



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:13 AM UTC

PDB ID : 7QF9 / pdb_00007qf9
Title : Crystal structure of PDE6D bound to HRas peptide
Authors : Yelland, T.; Ismail, I.
Deposited on : 2021-12-05
Resolution : 1.95 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
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

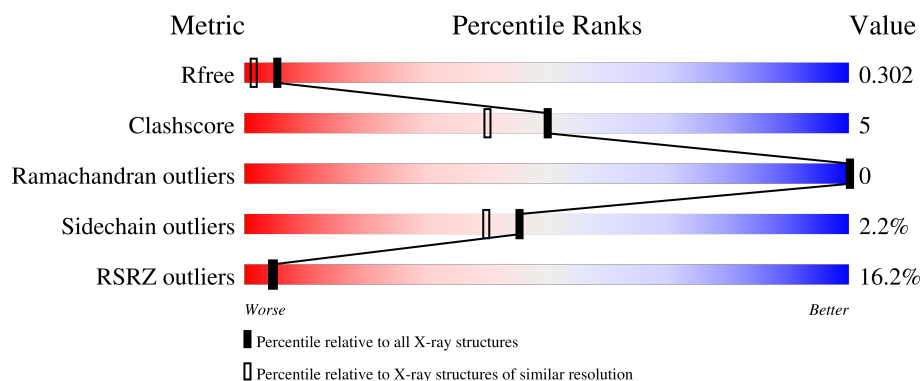
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	AAA	149	15% 85% 13% ..
1	BBB	149	16% 88% 11% .
2	EEE	10	30% 40% 20% 10% 30%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 2705 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.

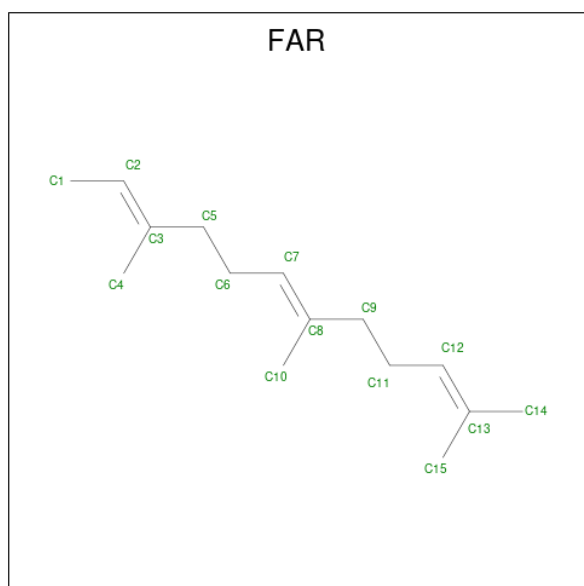
- Molecule 1 is a protein called Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit delta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	BBB	149	Total	C	N	O	S	0	6	0
			1258	809	212	231	6			
1	AAA	147	Total	C	N	O	S	0	1	0
			1205	774	201	224	6			

- Molecule 2 is a protein called HRas peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	EEE	7	Total	C	N	O	S	0	0	0
			47	26	8	9	4			

- Molecule 3 is FARNESYL (CCD ID: FAR) (formula: C₁₅H₂₆).



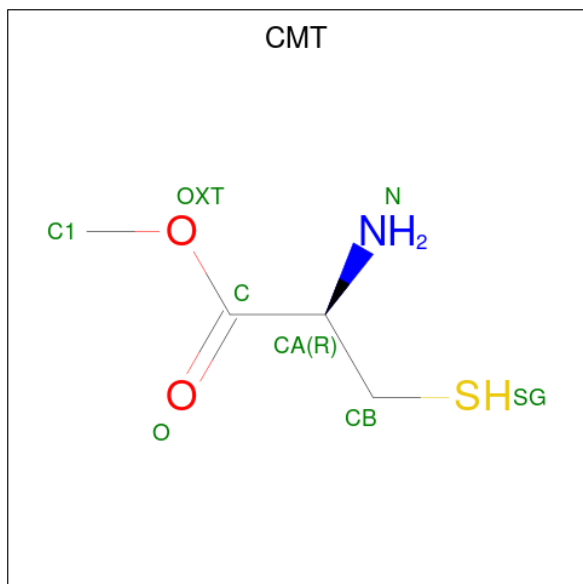
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	BBB	1	Total	C	0	0
			15	15		

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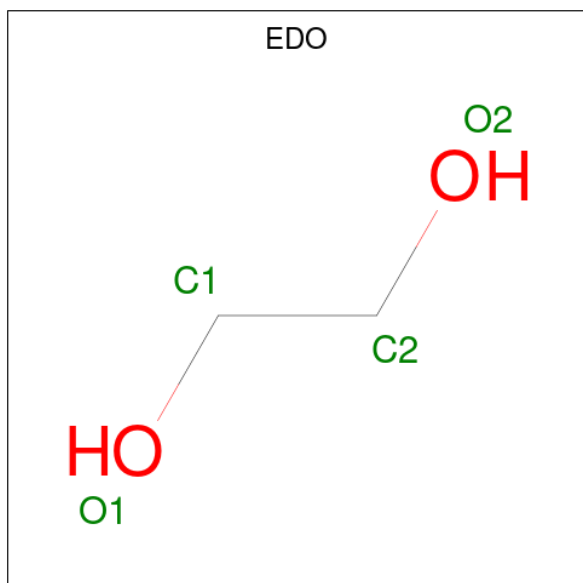
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	EEE	1	Total	C	0	0
			15	15		

- Molecule 4 is O-METHYLCYSTEINE (CCD ID: CMT) (formula: $C_4H_9NO_2S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	BBB	1	Total	C	N	O	S	0	0
			8	4	1	2	1		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	BBB	1	Total C O 4 2 2	0	0
5	BBB	1	Total C O 4 2 2	0	0
5	BBB	1	Total C O 4 2 2	0	0
5	AAA	1	Total C O 4 2 2	0	0
5	AAA	1	Total C O 4 2 2	0	0

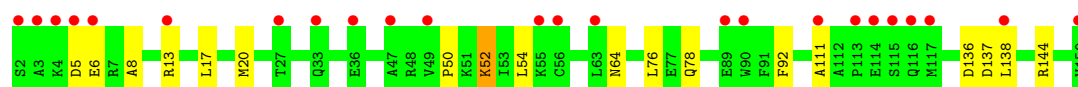
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	BBB	72	Total O 72 72	0	0
6	AAA	64	Total O 64 64	0	0
6	EEE	1	Total O 1 1	0	0

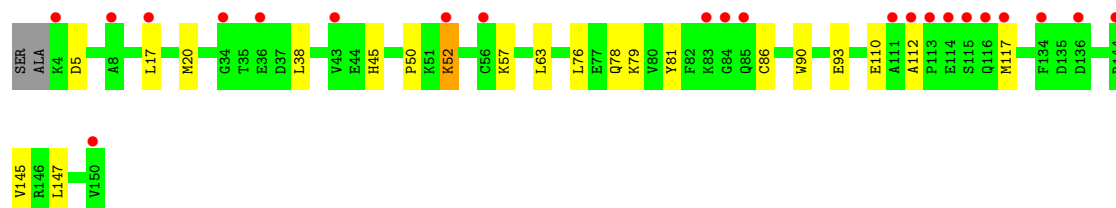
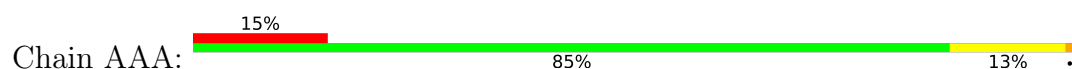
3 Residue-property plots [i](#)

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.

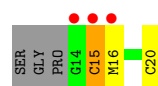
- Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit delta



- Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit delta



- Molecule 2: HRas peptide



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	34.63Å 82.79Å 112.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	56.23 – 1.95 56.23 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.8 (56.23-1.95) 99.7 (56.23-1.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.00 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.230 , 0.299 0.234 , 0.302	Depositor DCC
R_{free} test set	1197 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	38.1	Xtriage
Anisotropy	0.043	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 35.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2705	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.03% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, CMT, FAR

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	AAA	0.92	0/1231	0.88	0/1660
1	BBB	0.92	0/1289	0.89	0/1743
2	EEE	1.05	0/38	0.85	0/47
All	All	0.92	0/2558	0.89	0/3450

There are no bond length outliers.

There are no bond angle outliers.

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	AAA	1205	0	1190	15	0
1	BBB	1258	0	1238	11	0
2	EEE	47	0	46	3	0
3	BBB	15	0	24	0	0
3	EEE	15	0	24	2	0
4	BBB	8	0	8	2	0
5	AAA	8	0	12	0	0
5	BBB	12	0	18	0	0
6	AAA	64	0	0	1	0
6	BBB	72	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	EEE	1	0	0	0	0
All	All	2705	0	2560	27	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 (27) 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:AAA:50:PRO:HB2	1:AAA:52:LYS:HG2	1.67	0.74
1:AAA:17:LEU:HG	1:AAA:63:LEU:HD11	1.80	0.62
1:AAA:147:LEU:HD21	3:EEE:201:FAR:H52	1.84	0.60
1:BBB:6[B]:GLU:OE2	1:BBB:13:ARG:NH1	2.39	0.56
1:BBB:76[A]:LEU:HD11	1:BBB:92:PHE:HD2	1.72	0.54
1:BBB:76[A]:LEU:HD13	1:BBB:78:GLN:HG3	1.91	0.52
1:BBB:8:ALA:HB2	1:BBB:138:LEU:HD22	1.92	0.52
1:AAA:110[A]:GLU:N	2:EEE:15:CYS:O	2.44	0.49
1:AAA:112:ALA:HA	2:EEE:16:MET:HE2	1.94	0.49
1:AAA:90:TRP:CG	2:EEE:15:CYS:HG	2.30	0.49
1:BBB:144:ARG:NH1	6:BBB:304:HOH:O	2.46	0.48
1:BBB:17:LEU:HD12	1:BBB:64:ASN:O	2.12	0.48
1:AAA:117:MET:HE3	1:AAA:117:MET:HB3	1.70	0.47
1:AAA:93:GLU:HG3	6:AAA:357:HOH:O	2.14	0.47
1:BBB:50:PRO:HB2	1:BBB:52:LYS:HG2	1.97	0.46
1:BBB:111:ALA:HB2	4:BBB:202:CMT:H12	1.96	0.46
1:AAA:79:LYS:HE2	1:AAA:81:TYR:OH	2.17	0.45
1:BBB:54:LEU:HD23	4:BBB:202:CMT:HA	1.98	0.44
1:AAA:79:LYS:HE3	1:AAA:86:CYS:SG	2.57	0.44
3:EEE:201:FAR:H112	3:EEE:201:FAR:H101	1.65	0.44
1:AAA:45:HIS:HB2	1:AAA:145:VAL:HG22	2.00	0.43
1:AAA:20:MET:HE1	1:AAA:38:LEU:HD12	2.00	0.43
1:AAA:76:LEU:HD13	1:AAA:78:GLN:HG3	2.00	0.43
1:BBB:13:ARG:HD3	6:BBB:364:HOH:O	2.20	0.42
1:AAA:57:LYS:HD2	1:AAA:57:LYS:HA	1.74	0.40
1:BBB:136:ASP:HB3	1:BBB:137:ASP:H	1.69	0.40
1:AAA:17:LEU:HG	1:AAA:63:LEU:CD1	2.49	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 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	AAA	146/149 (98%)	144 (99%)	2 (1%)	0	100	100
1	BBB	153/149 (103%)	149 (97%)	4 (3%)	0	100	100
2	EEE	5/10 (50%)	5 (100%)	0	0	100	100
All	All	304/308 (99%)	298 (98%)	6 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	AAA	132/134 (98%)	130 (98%)	2 (2%)	57	54
1	BBB	137/134 (102%)	134 (98%)	3 (2%)	45	40
2	EEE	5/7 (71%)	4 (80%)	1 (20%)	1	0
All	All	274/275 (100%)	268 (98%)	6 (2%)	45	40

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	BBB	5	ASP
1	BBB	20	MET
1	BBB	52	LYS
1	AAA	5	ASP
1	AAA	52	LYS

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Mol	Chain	Res	Type
2	EEE	15	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
2	CMT	EEE	20	2,3	7,7,7	1.97	1 (14%)	6,8,8	1.39	0

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
2	CMT	EEE	20	2,3	-	1/8/8/8	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	EEE	20	CMT	OXT-C	5.00	1.45	1.33

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	EEE	20	CMT	N-CA-CB-SG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

8 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	FAR	EEE	201	2	14,14,14	0.23	0	15,16,16	0.39	0
5	EDO	BBB	205	-	3,3,3	0.06	0	2,2,2	0.05	0
3	FAR	BBB	201	4	14,14,14	0.24	0	15,16,16	0.15	0
5	EDO	AAA	202	-	3,3,3	0.07	0	2,2,2	0.06	0
5	EDO	AAA	201	-	3,3,3	0.06	0	2,2,2	0.06	0
5	EDO	BBB	203	-	3,3,3	0.06	0	2,2,2	0.04	0
5	EDO	BBB	204	-	3,3,3	0.06	0	2,2,2	0.02	0
4	CMT	BBB	202	3	7,7,7	1.99	1 (14%)	6,8,8	0.82	0

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	FAR	EEE	201	2	-	5/14/14/14	-
5	EDO	BBB	205	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	FAR	BBB	201	4	-	6/14/14/14	-
5	EDO	AAA	202	-	-	0/1/1/1	-
5	EDO	AAA	201	-	-	0/1/1/1	-
5	EDO	BBB	203	-	-	0/1/1/1	-
5	EDO	BBB	204	-	-	1/1/1/1	-
4	CMT	BBB	202	3	-	4/8/8/8	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	BBB	202	CMT	OXT-C	5.05	1.45	1.33

There are no bond angle outliers.

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	BBB	202	CMT	CA-C-OXT-C1
4	BBB	202	CMT	O-C-OXT-C1
3	EEE	201	FAR	C10-C8-C9-C11
3	EEE	201	FAR	C7-C8-C9-C11
3	BBB	201	FAR	C12-C11-C9-C8
3	BBB	201	FAR	C10-C8-C9-C11
3	BBB	201	FAR	C2-C3-C5-C6
3	BBB	201	FAR	C7-C8-C9-C11
3	EEE	201	FAR	C4-C3-C5-C6
5	BBB	204	EDO	O1-C1-C2-O2
3	BBB	201	FAR	C4-C3-C5-C6
3	EEE	201	FAR	C2-C3-C5-C6
3	EEE	201	FAR	C3-C5-C6-C7
4	BBB	202	CMT	N-CA-CB-SG
3	BBB	201	FAR	C5-C6-C7-C8
4	BBB	202	CMT	O-C-CA-N

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	EEE	201	FAR	2	0
4	BBB	202	CMT	2	0

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 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	AAA	147/149 (98%)	0.97	22 (14%) 5 6	26, 42, 65, 92	1 (0%)
1	BBB	149/149 (100%)	1.03	24 (16%) 4 5	16, 41, 70, 95	6 (4%)
2	EEE	6/10 (60%)	2.01	3 (50%) 0 0	43, 50, 83, 96	0
All	All	302/308 (98%)	1.02	49 (16%) 4 5	16, 42, 76, 96	7 (2%)

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	3	ALA	7.0
1	BBB	117	MET	4.1
1	AAA	84	GLY	3.8
1	BBB	114	GLU	3.8
1	BBB	4	LYS	3.8
1	BBB	2	SER	3.6
1	AAA	114	GLU	3.6
1	BBB	5	ASP	3.5
1	BBB	113	PRO	3.5
1	AAA	111	ALA	3.4
2	EEE	15	CYS	3.3
1	BBB	36	GLU	3.3
1	BBB	150	VAL	3.3
1	AAA	115	SER	3.2
2	EEE	14	GLY	3.2
1	AAA	4	LYS	3.1
1	BBB	116	GLN	2.9
1	AAA	52	LYS	2.8
1	AAA	43	VAL	2.8
1	BBB	115	SER	2.7
1	BBB	111	ALA	2.7
1	AAA	8	ALA	2.7
1	AAA	36	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
1	AAA	112	ALA	2.7
2	EEE	16	MET	2.6
1	AAA	113	PRO	2.6
1	BBB	55	LYS	2.5
1	BBB	6[A]	GLU	2.5
1	AAA	117	MET	2.5
1	AAA	83	LYS	2.5
1	BBB	138	LEU	2.4
1	AAA	17	LEU	2.4
1	AAA	34	GLY	2.4
1	BBB	33	GLN	2.3
1	AAA	116	GLN	2.3
1	BBB	90[A]	TRP	2.3
1	BBB	56	CYS	2.3
1	AAA	134	PHE	2.2
1	BBB	49[A]	VAL	2.2
1	BBB	13	ARG	2.2
1	AAA	56	CYS	2.2
1	BBB	63	LEU	2.2
1	AAA	85	GLN	2.1
1	BBB	27	THR	2.1
1	BBB	89	GLU	2.1
1	AAA	150	VAL	2.1
1	AAA	136	ASP	2.1
1	BBB	47	ALA	2.0
1	AAA	144	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
2	CMT	EEE	20	8/8	0.96	0.08	30,36,36,43	0

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(Å ²)	Q<0.9
5	EDO	BBB	204	4/4	0.76	0.19	27,28,31,33	4
4	CMT	BBB	202	8/8	0.80	0.23	78,85,92,95	0
3	FAR	EEE	201	15/15	0.85	0.16	36,44,55,63	0
5	EDO	AAA	202	4/4	0.85	0.14	40,41,44,44	0
3	FAR	BBB	201	15/15	0.86	0.17	55,68,79,83	0
5	EDO	BBB	205	4/4	0.88	0.12	38,44,46,51	0
5	EDO	AAA	201	4/4	0.90	0.12	31,31,31,34	0
5	EDO	BBB	203	4/4	0.90	0.10	32,34,38,38	0

6.5 Other polymers [i](#)

There are no such residues in this entry.