	2.20	0.41
1:A:132:MET:HA	1:A:136:VAL:O	2.21	0.41
1:A:137:VAL:HG21	1:A:144:TYR:OH	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:132:MET:HB2	1:A:137:VAL:N	2.35	0.41
1:A:57:THR:C	1:A:185:LEU:HD22	2.46	0.41
1:A:123:LEU:HD23	1:A:128:LEU:HD12	2.03	0.41
1:A:60:LEU:HD21	1:A:298:HIS:ND1	2.36	0.41
1:A:197:HIS:CD2	1:A:199:SER:OG	2.62	0.41
1:A:83:SER:C	1:A:85:LEU:N	2.80	0.41
1:A:258:ARG:HH22	2:B:87:GLU:CD	2.29	0.41
1:A:130:THR:O	1:A:138:ALA:HB3	2.22	0.40
1:A:235:ARG:HE	1:A:235:ARG:HB3	1.66	0.40
2:B:105:LEU:HD12	2:B:125:ILE:HD11	2.03	0.40

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 X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	347/358 (97%)	315 (91%)	23 (7%)	9 (3%)	4	2
2	B	67/69 (97%)	63 (94%)	2 (3%)	2 (3%)	3	1
All	All	414/427 (97%)	378 (91%)	25 (6%)	11 (3%)	4	2

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	86	PHE
1	A	135	GLY
1	A	155	SER
1	A	210	THR
2	B	143	GLN
2	B	145	MET
1	A	84	LYS
1	A	153	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	234	ASP
1	A	179	ASN
1	A	131	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	271/274 (99%)	242 (89%)	29 (11%)	6	6
2	B	59/59 (100%)	51 (86%)	8 (14%)	3	3
All	All	330/333 (99%)	293 (89%)	37 (11%)	6	5

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	SER
1	A	57	THR
1	A	91	GLU
1	A	92	VAL
1	A	97	ASP
1	A	102	SER
1	A	119	ARG
1	A	129	VAL
1	A	134	ASP
1	A	137	VAL
1	A	140	ASN
1	A	150	ARG
1	A	154	THR
1	A	155	SER
1	A	165	ARG
1	A	166	LYS
1	A	170	ASP
1	A	174	VAL
1	A	204	SER
1	A	207	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	211	SER
1	A	223	ARG
1	A	224	ARG
1	A	253	VAL
1	A	256	GLU
1	A	290	VAL
1	A	297	GLN
1	A	304	ASN
1	A	327	ARG
2	B	79	THR
2	B	95	ASP
2	B	105	LEU
2	B	125	ILE
2	B	127	GLU
2	B	137	ASN
2	B	144	MET
2	B	145	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	ASN
1	A	46	HIS
1	A	101	ASN
1	A	108	HIS
1	A	162	GLN
1	A	197	HIS
1	A	260	GLN
1	A	293	GLN
1	A	297	GLN
1	A	298	HIS
1	A	302	GLN
1	A	304	ASN
2	B	111	ASN
2	B	137	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 5 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	EMA	A	900	3	26,27,27	7.12	8 (30%)	35,41,41	2.08	9 (25%)

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
4	EMA	A	900	3	-	6/17/20/20	0/2/2/2

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	900	EMA	PA-O3A	26.53	1.87	1.58
4	A	900	EMA	PA-C5'	-20.02	1.31	1.80
4	A	900	EMA	PB-O3B	8.80	1.69	1.59
4	A	900	EMA	PA-O2A	-7.09	1.39	1.56
4	A	900	EMA	PB-O3A	5.70	1.65	1.59
4	A	900	EMA	C1'-N9	3.63	1.54	1.47
4	A	900	EMA	O5'-C5'	3.37	1.47	1.42
4	A	900	EMA	C4-N3	2.87	1.39	1.34

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	900	EMA	O2A-PA-O1A	7.19	133.37	109.95
4	A	900	EMA	PA-O3A-PB	5.44	150.13	132.37
4	A	900	EMA	O1A-PA-C5'	-2.90	102.81	112.86
4	A	900	EMA	C1'-N9-C8	2.84	132.96	127.05
4	A	900	EMA	C4-N9-C8	-2.81	103.72	105.75
4	A	900	EMA	O3A-PB-O1B	-2.75	102.44	110.70
4	A	900	EMA	C4'-C1'-N9	2.68	121.58	112.30
4	A	900	EMA	O2B-PB-O3A	2.16	113.11	107.27
4	A	900	EMA	C1'-N9-C4	-2.03	123.32	126.63

There are no chirality outliers.

All (6) torsion outliers are listed below:

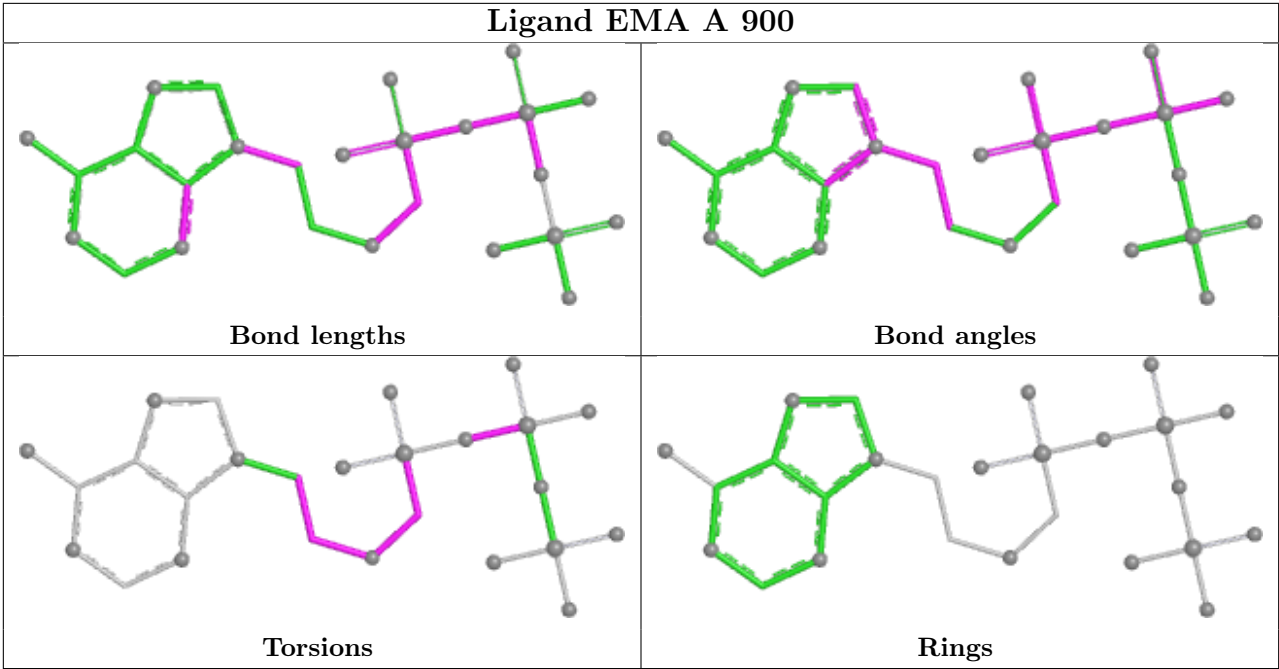
Mol	Chain	Res	Type	Atoms
4	A	900	EMA	PA-C5'-O5'-C4'
4	A	900	EMA	N9-C1'-C4'-O5'
4	A	900	EMA	PA-O3A-PB-O1B
4	A	900	EMA	C1'-C4'-O5'-C5'
4	A	900	EMA	PA-O3A-PB-O2B
4	A	900	EMA	O5'-C5'-PA-O1A

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	900	EMA	1	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	233:LEU	C	234:ASP	N	1.04
1	A	134:ASP	C	135:GLY	N	1.00

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	351/358 (98%)	0.87	53 (15%) 5 4	9, 26, 47, 58	0
2	B	69/69 (100%)	0.69	7 (10%) 12 10	14, 22, 36, 51	0
All	All	420/427 (98%)	0.84	60 (14%) 6 4	9, 25, 47, 58	0

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	364	ALA	6.7
1	A	167	GLY	5.8
1	A	130	THR	5.4
1	A	363	GLY	5.2
1	A	233	LEU	5.0
2	B	145	MET	4.7
1	A	362	LEU	4.6
1	A	133	ALA	4.5
2	B	146	THR	4.4
2	B	143	GLN	4.0
1	A	176	VAL	3.9
2	B	147	ALA	3.9
1	A	134	ASP	3.8
1	A	168	GLY	3.7
1	A	8	GLY	3.7
1	A	124	ARG	3.4
1	A	132	MET	3.3
1	A	159	TYR	2.9
1	A	98	ASN	2.9
1	A	92	VAL	2.8
1	A	151	VAL	2.8
1	A	169	ASP	2.8
1	A	225	ALA	2.8
1	A	126	ALA	2.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	135	GLY	2.7
2	B	96	GLY	2.6
1	A	54	GLY	2.5
1	A	106	HIS	2.5
1	A	99	ASP	2.5
1	A	86	PHE	2.5
1	A	246	ARG	2.5
1	A	309	ALA	2.5
2	B	144	MET	2.4
1	A	173	ALA	2.4
1	A	140	ASN	2.4
1	A	7	ALA	2.4
1	A	131	GLY	2.4
1	A	211	SER	2.4
1	A	155	SER	2.3
1	A	359	ASP	2.3
1	A	105	ALA	2.3
1	A	352	VAL	2.3
1	A	290	VAL	2.3
1	A	210	THR	2.3
2	B	97	ASN	2.2
1	A	89	ALA	2.2
1	A	269	ILE	2.2
1	A	223	ARG	2.2
1	A	96	ALA	2.2
1	A	166	LYS	2.1
1	A	361	GLY	2.1
1	A	138	ALA	2.1
1	A	91	GLU	2.1
1	A	101	ASN	2.1
1	A	179	ASN	2.1
1	A	110	ALA	2.1
1	A	129	VAL	2.1
1	A	52	ALA	2.0
1	A	78	VAL	2.0
1	A	171	PHE	2.0

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

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

6.3 Carbohydrates [i](#)

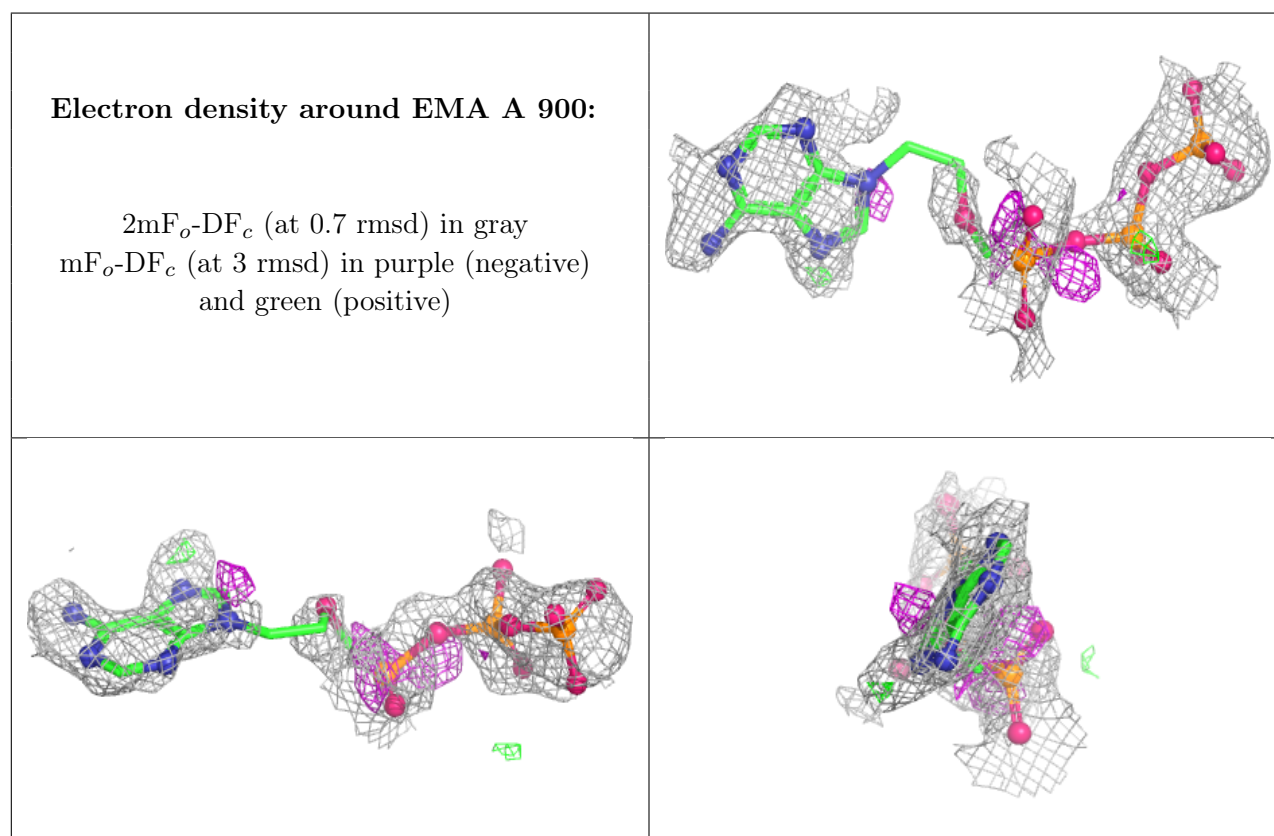
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	EMA	A	900	26/26	0.61	0.18	54,64,67,68	0
3	MG	A	903	1/1	0.87	0.14	48,48,48,48	0
3	MG	A	902	1/1	0.95	0.07	19,19,19,19	0
5	CA	B	800	1/1	0.96	0.04	25,25,25,25	0
5	CA	B	801	1/1	0.96	0.05	34,34,34,34	0
3	MG	A	901	1/1	0.97	0.07	19,19,19,19	0

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



6.5 Other polymers [i](#)

There are no such residues in this entry.