



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:35 PM UTC

PDB ID : 6R0E / pdb_00006r0e
Title : Structure of F11TCR in complex with DR1 MHC Class II presenting PKYVKQNTLKLAT
Authors : Rizkallah, P.J.; Greenshields-Watson, A.L.
Deposited on : 2019-03-12
Resolution : 1.91 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

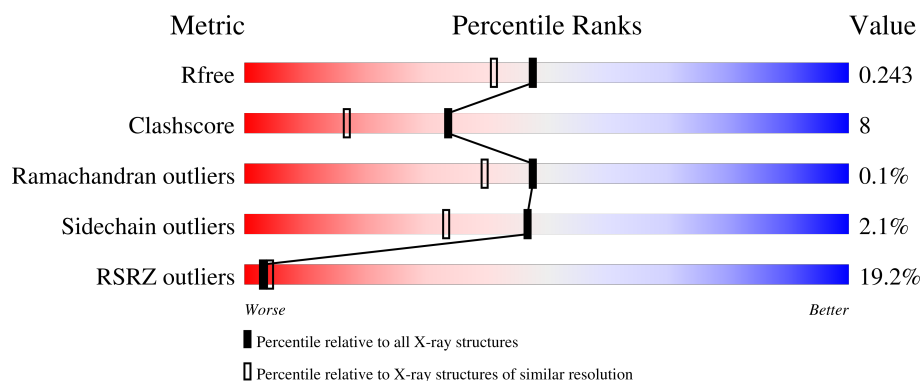
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.91 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	1188 (1.92-1.92)
Clashscore	190562	1209 (1.92-1.92)
Ramachandran outliers	187476	1195 (1.92-1.92)
Sidechain outliers	187428	1195 (1.92-1.92)
RSRZ outliers	180081	1188 (1.92-1.92)

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	183	30% 84% 13% ..
2	BBB	191	37% 76% 23% ..
3	CCC	13	23% 92% 8%
4	DDD	202	10% 84% 15%
5	EEE	240	4% 87% 13%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	EDO	DDD	301	-	-	X	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 6958 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 HLA class II histocompatibility antigen, DR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	178	Total	C	N	O	S	0	0	0
			1447	940	234	268	5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	0	MET	-	initiating methionine	UNP P01903

- Molecule 2 is a protein called HLA class II histocompatibility antigen, DRB1-1 beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	BBB	190	Total	C	N	O	S	0	0	0
			1522	960	272	283	7			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BBB	0	MET	-	initiating methionine	UNP P04229

- Molecule 3 is a protein called Hemagglutinin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	CCC	13	Total	C	N	O	0	0	0
			106	69	18	19			

- Molecule 4 is a protein called F11-TCR Alpha Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	DDD	202	Total	C	N	O	S	0	3	0
			1597	1007	263	317	10			

- Molecule 5 is a protein called F11-TCR Beta Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	EEE	240	Total 1935	C 1211	N 338	O 377	S 9	0	3	0

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



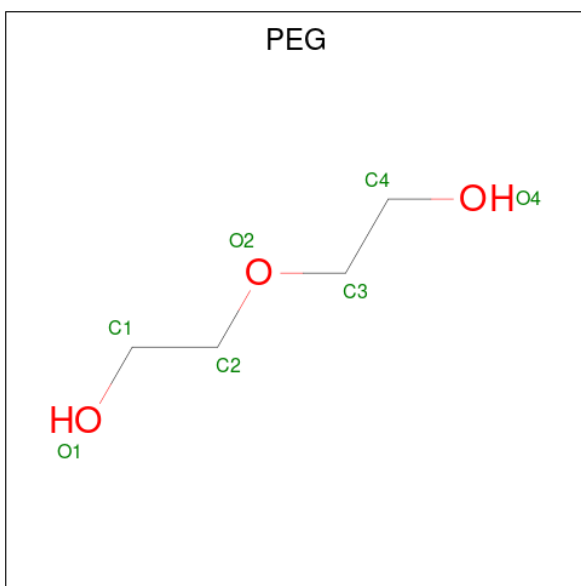
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	BBB	1	Total 4	C 2	O 2	0	0
6	BBB	1	Total 4	C 2	O 2	0	0
6	DDD	1	Total 4	C 2	O 2	0	0
6	DDD	1	Total 4	C 2	O 2	0	0
6	DDD	1	Total 4	C 2	O 2	0	0
6	EEE	1	Total 4	C 2	O 2	0	0

- Molecule 7 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	DDD	1	Total	O	S	0	0
			5	4	1		

- Molecule 8 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	DDD	1	Total	C	O	0	0
			7	4	3		
8	EEE	1	Total	C	O	0	0
			7	4	3		

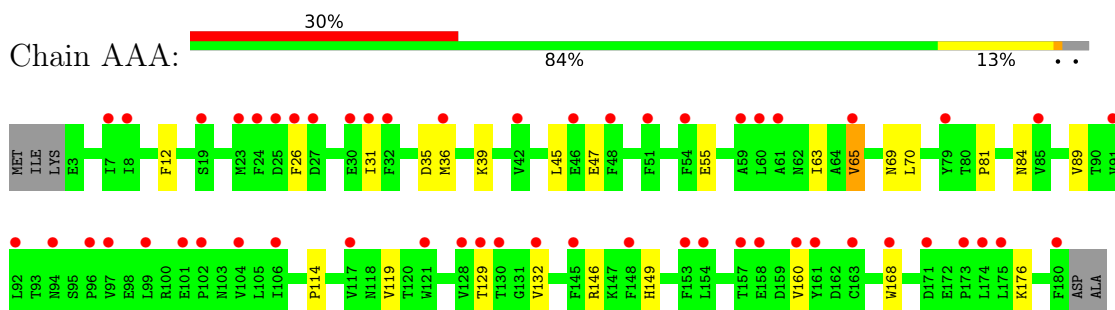
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	AAA	37	Total 37	O 37	0	0
9	BBB	23	Total 23	O 23	0	0
9	CCC	4	Total 4	O 4	0	0
9	DDD	118	Total 118	O 118	0	0
9	EEE	126	Total 126	O 126	0	0

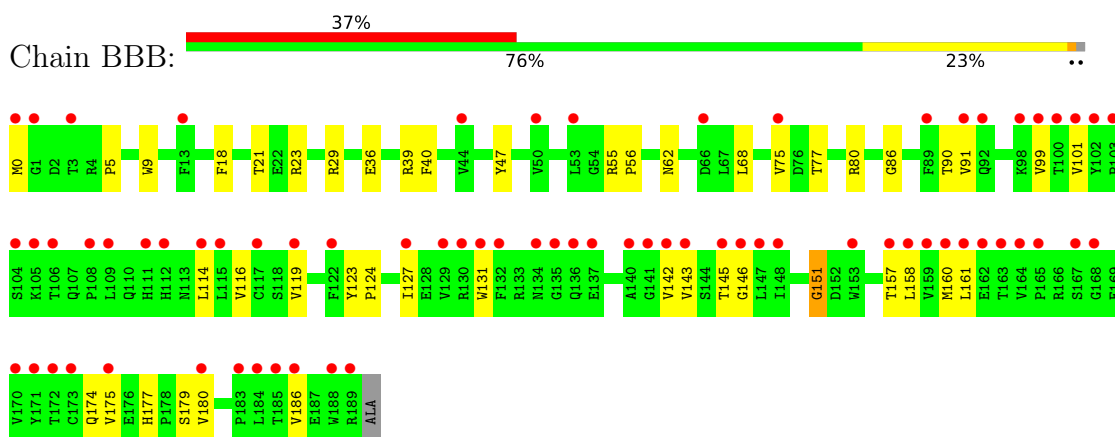
3 Residue-property plots [i](#)

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.

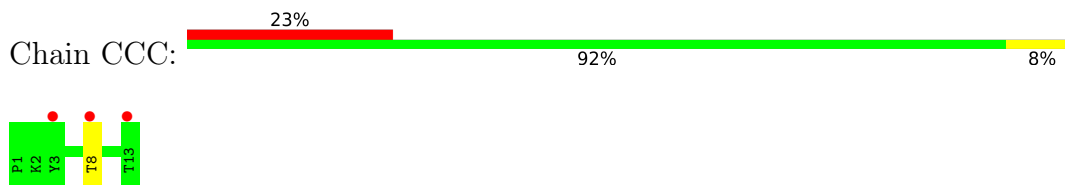
- Molecule 1: HLA class II histocompatibility antigen, DR alpha chain



- Molecule 2: HLA class II histocompatibility antigen, DRB1-1 beta chain

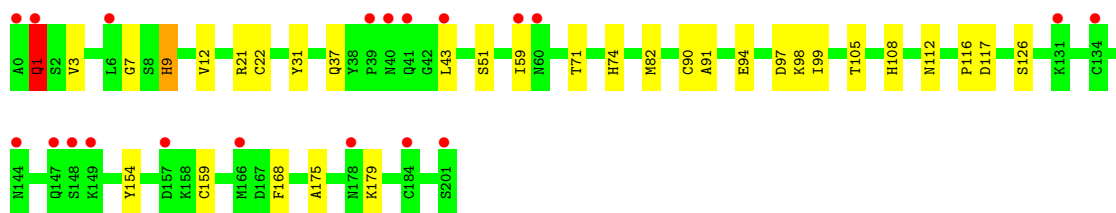


- Molecule 3: Hemagglutinin

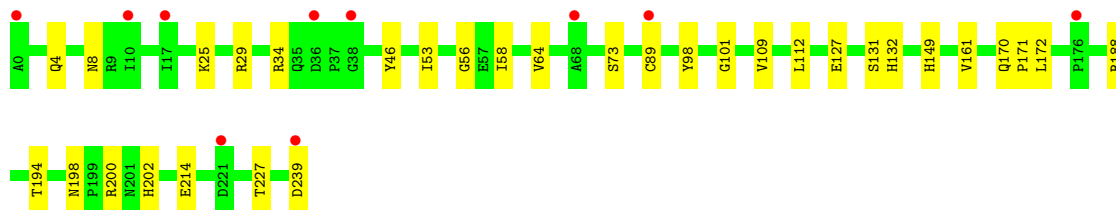
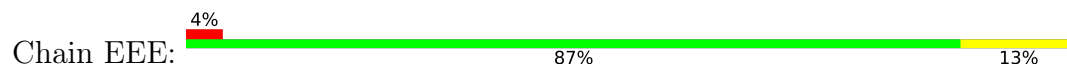


- Molecule 4: F11-TCR Alpha Chain





● Molecule 5: F11-TCR Beta Chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	132.28Å 184.90Å 50.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	92.45 – 1.91 92.45 – 1.91	Depositor EDS
% Data completeness (in resolution range)	99.9 (92.45-1.91) 99.9 (92.45-1.91)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.06 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.205 , 0.233 0.212 , 0.243	Depositor DCC
R_{free} test set	4763 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	36.2	Xtriage
Anisotropy	0.178	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 33.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6958	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.32% 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: SO4, PEG, EDO

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	1.11	0/1492	1.35	3/2038 (0.1%)
2	BBB	1.12	0/1561	1.38	2/2124 (0.1%)
3	CCC	1.03	0/107	1.38	0/141
4	DDD	1.16	2/1634 (0.1%)	1.31	3/2216 (0.1%)
5	EEE	1.08	0/1983	1.31	5/2693 (0.2%)
All	All	1.11	2/6777 (0.0%)	1.34	13/9212 (0.1%)

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
2	BBB	0	1
4	DDD	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	DDD	9	HIS	C-O	6.15	1.31	1.24
4	DDD	12	VAL	C-O	5.29	1.29	1.23

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	EEE	56	GLY	CA-C-N	5.95	128.17	120.44
5	EEE	56	GLY	C-N-CA	5.95	128.17	120.44
1	AAA	65	VAL	CA-C-O	-5.78	114.72	120.85
5	EEE	227	THR	CA-CB-OG1	-5.61	101.18	109.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	DDD	1	GLN	CB-CA-C	5.47	118.47	110.26
5	EEE	214	GLU	CA-C-N	5.45	127.84	120.65
5	EEE	214	GLU	C-N-CA	5.45	127.84	120.65
4	DDD	179	LYS	CA-C-N	5.19	127.23	120.28
4	DDD	179	LYS	C-N-CA	5.19	127.23	120.28
1	AAA	35	ASP	CA-C-N	5.12	127.13	120.28
1	AAA	35	ASP	C-N-CA	5.12	127.13	120.28
2	BBB	151	GLY	CA-C-N	5.01	130.10	122.23
2	BBB	151	GLY	C-N-CA	5.01	130.10	122.23

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	BBB	151	GLY	Peptide
4	DDD	112	ASN	Mainchain

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	1447	0	1373	21	0
2	BBB	1522	0	1436	31	0
3	CCC	106	0	121	1	0
4	DDD	1597	0	1521	38	0
5	EEE	1935	0	1843	22	0
6	BBB	8	0	12	0	0
6	DDD	12	0	18	8	0
6	EEE	4	0	6	0	0
7	DDD	5	0	0	1	0
8	DDD	7	0	10	0	0
8	EEE	7	0	10	3	0
9	AAA	37	0	0	2	0
9	BBB	23	0	0	0	0
9	CCC	4	0	0	0	0
9	DDD	118	0	0	2	0
9	EEE	126	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	6958	0	6350	100	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 8.

All (100) 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)
4:DDD:3:VAL:CG2	4:DDD:90[B]:CYS:SG	2.60	0.90
4:DDD:3:VAL:HG21	4:DDD:90[B]:CYS:SG	2.18	0.84
4:DDD:3:VAL:HG23	4:DDD:22:CYS:SG	2.34	0.68
4:DDD:9:HIS:HD2	4:DDD:108:HIS:HE1	1.40	0.67
5:EEE:53:ILE:HD12	5:EEE:64:VAL:HG23	1.81	0.62
1:AAA:45:LEU:HB3	1:AAA:47:GLU:OE1	2.01	0.60
4:DDD:108:HIS:HD2	6:DDD:301:EDO:C1	2.15	0.60
2:BBB:99:VAL:HG22	2:BBB:119:VAL:HG23	1.84	0.58
5:EEE:161:VAL:HG12	8:EEE:301:PEG:H32	1.85	0.58
4:DDD:82:MET:HE3	9:DDD:495:HOH:O	2.03	0.58
2:BBB:99:VAL:HG12	2:BBB:186:VAL:HG11	1.86	0.58
1:AAA:119:VAL:HG21	1:AAA:149:HIS:CE1	2.38	0.57
8:EEE:301:PEG:H12	9:EEE:407:HOH:O	2.02	0.57
1:AAA:26:PHE:N	1:AAA:31:ILE:HD11	2.20	0.56
5:EEE:34:ARG:HD3	5:EEE:58:ILE:HD12	1.87	0.56
4:DDD:3:VAL:CG2	4:DDD:22:CYS:SG	2.94	0.56
4:DDD:97:ASP:CG	5:EEE:29:ARG:HE	2.14	0.56
1:AAA:65:VAL:HB	3:CCC:8:THR:HG23	1.88	0.55
4:DDD:98:LYS:HE2	5:EEE:46:TYR:CZ	2.41	0.55
4:DDD:168:PHE:CE1	6:DDD:303:EDO:H11	2.42	0.55
5:EEE:198:ASN:HD21	5:EEE:200:ARG:NH2	2.04	0.55
2:BBB:90:THR:HG22	2:BBB:91:VAL:H	1.72	0.54
2:BBB:146:GLY:O	2:BBB:157:THR:HG23	2.07	0.54
2:BBB:90:THR:HG22	2:BBB:91:VAL:N	2.22	0.54
4:DDD:21[B]:ARG:HA	4:DDD:74:HIS:CD2	2.43	0.53
1:AAA:168:TRP:HE1	2:BBB:0:MET:HB3	1.72	0.53
4:DDD:99:ILE:CD1	5:EEE:98:TYR:CE1	2.92	0.53
5:EEE:202:HIS:HD2	9:EEE:486:HOH:O	1.91	0.52
4:DDD:3:VAL:HG22	4:DDD:90[B]:CYS:SG	2.47	0.52
4:DDD:91:ALA:HB1	4:DDD:99:ILE:HG23	1.91	0.52
2:BBB:77:THR:HG21	4:DDD:51:SER:CB	2.40	0.51
4:DDD:1:GLN:CB	4:DDD:94:GLU:HG3	2.41	0.51
1:AAA:129:THR:O	1:AAA:132:VAL:HG12	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BBB:62:ASN:HA	2:BBB:68:LEU:HD11	1.92	0.51
4:DDD:7:GLY:O	4:DDD:105:THR:HG23	2.11	0.50
5:EEE:8:ASN:OD1	5:EEE:149:HIS:HE1	1.93	0.50
2:BBB:40:PHE:HB2	2:BBB:47:TYR:CE1	2.46	0.50
1:AAA:31:ILE:HD12	1:AAA:31:ILE:N	2.27	0.49
2:BBB:131:TRP:CD1	2:BBB:161:LEU:HB2	2.47	0.49
2:BBB:177:HIS:O	2:BBB:180:VAL:HG22	2.12	0.49
2:BBB:177:HIS:HD2	2:BBB:179:SER:OG	1.95	0.49
4:DDD:9:HIS:CD2	4:DDD:108:HIS:HE1	2.27	0.49
4:DDD:9:HIS:HD2	4:DDD:108:HIS:CE1	2.28	0.48
5:EEE:4:GLN:HE21	5:EEE:101:GLY:HA3	1.79	0.48
5:EEE:194:THR:HG23	9:EEE:513:HOH:O	2.13	0.47
4:DDD:99:ILE:HD12	5:EEE:98:TYR:CE1	2.48	0.47
1:AAA:26:PHE:CG	2:BBB:90:THR:HG23	2.49	0.47
4:DDD:31:TYR:CD2	7:DDD:304:SO4:O4	2.67	0.47
4:DDD:108:HIS:CD2	6:DDD:301:EDO:C1	2.96	0.47
2:BBB:18:PHE:HB2	2:BBB:23:ARG:HB3	1.96	0.47
4:DDD:154:TYR:O	4:DDD:175:ALA:HA	2.14	0.47
4:DDD:108:HIS:HD2	6:DDD:301:EDO:H11	1.79	0.47
5:EEE:172:LEU:HD12	5:EEE:172:LEU:C	2.40	0.47
4:DDD:99:ILE:HD12	5:EEE:98:TYR:CD1	2.50	0.46
5:EEE:64:VAL:HA	5:EEE:73:SER:O	2.15	0.46
5:EEE:170:GLN:HA	5:EEE:171:PRO:HD3	1.82	0.46
4:DDD:108:HIS:CD2	6:DDD:301:EDO:H11	2.51	0.46
4:DDD:21[A]:ARG:HA	4:DDD:74:HIS:CD2	2.49	0.46
2:BBB:75:VAL:O	2:BBB:80:ARG:HG3	2.16	0.46
1:AAA:26:PHE:CE2	2:BBB:90:THR:CG2	2.98	0.45
2:BBB:123:TYR:CD1	2:BBB:124:PRO:HA	2.52	0.45
5:EEE:4:GLN:NE2	5:EEE:89:CYS:H	2.15	0.45
1:AAA:26:PHE:CB	1:AAA:31:ILE:HD11	2.47	0.45
2:BBB:86:GLY:O	2:BBB:90:THR:HB	2.17	0.45
1:AAA:31:ILE:HD12	1:AAA:31:ILE:H	1.81	0.44
4:DDD:21[A]:ARG:HB2	6:DDD:302:EDO:H11	2.00	0.44
8:EEE:301:PEG:C1	9:EEE:407:HOH:O	2.59	0.44
1:AAA:81:PRO:HB3	2:BBB:5:PRO:HB2	1.99	0.44
5:EEE:34:ARG:HG2	5:EEE:58:ILE:HD11	2.00	0.44
1:AAA:39:LYS:NZ	9:AAA:203:HOH:O	2.51	0.44
1:AAA:84:ASN:HD22	1:AAA:114:PRO:CD	2.31	0.44
1:AAA:26:PHE:CD2	2:BBB:90:THR:CG2	3.01	0.43
1:AAA:12:PHE:HA	2:BBB:9:TRP:O	2.17	0.43
4:DDD:108:HIS:CD2	6:DDD:301:EDO:H12	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AAA:69:ASN:ND2	9:AAA:202:HOH:O	2.40	0.43
2:BBB:101:VAL:HA	2:BBB:116:VAL:O	2.19	0.43
4:DDD:91:ALA:HB1	4:DDD:99:ILE:CG2	2.48	0.43
4:DDD:117:ASP:OD1	5:EEE:132:HIS:HE1	2.02	0.43
2:BBB:21:THR:O	2:BBB:80:ARG:NH1	2.52	0.43
2:BBB:114:LEU:HD21	2:BBB:160:MET:HE3	2.01	0.43
2:BBB:36:GLU:OE2	2:BBB:39:ARG:HB3	2.20	0.42
6:DDD:301:EDO:C2	9:DDD:451:HOH:O	2.68	0.42
1:AAA:70:LEU:HD13	2:BBB:9:TRP:HB2	2.01	0.42
2:BBB:145:THR:HG23	2:BBB:158:LEU:HB2	2.02	0.41
4:DDD:37:GLN:HB2	4:DDD:43:LEU:HD23	2.02	0.41
4:DDD:1:GLN:HB3	4:DDD:94:GLU:HG3	2.02	0.41
5:EEE:109:VAL:CG2	5:EEE:112:LEU:HD23	2.49	0.41
1:AAA:36:MET:CE	1:AAA:63:ILE:HG13	2.51	0.41
2:BBB:127:ILE:HD11	2:BBB:175:VAL:HG13	2.02	0.41
1:AAA:26:PHE:CD1	2:BBB:90:THR:HG23	2.56	0.41
2:BBB:55:ARG:N	2:BBB:56:PRO:CD	2.84	0.41
5:EEE:34:ARG:HD3	5:EEE:58:ILE:CD1	2.50	0.41
5:EEE:127:GLU:HG3	9:EEE:481:HOH:O	2.20	0.41
4:DDD:1:GLN:HB2	4:DDD:94:GLU:HG3	2.03	0.41
2:BBB:29:ARG:HG2	2:BBB:36:GLU:OE2	2.21	0.40
1:AAA:89:VAL:O	1:AAA:176:LYS:HE2	2.22	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	AAA	176/183 (96%)	170 (97%)	6 (3%)	0	100	100
2	BBB	188/191 (98%)	182 (97%)	6 (3%)	0	100	100
3	CCC	11/13 (85%)	11 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	DDD	203/202 (100%)	196 (97%)	6 (3%)	1 (0%)	24	14
5	EEE	241/240 (100%)	232 (96%)	9 (4%)	0	100	100
All	All	819/829 (99%)	791 (97%)	27 (3%)	1 (0%)	48	40

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	DDD	71	THR

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	159/167 (95%)	156 (98%)	3 (2%)	50	37
2	BBB	163/172 (95%)	160 (98%)	3 (2%)	51	39
3	CCC	12/12 (100%)	12 (100%)	0	100	100
4	DDD	182/180 (101%)	176 (97%)	6 (3%)	33	17
5	EEE	213/210 (101%)	209 (98%)	4 (2%)	50	37
All	All	729/741 (98%)	713 (98%)	16 (2%)	47	32

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	55	GLU
1	AAA	146	ARG
1	AAA	160	VAL
2	BBB	142	VAL
2	BBB	143	VAL
2	BBB	174	GLN
4	DDD	1	GLN
4	DDD	59	ILE
4	DDD	116	PRO
4	DDD	126	SER

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Mol	Chain	Res	Type
4	DDD	159[A]	CYS
4	DDD	159[B]	CYS
5	EEE	25	LYS
5	EEE	131	SER
5	EEE	188	ARG
5	EEE	239	ASP

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

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

9 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	$\# Z > 2$
6	EDO	BBB	201	-	3,3,3	0.14	0	2,2,2	0.26	0
6	EDO	BBB	202	-	3,3,3	0.17	0	2,2,2	0.18	0
6	EDO	DDD	302	-	3,3,3	0.18	0	2,2,2	0.14	0
8	PEG	EEE	301	-	6,6,6	0.30	0	5,5,5	0.25	0
6	EDO	EEE	302	-	3,3,3	0.12	0	2,2,2	0.31	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	EDO	DDD	303	-	3,3,3	0.11	0	2,2,2	0.31	0
7	SO4	DDD	304	-	4,4,4	0.36	0	6,6,6	0.09	0
6	EDO	DDD	301	-	3,3,3	0.24	0	2,2,2	0.43	0
8	PEG	DDD	305	-	6,6,6	0.32	0	5,5,5	0.26	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
6	EDO	BBB	201	-	-	0/1/1/1	-
6	EDO	BBB	202	-	-	0/1/1/1	-
6	EDO	DDD	302	-	-	0/1/1/1	-
8	PEG	EEE	301	-	-	2/4/4/4	-
6	EDO	EEE	302	-	-	1/1/1/1	-
6	EDO	DDD	303	-	-	0/1/1/1	-
6	EDO	DDD	301	-	-	1/1/1/1	-
8	PEG	DDD	305	-	-	1/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	DDD	305	PEG	O2-C3-C4-O4
6	DDD	301	EDO	O1-C1-C2-O2
8	EEE	301	PEG	O1-C1-C2-O2
6	EEE	302	EDO	O1-C1-C2-O2
8	EEE	301	PEG	O2-C3-C4-O4

There are no ring outliers.

5 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	DDD	302	EDO	1	0
8	EEE	301	PEG	3	0
6	DDD	303	EDO	1	0
7	DDD	304	SO4	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	DDD	301	EDO	6	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	178/183 (97%)	1.58	54 (30%)  	39, 63, 103, 114	0
2	BBB	190/191 (99%)	1.84	71 (37%)  	40, 69, 94, 108	0
3	CCC	13/13 (100%)	1.14	3 (23%)  	41, 48, 61, 72	0
4	DDD	202/202 (100%)	0.63	20 (9%)  	15, 39, 69, 94	3 (1%)
5	EEE	240/240 (100%)	0.57	10 (4%)  	14, 42, 63, 91	3 (1%)
All	All	823/829 (99%)	1.11	158 (19%)  	14, 51, 92, 114	6 (0%)

All (158) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	BBB	170	VAL	6.5
1	AAA	180	PHE	6.3
4	DDD	1	GLN	5.8
2	BBB	1	GLY	5.6
1	AAA	99	LEU	5.4
2	BBB	173	CYS	5.3
4	DDD	40	ASN	5.0
5	EEE	0	ALA	4.9
2	BBB	159	VAL	4.7
1	AAA	25	ASP	4.4
2	BBB	161	LEU	4.2
1	AAA	97	VAL	4.1
4	DDD	39	PRO	4.1
2	BBB	132	PHE	4.1
4	DDD	0	ALA	4.1
5	EEE	239	ASP	4.1
2	BBB	142	VAL	4.0
2	BBB	186	VAL	4.0
2	BBB	130	ARG	3.9
2	BBB	143	VAL	3.9

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Mol	Chain	Res	Type	RSRZ
1	AAA	154	LEU	3.8
2	BBB	162	GLU	3.8
2	BBB	112	HIS	3.8
4	DDD	184	CYS	3.7
4	DDD	147	GLN	3.7
5	EEE	89	CYS	3.6
2	BBB	101	VAL	3.5
2	BBB	115	LEU	3.5
1	AAA	106	ILE	3.5
2	BBB	141	GLY	3.4
2	BBB	117	CYS	3.4
3	CCC	3	TYR	3.4
1	AAA	19	SER	3.3
2	BBB	185	THR	3.3
2	BBB	171	TYR	3.3
1	AAA	96	PRO	3.3
4	DDD	41	GLN	3.2
1	AAA	128	VAL	3.2
2	BBB	168	GLY	3.2
2	BBB	131	TRP	3.2
2	BBB	3	THR	3.1
2	BBB	160	MET	3.1
1	AAA	174	LEU	3.1
1	AAA	175	LEU	3.1
2	BBB	188	TRP	3.0
2	BBB	135	GLY	3.0
2	BBB	164	VAL	3.0
1	AAA	24	PHE	3.0
2	BBB	172	THR	3.0
1	AAA	26	PHE	3.0
2	BBB	148	ILE	3.0
2	BBB	146	GLY	2.9
1	AAA	91	VAL	2.9
2	BBB	108	PRO	2.9
4	DDD	43	LEU	2.9
2	BBB	129	VAL	2.9
2	BBB	145	THR	2.9
2	BBB	89	PHE	2.8
1	AAA	101	GLU	2.8
1	AAA	121	TRP	2.8
2	BBB	158	LEU	2.8
2	BBB	184	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
4	DDD	144	ASN	2.8
1	AAA	27	ASP	2.8
2	BBB	0	MET	2.8
2	BBB	104	SER	2.8
2	BBB	105	LYS	2.8
1	AAA	130	THR	2.8
1	AAA	102	PRO	2.8
1	AAA	160	VAL	2.8
2	BBB	50	VAL	2.8
1	AAA	51	PHE	2.7
1	AAA	30	GLU	2.7
2	BBB	111	HIS	2.7
1	AAA	8	ILE	2.7
4	DDD	59	ILE	2.7
4	DDD	157	ASP	2.7
3	CCC	13	THR	2.7
2	BBB	147	LEU	2.7
2	BBB	140	ALA	2.7
2	BBB	13	PHE	2.7
2	BBB	100	THR	2.7
2	BBB	189	ARG	2.7
2	BBB	99	VAL	2.7
1	AAA	23	MET	2.6
2	BBB	157	THR	2.6
2	BBB	114	LEU	2.6
2	BBB	137	GLU	2.6
1	AAA	48	PHE	2.6
5	EEE	221	ASP	2.6
1	AAA	46	GLU	2.6
2	BBB	134	ASN	2.6
4	DDD	60	ASN	2.6
2	BBB	183	PRO	2.5
2	BBB	122	PHE	2.5
2	BBB	136	GLN	2.5
1	AAA	92	LEU	2.5
1	AAA	117	VAL	2.5
2	BBB	180	VAL	2.5
2	BBB	103	PRO	2.5
2	BBB	66	ASP	2.5
2	BBB	102	TYR	2.5
1	AAA	148	PHE	2.5
1	AAA	153	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
5	EEE	38	GLY	2.5
2	BBB	75	VAL	2.5
2	BBB	53	LEU	2.5
1	AAA	85	VAL	2.5
1	AAA	158	GLU	2.4
1	AAA	168	TRP	2.4
2	BBB	119	VAL	2.4
1	AAA	65	VAL	2.4
4	DDD	149	LYS	2.4
1	AAA	171	ASP	2.4
2	BBB	175	VAL	2.4
2	BBB	153	TRP	2.4
4	DDD	201	SER	2.4
4	DDD	131	LYS	2.4
1	AAA	163	CYS	2.4
2	BBB	92	GLN	2.3
1	AAA	36	MET	2.3
1	AAA	60	LEU	2.3
1	AAA	31	ILE	2.3
1	AAA	132	VAL	2.3
2	BBB	44	VAL	2.3
2	BBB	98	LYS	2.3
1	AAA	145	PHE	2.2
2	BBB	106	THR	2.2
2	BBB	167	SER	2.2
5	EEE	36	ASP	2.2
5	EEE	68	ALA	2.2
1	AAA	42	VAL	2.2
1	AAA	157	THR	2.2
3	CCC	8	THR	2.2
2	BBB	165	PRO	2.2
1	AAA	61	ALA	2.2
2	BBB	127	ILE	2.2
1	AAA	173	PRO	2.2
1	AAA	59	ALA	2.2
1	AAA	161	TYR	2.1
5	EEE	10	ILE	2.1
1	AAA	129	THR	2.1
2	BBB	163	THR	2.1
4	DDD	6	LEU	2.1
5	EEE	176	PRO	2.1
4	DDD	178	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	AAA	79	TYR	2.1
5	EEE	17	ILE	2.1
4	DDD	148	SER	2.1
4	DDD	166	MET	2.1
1	AAA	94	ASN	2.1
4	DDD	134	CYS	2.1
1	AAA	32	PHE	2.0
1	AAA	54	PHE	2.0
2	BBB	91	VAL	2.0
2	BBB	109	LEU	2.0
1	AAA	7	ILE	2.0
1	AAA	104	VAL	2.0

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

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
7	SO4	DDD	304	5/5	0.65	0.26	38,47,59,62	5
8	PEG	DDD	305	7/7	0.78	0.28	62,67,73,75	0
8	PEG	EEE	301	7/7	0.78	0.26	48,64,74,76	0
6	EDO	EEE	302	4/4	0.83	0.18	54,63,67,75	0
6	EDO	DDD	303	4/4	0.86	0.19	63,65,65,68	0
6	EDO	BBB	201	4/4	0.87	0.17	56,60,62,65	0
6	EDO	DDD	302	4/4	0.88	0.17	50,55,55,61	0
6	EDO	BBB	202	4/4	0.89	0.11	52,55,60,60	0
6	EDO	DDD	301	4/4	0.92	0.14	48,54,60,66	0

6.5 Other polymers [i](#)

There are no such residues in this entry.