



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 06:36 PM UTC

PDB ID : 1NEX / pdb_00001nex
Title : Crystal Structure of ScSkp1-ScCdc4-CPD peptide complex
Authors : Orlicky, S.; Tang, X.; Willems, A.; Tyers, M.; Sicheri, F.
Deposited on : 2002-12-12
Resolution : 2.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

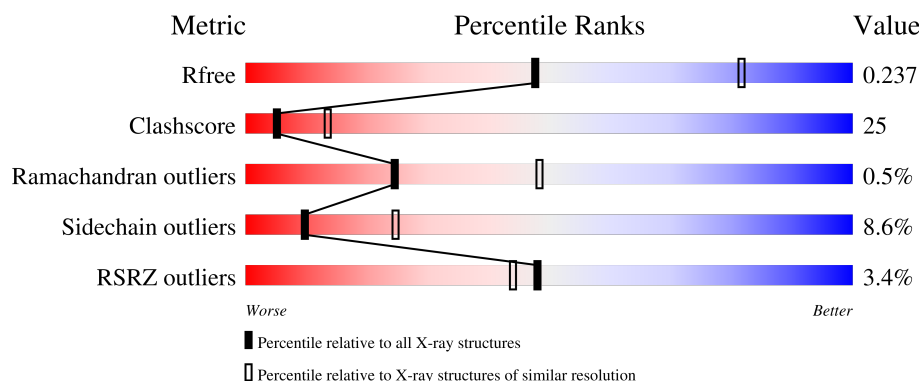
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	169	5% 42% 29% 5% 24%
1	C	169	6% 41% 29% 7% 23%
2	B	464	2% 51% 39% 6%
2	D	464	2% 54% 36% 5%
3	E	9	11% 22% 11% 56%

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Mol	Chain	Length	Quality of chain
3	F	9	56% 33% 44% 11% 11%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9435 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 Centromere DNA-binding protein complex CBF3 subunit D.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	129	Total	C	N	O	S	Se	0	0	0
			1047	666	182	195	1	3			
1	C	130	Total	C	N	O	S	Se	0	0	0
			1058	672	186	196	1	3			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	cloning artifact	UNP P52286
A	-1	ALA	-	cloning artifact	UNP P52286
A	0	HIS	-	cloning artifact	UNP P52286
A	1	MSE	MET	modified residue	UNP P52286
A	36	MSE	MET	modified residue	UNP P52286
A	?	-	HIS	deletion	UNP P52286
A	?	-	ASP	deletion	UNP P52286
A	?	-	SER	deletion	UNP P52286
A	?	-	ASN	deletion	UNP P52286
A	?	-	LEU	deletion	UNP P52286
A	?	-	GLN	deletion	UNP P52286
A	?	-	ASN	deletion	UNP P52286
A	?	-	ASN	deletion	UNP P52286
A	?	-	SER	deletion	UNP P52286
A	?	-	ASP	deletion	UNP P52286
A	?	-	SER	deletion	UNP P52286
A	?	-	GLU	deletion	UNP P52286
A	?	-	SER	deletion	UNP P52286
A	?	-	ASP	deletion	UNP P52286
A	?	-	SER	deletion	UNP P52286
A	?	-	ASP	deletion	UNP P52286
A	?	-	SER	deletion	UNP P52286
A	?	-	GLU	deletion	UNP P52286
A	?	-	THR	deletion	UNP P52286
A	?	-	ASN	deletion	UNP P52286

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	HIS	deletion	UNP P52286
A	?	-	LYS	deletion	UNP P52286
A	?	-	SER	deletion	UNP P52286
A	?	-	LYS	deletion	UNP P52286
A	?	-	ASP	deletion	UNP P52286
A	?	-	ASN	deletion	UNP P52286
A	?	-	ASN	deletion	UNP P52286
A	?	-	ASN	deletion	UNP P52286
A	77	MSE	MET	modified residue	UNP P52286
A	130	MSE	MET	modified residue	UNP P52286
A	157	MSE	MET	modified residue	UNP P52286
C	-2	GLY	-	cloning artifact	UNP P52286
C	-1	ALA	-	cloning artifact	UNP P52286
C	0	HIS	-	cloning artifact	UNP P52286
C	1	MSE	MET	modified residue	UNP P52286
C	36	MSE	MET	modified residue	UNP P52286
C	?	-	HIS	deletion	UNP P52286
C	?	-	ASP	deletion	UNP P52286
C	?	-	SER	deletion	UNP P52286
C	?	-	ASN	deletion	UNP P52286
C	?	-	LEU	deletion	UNP P52286
C	?	-	GLN	deletion	UNP P52286
C	?	-	ASN	deletion	UNP P52286
C	?	-	ASN	deletion	UNP P52286
C	?	-	SER	deletion	UNP P52286
C	?	-	ASP	deletion	UNP P52286
C	?	-	SER	deletion	UNP P52286
C	?	-	GLU	deletion	UNP P52286
C	?	-	SER	deletion	UNP P52286
C	?	-	ASP	deletion	UNP P52286
C	?	-	SER	deletion	UNP P52286
C	?	-	ASP	deletion	UNP P52286
C	?	-	SER	deletion	UNP P52286
C	?	-	GLU	deletion	UNP P52286
C	?	-	THR	deletion	UNP P52286
C	?	-	ASN	deletion	UNP P52286
C	?	-	HIS	deletion	UNP P52286
C	?	-	LYS	deletion	UNP P52286
C	?	-	SER	deletion	UNP P52286
C	?	-	LYS	deletion	UNP P52286
C	?	-	ASP	deletion	UNP P52286
C	?	-	ASN	deletion	UNP P52286

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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	ASN	deletion	UNP P52286
C	?	-	ASN	deletion	UNP P52286
C	77	MSE	MET	modified residue	UNP P52286
C	130	MSE	MET	modified residue	UNP P52286
C	157	MSE	MET	modified residue	UNP P52286

- Molecule 2 is a protein called CDC4 protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	444	Total	C	N	O	S	Se	0	0	0
			3582	2296	618	656	6	6			
2	D	444	Total	C	N	O	S	Se	0	0	0
			3582	2296	618	656	6	6			

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	261	GLY	-	cloning artifact	UNP P07834
B	262	ALA	-	cloning artifact	UNP P07834
B	381	MSE	MET	modified residue	UNP P07834
B	403	MSE	MET	modified residue	UNP P07834
B	530	MSE	MET	modified residue	UNP P07834
B	560	MSE	MET	modified residue	UNP P07834
B	590	MSE	MET	modified residue	UNP P07834
B	?	-	ASN	deletion	UNP P07834
B	?	-	ILE	deletion	UNP P07834
B	?	-	TRP	deletion	UNP P07834
B	?	-	ASN	deletion	UNP P07834
B	608	LEU	CYS	engineered mutation	UNP P07834
B	?	-	SER	deletion	UNP P07834
B	?	-	TYR	deletion	UNP P07834
B	?	-	ALA	deletion	UNP P07834
B	?	-	THR	deletion	UNP P07834
B	?	-	ASN	deletion	UNP P07834
B	?	-	SER	deletion	UNP P07834
B	?	-	ALA	deletion	UNP P07834
B	?	-	SER	deletion	UNP P07834
B	?	-	PRO	deletion	UNP P07834
B	?	-	CYS	deletion	UNP P07834
B	?	-	ALA	deletion	UNP P07834
B	?	-	LYS	deletion	UNP P07834
B	?	-	ILE	deletion	UNP P07834

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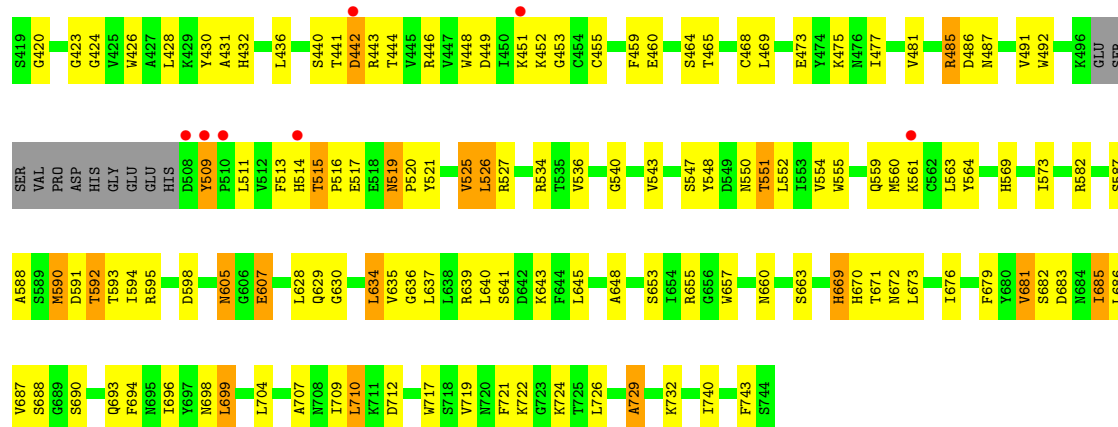
Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	GLY	deletion	UNP P07834
B	?	-	ALA	deletion	UNP P07834
B	625	MSE	MET	modified residue	UNP P07834
D	261	GLY	-	cloning artifact	UNP P07834
D	262	ALA	-	cloning artifact	UNP P07834
D	381	MSE	MET	modified residue	UNP P07834
D	403	MSE	MET	modified residue	UNP P07834
D	530	MSE	MET	modified residue	UNP P07834
D	560	MSE	MET	modified residue	UNP P07834
D	590	MSE	MET	modified residue	UNP P07834
D	?	-	ASN	deletion	UNP P07834
D	?	-	ILE	deletion	UNP P07834
D	?	-	TRP	deletion	UNP P07834
D	?	-	ASN	deletion	UNP P07834
D	608	LEU	CYS	engineered mutation	UNP P07834
D	?	-	SER	deletion	UNP P07834
D	?	-	TYR	deletion	UNP P07834
D	?	-	ALA	deletion	UNP P07834
D	?	-	THR	deletion	UNP P07834
D	?	-	ASN	deletion	UNP P07834
D	?	-	SER	deletion	UNP P07834
D	?	-	ALA	deletion	UNP P07834
D	?	-	SER	deletion	UNP P07834
D	?	-	PRO	deletion	UNP P07834
D	?	-	CYS	deletion	UNP P07834
D	?	-	ALA	deletion	UNP P07834
D	?	-	LYS	deletion	UNP P07834
D	?	-	ILE	deletion	UNP P07834
D	?	-	GLY	deletion	UNP P07834
D	?	-	ALA	deletion	UNP P07834
D	625	MSE	MET	modified residue	UNP P07834

- Molecule 3 is a protein called GLL(TPO)PPQSG.

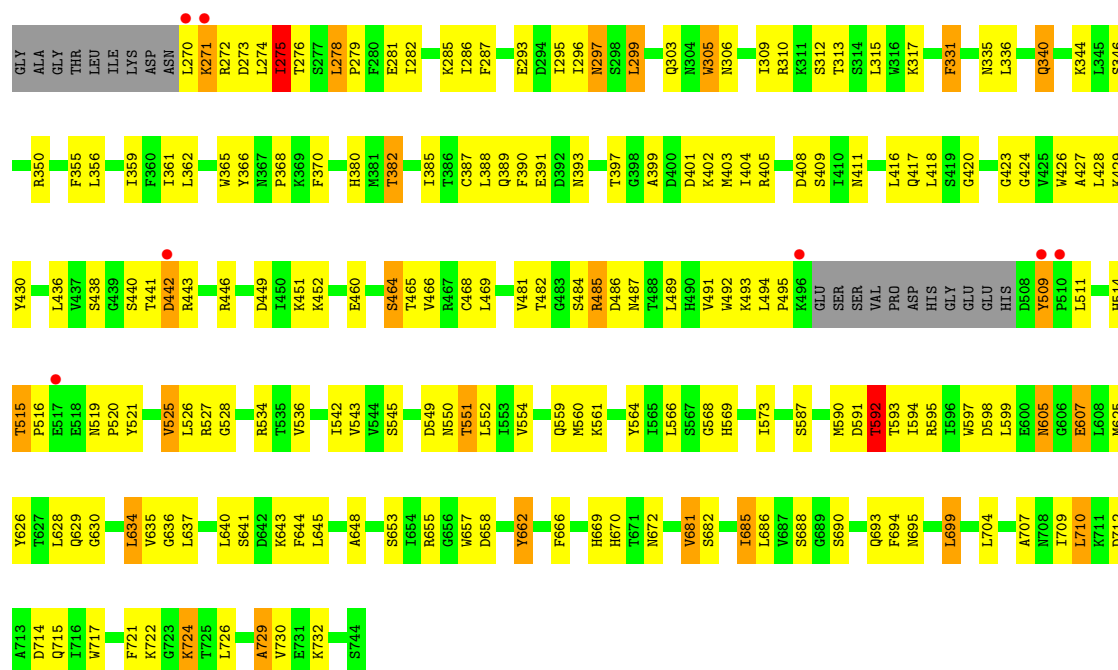
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	4	Total	C	N	O	P	0	0	0
			33	20	4	8	1			
3	F	8	Total	C	N	O	P	0	0	0
			61	36	9	15	1			

- Molecule 4 is water.

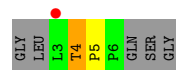
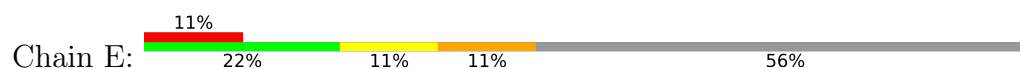
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	9	Total 9	O 9	0	0
4	B	25	Total 25	O 25	0	0
4	C	9	Total 9	O 9	0	0
4	D	27	Total 27	O 27	0	0
4	E	2	Total 2	O 2	0	0



• Molecule 2: CDC4 protein

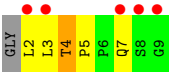


• Molecule 3: GLL(TPO)PPQSG



• Molecule 3: GLL(TPO)PPQSG





4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	107.67Å 107.67Å 168.30Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.99 – 2.70 19.99 – 2.70	Depositor EDS
% Data completeness (in resolution range)	95.7 (19.99-2.70) 96.7 (19.99-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.33 (at 2.71Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.239 , 0.273 0.240 , 0.237	Depositor DCC
R_{free} test set	9884 reflections (8.51%)	wwPDB-VP
Wilson B-factor (Å ²)	41.6	Xtriage
Anisotropy	0.034	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 47.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	0.244 for -h,-k,l 0.085 for h,-h-k,-l 0.078 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	9435	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.70% 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: TPO

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	0.55	0/1061	0.96	2/1428 (0.1%)
1	C	0.56	0/1072	0.96	2/1442 (0.1%)
2	B	0.52	0/3657	0.98	13/4939 (0.3%)
2	D	0.53	1/3657 (0.0%)	1.02	19/4939 (0.4%)
3	E	0.46	0/22	0.74	0/28
3	F	0.46	0/50	0.78	0/64
All	All	0.53	1/9519 (0.0%)	0.99	36/12840 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	275	ILE	CA-CB	-5.79	1.47	1.54

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	681	VAL	N-CA-C	7.96	120.42	108.80
2	B	645	LEU	N-CA-C	-7.35	96.53	108.52
2	B	685	ILE	N-CA-C	6.56	119.44	108.81
2	D	275	ILE	N-CA-C	6.32	117.06	110.62
2	B	401	ASP	N-CA-C	-6.22	105.63	112.72

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	1047	0	1055	64	0
1	C	1058	0	1068	67	0
2	B	3582	0	3581	185	0
2	D	3582	0	3581	165	0
3	E	33	0	30	5	0
3	F	61	0	56	7	0
4	A	9	0	0	3	0
4	B	25	0	0	5	0
4	C	9	0	0	1	0
4	D	27	0	0	1	0
4	E	2	0	0	0	0
All	All	9435	0	9371	461	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 25.

The worst 5 of 461 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:167:ARG:HG2	1:A:172:ILE:HG22	1.30	1.12
2:D:491:VAL:HB	2:D:560:MSE:HE1	1.34	1.07
2:D:275:ILE:HG21	2:D:305:TRP:NE1	1.72	1.04
2:D:270:LEU:HD23	2:D:271:LYS:H	1.24	1.03
1:C:171:ASN:HD22	2:D:271:LYS:HD2	1.19	1.02

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	123/169 (73%)	114 (93%)	9 (7%)	0	100	100
1	C	124/169 (73%)	115 (93%)	8 (6%)	1 (1%)	16	37
2	B	440/464 (95%)	406 (92%)	31 (7%)	3 (1%)	18	41
2	D	440/464 (95%)	423 (96%)	15 (3%)	2 (0%)	24	48
3	E	1/9 (11%)	1 (100%)	0	0	100	100
3	F	5/9 (56%)	3 (60%)	2 (40%)	0	100	100
All	All	1133/1284 (88%)	1062 (94%)	65 (6%)	6 (0%)	24	48

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	605	ASN
2	D	605	ASN
2	B	673	LEU
2	B	331	PHE
1	C	24	GLU

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	117/147 (80%)	106 (91%)	11 (9%)	8	21
1	C	118/147 (80%)	105 (89%)	13 (11%)	6	15
2	B	400/410 (98%)	368 (92%)	32 (8%)	11	28
2	D	400/410 (98%)	366 (92%)	34 (8%)	10	25
3	E	3/6 (50%)	3 (100%)	0	100	100
3	F	6/6 (100%)	6 (100%)	0	100	100
All	All	1044/1126 (93%)	954 (91%)	90 (9%)	10	25

5 of 90 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	272	ARG

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Mol	Chain	Res	Type
2	D	464	SER
2	D	278	LEU
2	D	313	THR
2	D	525	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	340	GLN
2	D	457	HIS
2	D	358	ASN
2	D	389	GLN
2	D	487	ASN

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	TPO	F	4	3	8,10,11	2.02	2 (25%)	10,14,16	0.87	0
3	TPO	E	4	3	8,10,11	2.31	3 (37%)	10,14,16	0.80	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	TPO	F	4	3	-	2/9/11/13	-
3	TPO	E	4	3	-	2/9/11/13	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	4	TPO	P-OG1	4.17	1.66	1.59
3	E	4	TPO	O-C	3.65	1.33	1.20
3	F	4	TPO	O-C	3.54	1.33	1.20
3	F	4	TPO	P-OG1	3.39	1.65	1.59
3	E	4	TPO	P-O1P	2.36	1.57	1.50

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	4	TPO	O-C-CA-CB
3	F	4	TPO	O-C-CA-CB
3	E	4	TPO	CG2-CB-OG1-P
3	F	4	TPO	CG2-CB-OG1-P

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	4	TPO	1	0
3	E	4	TPO	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	126/169 (74%)	0.36	8 (6%) 26 23	24, 42, 71, 92	0
1	C	127/169 (75%)	0.30	10 (7%) 18 16	24, 41, 74, 90	0
2	B	438/464 (94%)	-0.02	8 (1%) 67 65	21, 38, 57, 87	0
2	D	438/464 (94%)	-0.09	7 (1%) 70 68	19, 35, 53, 85	0
3	E	3/9 (33%)	1.88	1 (33%) 1 1	78, 78, 82, 86	0
3	F	7/9 (77%)	2.96	5 (71%) 0 0	79, 85, 90, 92	0
All	All	1139/1284 (88%)	0.06	39 (3%) 48 44	19, 38, 64, 92	0

The worst 5 of 39 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	509	TYR	4.7
1	C	116	VAL	4.7
1	A	116	VAL	4.4
3	F	3	LEU	4.2
1	A	103	PRO	4.1

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	TPO	E	4	11/12	0.90	0.12	72,76,79,79	0
3	TPO	F	4	11/12	0.90	0.17	71,75,79,80	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.