



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 9, 2025 – 02:08 PM EST

PDB ID : 9NXF / pdb_00009nxf
Title : Crystal structure of CN:Tak1 complex
Authors : Shirakawa, K.T.; Parikh, T.; Page, R.; Peti, W.
Deposited on : 2025-03-25
Resolution : 3.13 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 : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.47

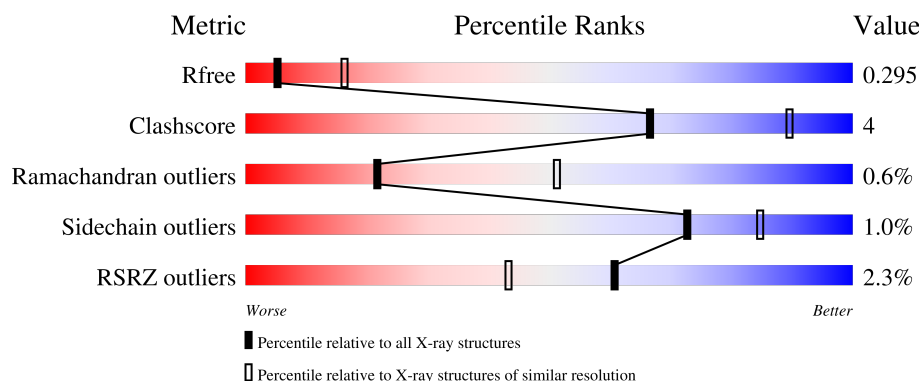
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.13 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}	164625	2149 (3.18-3.10)
Clashscore	180529	2290 (3.18-3.10)
Ramachandran outliers	177936	2178 (3.18-3.10)
Sidechain outliers	177891	2178 (3.18-3.10)
RSRZ outliers	164620	2149 (3.18-3.10)

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	370	<div> <div>88%</div> <div>8%</div> <div>.</div> </div>
1	D	370	<div> <div>86%</div> <div>10%</div> <div>.</div> </div>
2	B	156	<div> <div>4%</div> <div>79%</div> <div>13%</div> <div>7%</div> </div>
2	E	156	<div> <div>4%</div> <div>81%</div> <div>12%</div> <div>6%</div> </div>
3	C	53	<div> <div>11%</div> <div>68%</div> <div>6%</div> <div>25%</div> </div>

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Mol	Chain	Length	Quality of chain
3	F	53	<div><div></div><div>6%</div><div>53%</div><div>15%</div><div>28%</div></div>

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 8795 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 Protein phosphatase 3 catalytic subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	357	Total	C	N	O	S	0	0	0
			2889	1863	482	524	20			
1	D	356	Total	C	N	O	S	0	0	0
			2886	1861	483	522	20			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	90	ALA	ASP	engineered mutation	UNP Q08209
D	90	ALA	ASP	engineered mutation	UNP Q08209

- Molecule 2 is a protein called Calcineurin subunit B type 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	145	Total	C	N	O	S	0	0	0
			1154	727	192	230	5			
2	E	146	Total	C	N	O	S	0	0	0
			1162	731	193	233	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	14	MET	-	expression tag	UNP P63098
E	14	MET	-	expression tag	UNP P63098

- Molecule 3 is a protein called IkB-like protein,Mitogen-activated protein kinase kinase kinase 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	40	Total	C	N	O	P S	0	1	0
			338	211	61	63	1 2			

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	F	38	Total	C	N	O	P	S	0	0	0
			308	192	55	58	1	2			

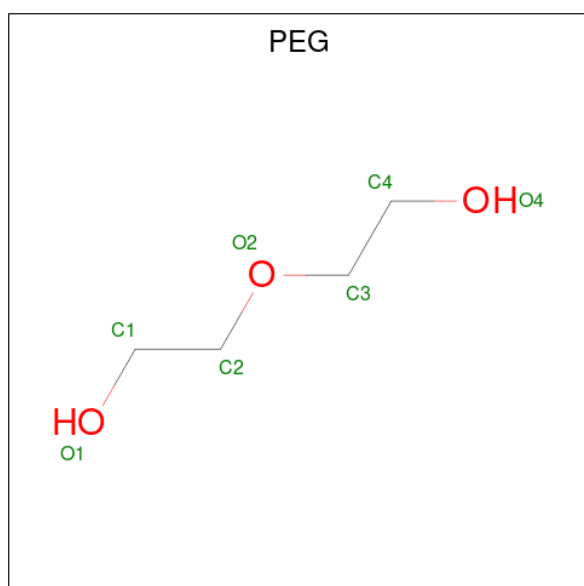
There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	390	GLY	-	expression tag	UNP O36972
C	391	HIS	-	expression tag	UNP O36972
C	392	MET	-	expression tag	UNP O36972
C	441	ARG	GLN	engineered mutation	UNP O43318
C	442	PRO	ASP	engineered mutation	UNP O43318
F	390	GLY	-	expression tag	UNP O36972
F	391	HIS	-	expression tag	UNP O36972
F	392	MET	-	expression tag	UNP O36972
F	441	ARG	GLN	engineered mutation	UNP O43318
F	442	PRO	ASP	engineered mutation	UNP O43318

- Molecule 4 is FE (III) ION (CCD ID: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Fe	0	0
			1	1		
4	D	1	Total	Fe	0	0
			1	1		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).

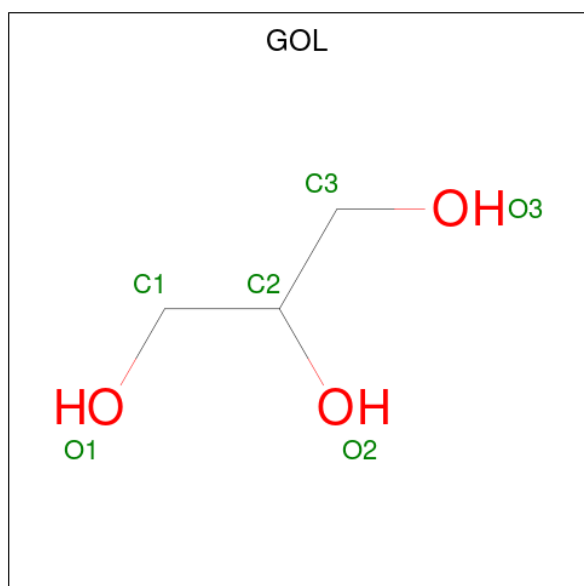


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 7 4 3	0	0
5	B	1	Total C O 7 4 3	0	0
5	D	1	Total C O 7 4 3	0	0

- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	4	Total Ca 4 4	0	0
6	E	4	Total Ca 4 4	0	0

- Molecule 7 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	D	1	Total C O 6 3 3	0	0

- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	11	Total O 11 11	0	0

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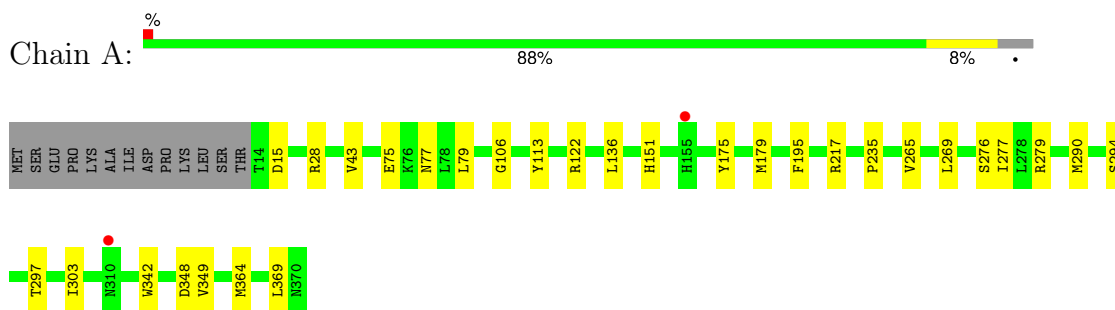
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	1	Total 1	O 1	0	0
8	D	3	Total 3	O 3	0	0
8	E	2	Total 2	O 2	0	0
8	F	4	Total 4	O 4	0	0

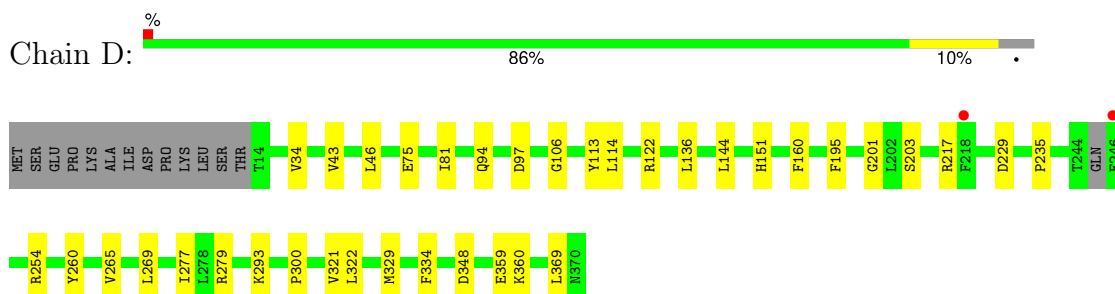
3 Residue-property plots [i](#)

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.

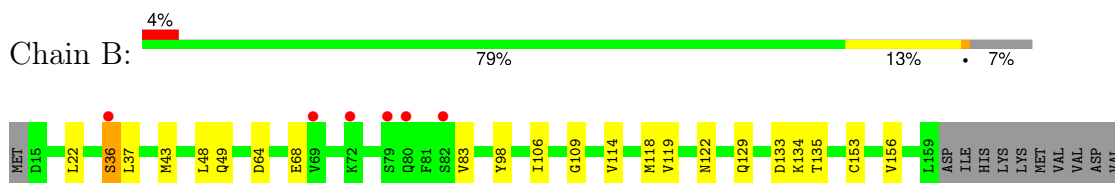
- Molecule 1: Protein phosphatase 3 catalytic subunit alpha



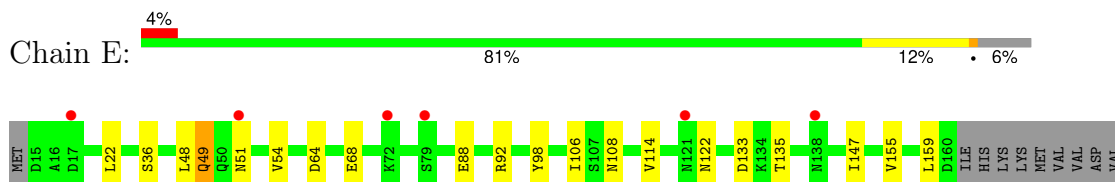
- Molecule 1: Protein phosphatase 3 catalytic subunit alpha



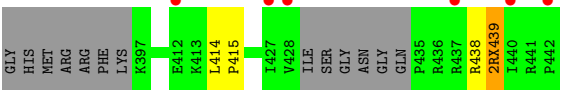
- Molecule 2: Calcineurin subunit B type 1



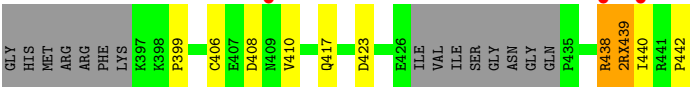
- Molecule 2: Calcineurin subunit B type 1



- Molecule 3: IkB-like protein, Mitogen-activated protein kinase kinase kinase 7



● Molecule 3: IκB-like protein,Mitogen-activated protein kinase kinase kinase 7



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	224.08Å 49.59Å 158.90Å 90.00° 128.72° 90.00°	Depositor
Resolution (Å)	34.94 – 3.13 34.94 – 3.13	Depositor EDS
% Data completeness (in resolution range)	95.8 (34.94-3.13) 95.7 (34.94-3.13)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.60 (at 3.12Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.248 , 0.295 0.248 , 0.295	Depositor DCC
R_{free} test set	1179 reflections (4.78%)	wwPDB-VP
Wilson B-factor (Å ²)	52.3	Xtriage
Anisotropy	0.208	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 60.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	8795	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.44% 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: 2RX, GOL, CA, PEG, FE

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.07	0/2968	0.23	0/4030
1	D	0.07	0/2964	0.23	0/4022
2	B	0.07	0/1168	0.19	0/1562
2	E	0.06	0/1176	0.18	0/1573
3	C	0.06	0/332	0.20	0/444
3	F	0.11	0/302	0.27	0/404
All	All	0.07	0/8910	0.22	0/12035

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	A	2889	0	2817	19	0
1	D	2886	0	2819	23	0
2	B	1154	0	1137	15	0
2	E	1162	0	1141	12	0
3	C	338	0	343	3	0
3	F	308	0	308	8	0
4	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	1	0	0	0	0
5	A	7	0	10	0	0
5	B	7	0	10	0	0
5	D	7	0	10	0	0
6	B	4	0	0	0	0
6	E	4	0	0	0	0
7	D	6	0	8	0	0
8	A	11	0	0	0	0
8	B	1	0	0	0	0
8	D	3	0	0	0	0
8	E	2	0	0	0	0
8	F	4	0	0	0	0
All	All	8795	0	8603	63	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 4.

All (63) 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)
2:B:43:MET:O	2:B:49:GLN:NE2	2.24	0.70
2:E:108:ASN:ND2	2:E:133:ASP:OD1	2.32	0.61
2:B:129:GLN:NE2	2:B:133:ASP:OD1	2.35	0.60
1:D:359:GLU:OE2	1:D:360:LYS:NZ	2.37	0.57
2:B:36:SER:HB3	2:B:68:GLU:HB3	1.87	0.56
1:A:364:MET:HG3	2:B:48:LEU:HD21	1.89	0.55
1:A:151:HIS:NE2	3:C:439:2RX:S41	2.74	0.52
1:D:265:VAL:HG13	1:D:277:ILE:HD12	1.93	0.50
2:E:106:ILE:HB	2:E:147:ILE:HB	1.92	0.50
1:A:235:PRO:O	3:C:438:ARG:NH2	2.45	0.49
1:D:106:GLY:O	1:D:113:TYR:OH	2.24	0.49
2:E:36:SER:HB3	2:E:68:GLU:HB3	1.95	0.49
2:E:51:ASN:HB3	2:E:54:VAL:HG23	1.94	0.48
1:A:15:ASP:O	2:B:109:GLY:N	2.47	0.48
1:D:254:ARG:O	3:F:442:PRO:HD2	2.13	0.48
1:A:348:ASP:HB2	2:B:135:THR:HG23	1.97	0.47
1:A:106:GLY:O	1:A:113:TYR:OH	2.28	0.46
1:D:122:ARG:HH12	3:F:439:2RX:H7	1.80	0.46
1:D:293:LYS:HA	1:D:300:PRO:HA	1.97	0.46
1:A:349:VAL:HG22	2:B:135:THR:HG21	1.97	0.46
1:D:269:LEU:HD21	1:D:277:ILE:HG13	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:43:VAL:HG11	1:A:136:LEU:HD23	1.98	0.46
2:E:122:ASN:O	3:F:417:GLN:NE2	2.48	0.46
1:A:269:LEU:HD21	1:A:277:ILE:HG13	1.97	0.46
1:D:235:PRO:O	3:F:438:ARG:NH2	2.43	0.45
1:A:75:GLU:HB3	1:A:79:LEU:HD21	1.97	0.45
1:A:265:VAL:HG13	1:A:277:ILE:HD12	1.97	0.45
1:A:195:PHE:HD1	1:A:276:SER:HB3	1.82	0.45
2:B:98:TYR:HB2	2:B:106:ILE:HD13	1.98	0.45
2:B:114:VAL:HG12	2:B:118:MET:HE2	1.98	0.45
1:D:43:VAL:HG11	1:D:136:LEU:HD23	1.99	0.45
1:A:369:LEU:HD22	2:B:22:LEU:HD22	1.98	0.45
1:D:322:LEU:HD21	1:D:329:MET:HE3	1.99	0.45
1:D:81:ILE:HD12	1:D:114:LEU:HD22	1.99	0.45
1:A:290:MET:HG2	1:A:303:ILE:HG12	1.99	0.44
2:B:153:CYS:HA	2:B:156:VAL:HG22	1.99	0.44
1:D:34:VAL:HG13	1:D:46:LEU:HD11	1.98	0.44
2:B:98:TYR:HA	2:B:114:VAL:HG21	1.99	0.44
2:E:98:TYR:HA	2:E:114:VAL:HG21	2.00	0.43
3:F:423:ASP:OD1	3:F:423:ASP:N	2.44	0.43
1:D:321:VAL:HG13	1:D:334:PHE:HE1	1.84	0.43
1:D:348:ASP:HB2	2:E:135:THR:HG23	1.99	0.43
2:E:64:ASP:OD1	2:E:64:ASP:N	2.50	0.43
1:A:294:SER:HB3	1:A:297:THR:OG1	2.18	0.43
3:C:414:LEU:HD12	3:C:415:PRO:HD2	1.99	0.43
1:D:136:LEU:HB3	1:D:144:LEU:HD13	2.00	0.43
2:E:88:GLU:O	2:E:92:ARG:N	2.52	0.43
1:D:195:PHE:HZ	3:F:399:PRO:HG2	1.84	0.42
1:D:369:LEU:HD22	2:E:22:LEU:HD22	2.01	0.42
2:E:48:LEU:HB3	2:E:49:GLN:H	1.61	0.42
2:E:122:ASN:HD22	3:F:423:ASP:HA	1.85	0.42
1:D:203:SER:HB2	1:D:229:ASP:HB2	2.02	0.42
1:A:342:TRP:CZ2	2:B:134:LYS:HD2	2.55	0.42
2:B:119:VAL:HG22	2:B:122:ASN:HB2	2.02	0.42
1:D:94:GLN:NE2	1:D:97:ASP:OD2	2.53	0.42
1:A:175:TYR:O	1:A:179:MET:HG2	2.20	0.41
1:D:322:LEU:HD11	1:D:329:MET:HB3	2.02	0.41
1:A:195:PHE:CD1	1:A:276:SER:HB3	2.56	0.41
1:D:201:GLY:HA3	1:D:260:TYR:CE2	2.55	0.41
1:D:75:GLU:O	1:D:217:ARG:NH2	2.45	0.41
1:A:77:ASN:OD1	1:A:217:ARG:NH1	2.51	0.40
1:D:151:HIS:NE2	3:F:439:2RX:O43	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:37:LEU:HD23	2:B:37:LEU:HA	1.94	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	355/370 (96%)	332 (94%)	22 (6%)	1 (0%)	37	65
1	D	352/370 (95%)	326 (93%)	25 (7%)	1 (0%)	37	65
2	B	143/156 (92%)	135 (94%)	8 (6%)	0	100	100
2	E	144/156 (92%)	139 (96%)	4 (3%)	1 (1%)	19	48
3	C	36/53 (68%)	35 (97%)	1 (3%)	0	100	100
3	F	33/53 (62%)	28 (85%)	2 (6%)	3 (9%)	0	3
All	All	1063/1158 (92%)	995 (94%)	62 (6%)	6 (1%)	22	51

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	F	440	ILE
1	A	122	ARG
2	E	49	GLN
3	F	406	CYS
3	F	438	ARG
1	D	160	PHE

5.3.2 Protein sidechains [i](#)

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	316/330 (96%)	314 (99%)	2 (1%)	84	91
1	D	316/330 (96%)	315 (100%)	1 (0%)	91	95
2	B	128/139 (92%)	125 (98%)	3 (2%)	45	67
2	E	129/139 (93%)	127 (98%)	2 (2%)	58	77
3	C	38/48 (79%)	38 (100%)	0	100	100
3	F	34/48 (71%)	32 (94%)	2 (6%)	16	41
All	All	961/1034 (93%)	951 (99%)	10 (1%)	73	85

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	ARG
1	A	279	ARG
2	B	36	SER
2	B	64	ASP
2	B	83	VAL
1	D	279	ARG
2	E	155	VAL
2	E	159	LEU
3	F	408	ASP
3	F	410	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	49	HIS
1	A	110	ASN
1	A	245	GLN
1	A	270	GLN
1	A	284	GLN
2	B	127	GLN
1	D	270	GLN
1	D	284	GLN
1	D	330	ASN
1	D	339	HIS
2	E	80	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	2RX	F	439	4,3	6,9,10	1.72	1 (16%)	3,12,14	4.43	1 (33%)
3	2RX	C	439	4,3	6,9,10	1.76	1 (16%)	3,12,14	4.46	1 (33%)

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	2RX	F	439	4,3	-	2/5/8/10	-
3	2RX	C	439	4,3	-	2/5/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	439	2RX	P40-O42	-3.57	1.47	1.56
3	F	439	2RX	P40-O42	-3.46	1.48	1.56

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	439	2RX	O42-P40-O43	7.52	126.25	109.86
3	F	439	2RX	O42-P40-O43	7.41	126.03	109.86

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	439	2RX	N-CA-CB-OG
3	C	439	2RX	CB-OG-P40-O42
3	F	439	2RX	N-CA-CB-OG
3	F	439	2RX	C-CA-CB-OG

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	439	2RX	2	0
3	C	439	2RX	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 10 are monoatomic - leaving 4 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	$\# Z > 2$
7	GOL	D	402	-	5,5,5	0.93	0	5,5,5	1.07	0
5	PEG	A	402	-	6,6,6	0.12	0	5,5,5	0.08	0
5	PEG	B	205	-	6,6,6	0.11	0	5,5,5	0.09	0
5	PEG	D	403	-	6,6,6	0.11	0	5,5,5	0.10	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
7	GOL	D	402	-	-	2/4/4/4	-
5	PEG	A	402	-	-	0/4/4/4	-
5	PEG	B	205	-	-	0/4/4/4	-
5	PEG	D	403	-	-	1/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	D	402	GOL	O1-C1-C2-C3
7	D	402	GOL	O1-C1-C2-O2
5	D	403	PEG	C4-C3-O2-C2

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.

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	357/370 (96%)	0.22	2 (0%) 85 73	21, 39, 55, 70	0
1	D	356/370 (96%)	0.23	2 (0%) 85 73	23, 38, 55, 79	0
2	B	145/156 (92%)	0.56	6 (4%) 42 25	32, 54, 75, 88	0
2	E	146/156 (93%)	0.65	6 (4%) 42 25	33, 53, 80, 95	0
3	C	39/53 (73%)	1.02	6 (15%) 6 3	28, 52, 80, 83	1 (2%)
3	F	37/53 (69%)	0.63	3 (8%) 19 11	42, 55, 72, 73	0
All	All	1080/1158 (93%)	0.37	25 (2%) 61 43	21, 42, 72, 95	1 (0%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	412	GLU	4.2
3	C	440	ILE	4.1
2	B	79	SER	3.9
3	C	437[A]	ARG	3.8
3	C	428	VAL	3.3
2	E	17	ASP	3.1
1	D	246	GLU	3.0
2	E	121	ASN	2.9
2	E	138	ASN	2.9
2	B	80	GLN	2.8
3	F	440	ILE	2.8
2	B	69	VAL	2.7
3	C	442	PRO	2.6
2	B	36	SER	2.6
2	B	72	LYS	2.3
1	D	218	PHE	2.2
2	E	72	LYS	2.2
3	F	438	ARG	2.2
1	A	155	HIS	2.1

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Mol	Chain	Res	Type	RSRZ
2	E	51	ASN	2.1
3	F	409	ASN	2.1
3	C	427	ILE	2.1
1	A	310	ASN	2.1
2	B	82	SER	2.0
2	E	79	SER	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
3	2RX	C	439	10/11	0.71	0.17	48,72,85,87	0
3	2RX	F	439	10/11	0.78	0.15	49,58,67,75	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	PEG	B	205	7/7	0.65	0.20	43,48,56,57	0
5	PEG	D	403	7/7	0.73	0.19	40,51,61,62	0
7	GOL	D	402	6/6	0.76	0.12	50,54,57,59	0
5	PEG	A	402	7/7	0.85	0.14	32,40,47,47	0
6	CA	E	201	1/1	0.90	0.17	73,73,73,73	0
6	CA	B	202	1/1	0.94	0.12	77,77,77,77	0
6	CA	E	202	1/1	0.95	0.12	71,71,71,71	0
6	CA	E	203	1/1	0.96	0.06	53,53,53,53	0
6	CA	B	204	1/1	0.97	0.05	47,47,47,47	0
6	CA	B	203	1/1	0.98	0.03	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	CA	B	201	1/1	0.98	0.10	60,60,60,60	0
6	CA	E	204	1/1	0.98	0.04	38,38,38,38	0
4	FE	D	401	1/1	0.98	0.05	57,57,57,57	0
4	FE	A	401	1/1	0.99	0.08	39,39,39,39	0

6.5 Other polymers [i](#)

There are no such residues in this entry.