



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 09:05 PM GMT

PDB ID : 1NEX
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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

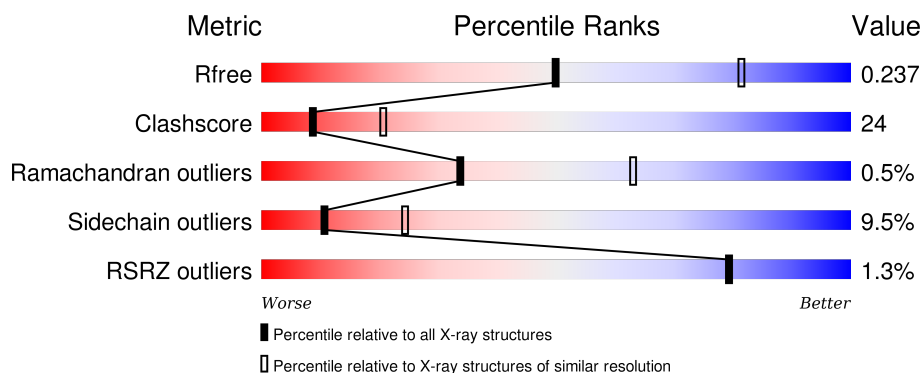
1 Overall quality at a glance

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}	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	<div> <div>2%</div> <div>42% 28% 6% 24%</div> </div>
1	C	169	<div> <div>2%</div> <div>41% 30% 7% 23%</div> </div>
2	B	464	<div> <div>53% 37% 6%</div> </div>
2	D	464	<div> <div>56% 34% 5%</div> </div>
3	E	9	<div> <div>11% 22% 22% 56%</div> </div>

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Mol	Chain	Length	Quality of chain
3	F	9	<div><div></div><div></div><div></div><div></div></div>

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	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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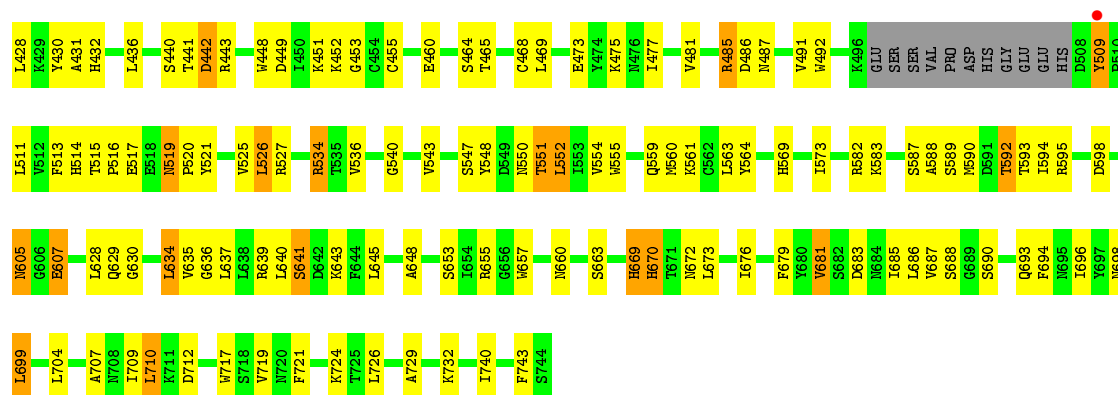
Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	GLY	DELETION	UNP P07834
B	?	-	ALA	DELETION	UNP P07834
B	625	MSE	MET	MODIFIED RESIDUE	UNP P07834
D	261	GLY	-	CLONING ARTIFACT	UNP P07834
D	262	ALA	-	CLONING ARTIFACT	UNP P07834
D	381	MSE	MET	MODIFIED RESIDUE	UNP P07834
D	403	MSE	MET	MODIFIED RESIDUE	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	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			

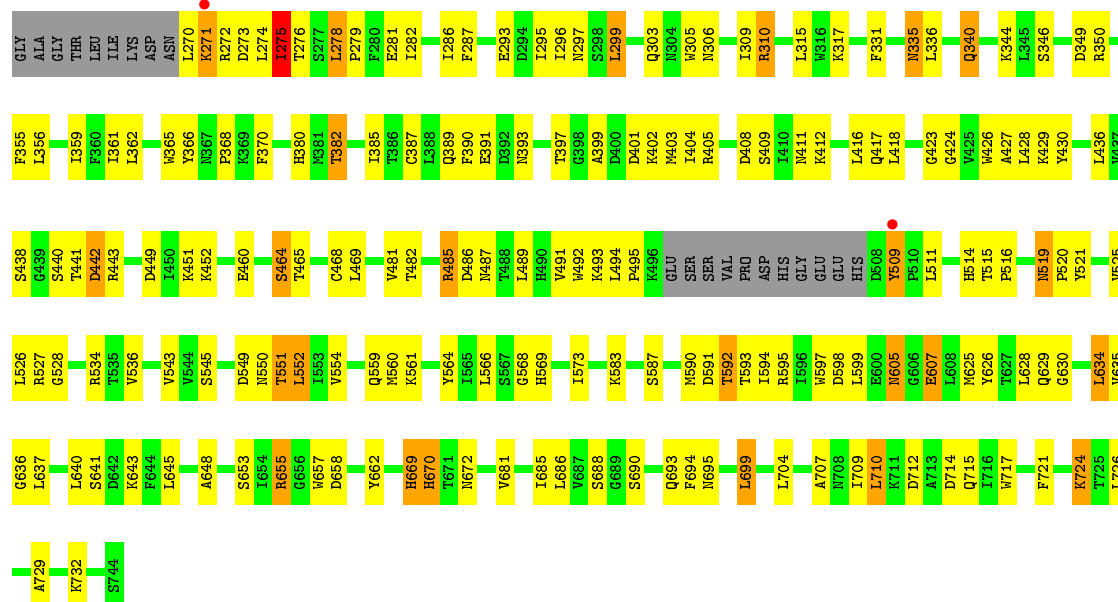
- Molecule 4 is water.

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

Chain D: 56% 34% 5%



• Molecule 3: GLL(TPO)PPQSG

Chain E: 11% 22% 22% 56%



• Molecule 3: GLL(TPO)PPQSG

Chain F: 33% 56% 33% 11%



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) 98.2 (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	5034 reflections (8.62%)	DCC
Wilson B-factor (Å ²)	41.6	Xtriage
Anisotropy	0.034	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 18.3	EDS
Estimated twinning fraction	0.244 for -h,-k,l 0.084 for h,-h-k,-l 0.078 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.24$	Xtriage
Outliers	0 of 116115 reflections	Xtriage
F_o, F_c correlation	0.93	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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.46	0/1061	0.65	0/1428
1	C	0.46	0/1072	0.63	0/1442
2	B	0.45	0/3657	0.69	3/4939 (0.1%)
2	D	0.45	0/3657	0.70	3/4939 (0.1%)
3	E	0.47	0/22	0.81	0/28
3	F	0.47	0/50	0.73	0/64
All	All	0.45	0/9519	0.68	6/12840 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	310	ARG	NE-CZ-NH1	7.12	123.86	120.30
2	B	310	ARG	NE-CZ-NH1	6.22	123.41	120.30
2	D	275	ILE	CG1-CB-CG2	5.58	123.67	111.40
2	B	310	ARG	NE-CZ-NH2	-5.58	117.51	120.30
2	B	645	LEU	N-CA-C	-5.36	96.53	111.00

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	60	0
1	C	1058	0	1068	65	0
2	B	3582	0	3581	181	0
2	D	3582	0	3581	157	0
3	E	33	0	29	5	0
3	F	61	0	56	6	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	9370	442	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 24.

The worst 5 of 442 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%)	24	51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	440/464 (95%)	406 (92%)	31 (7%)	3 (1%)	26	55
2	D	440/464 (95%)	423 (96%)	15 (3%)	2 (0%)	34	63
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%)	34	63

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%)	103 (88%)	14 (12%)	6	14
1	C	118/147 (80%)	105 (89%)	13 (11%)	8	18
2	B	400/410 (98%)	367 (92%)	33 (8%)	14	31
2	D	400/410 (98%)	361 (90%)	39 (10%)	10	23
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%)	945 (90%)	99 (10%)	11	24

5 of 99 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	699	LEU
1	C	156	GLU

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Mol	Chain	Res	Type
2	D	643	LYS
2	B	724	LYS
1	C	121	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	692	ASN
1	C	97	HIS
2	D	670	HIS
2	B	695	ASN
1	C	128	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	TPO	E	4	3	8,10,11	1.78	3 (37%)	7,14,16	0.70	0
3	TPO	F	4	3	8,10,11	1.58	1 (12%)	7,14,16	0.78	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	E	4	3	-	0/8/11/13	0/0/0/0
3	TPO	F	4	3	-	0/8/11/13	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	4	TPO	P-O1P	2.02	1.57	1.51
3	E	4	TPO	P-OG1	2.25	1.66	1.60
3	F	4	TPO	O-C	2.95	1.33	1.19
3	E	4	TPO	O-C	3.04	1.33	1.19

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

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

5.5 Carbohydrates [i](#)

There are no carbohydrates 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%)	0.16	4 (3%) 51 51	24, 42, 71, 92	0
1	C	127/169 (75%)	0.13	4 (3%) 52 52	24, 41, 74, 90	0
2	B	438/464 (94%)	0.03	1 (0%) 95 96	21, 38, 57, 87	0
2	D	438/464 (94%)	0.06	2 (0%) 91 93	19, 35, 53, 85	0
3	E	3/9 (33%)	1.72	1 (33%) 0 0	78, 78, 82, 86	0
3	F	7/9 (77%)	2.06	3 (42%) 0 0	79, 85, 90, 92	0
All	All	1139/1284 (88%)	0.08	15 (1%) 79 79	19, 38, 64, 92	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	9	GLY	3.7
2	B	509	TYR	3.4
3	F	6	PRO	3.4
2	D	271	LYS	3.2
1	C	103	PRO	3.1

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
3	TPO	F	4	11/12	0.92	0.25	-	71,75,79,80	0
3	TPO	E	4	11/12	0.90	0.19	-	72,76,79,79	0

6.3 Carbohydrates [i](#)

There are no carbohydrates 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.