



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 05:27 AM UTC

PDB ID : 1A1A / pdb_00001a1a
Title : C-SRC (SH2 DOMAIN WITH C188A MUTATION) COMPLEXED WITH
ACE-FORMYL PHOSPHOTYR-GLU-(N,N-DIPENTYL AMINE)
Authors : Shewchuk, L.; Jordan, S.
Deposited on : 1997-12-10
Resolution : 2.00 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

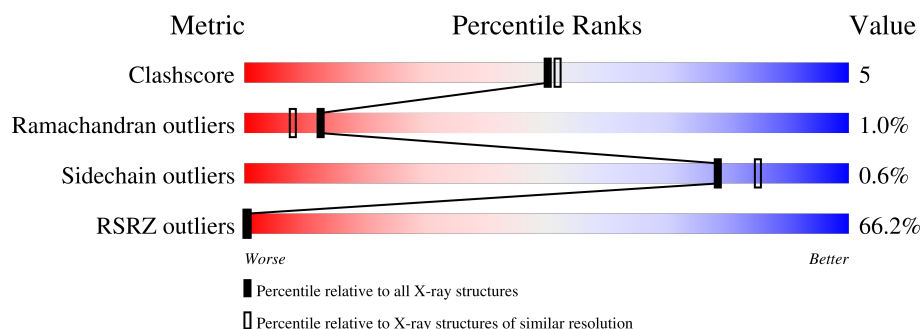
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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))
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	107	61% 79% 17% ..
1	B	107	69% 69% 25% 5%
2	C	4	75% 25%
2	D	4	75% 25%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2734 atoms, of which 800 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 C-SRC TYROSINE KINASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	106	Total	C	H	N	O	S	0	0	0
			1048	530	205	150	161	2			
1	B	102	Total	C	H	N	O	S	0	0	0
			1016	514	201	146	153	2			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	188	SER	CYS	engineered mutation	UNP P12931
B	188	SER	CYS	engineered mutation	UNP P12931

- Molecule 2 is a protein called ACE-FORMYL PHOSPHOTYR-GLU-(N,N-DIPENTYL AMINE).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	C	4	Total	C	H	N	O	P	0	0	0
			44	27	3	3	10	1			
2	D	4	Total	C	H	N	O	P	0	0	0
			44	27	3	3	10	1			

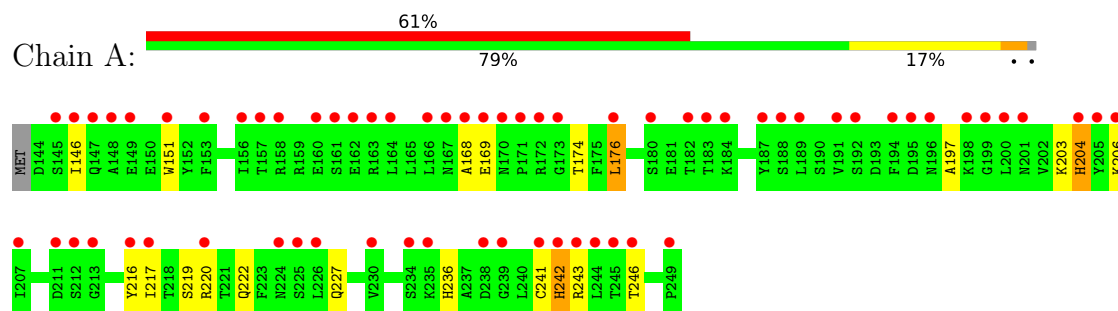
- Molecule 3 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	113	Total	H	O	0	0
			339	226	113		
3	C	3	Total	H	O	0	0
			9	6	3		
3	B	76	Total	H	O	0	0
			228	152	76		
3	D	2	Total	H	O	0	0
			6	4	2		

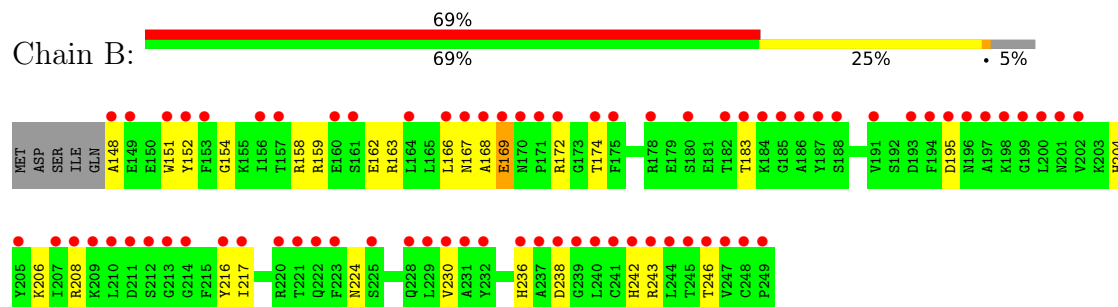
3 Residue-property plots

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.

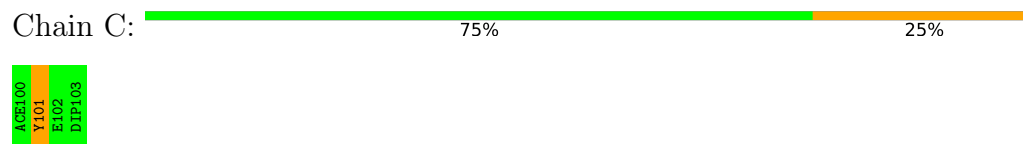
• Molecule 1: C-SRC TYROSINE KINASE



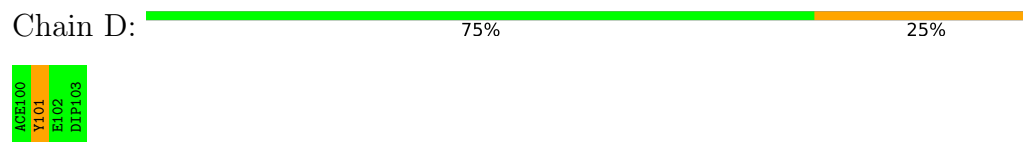
• Molecule 1: C-SRC TYROSINE KINASE



• Molecule 2: ACE-FORMYL PHOSPHOTYR-GLU-(N,N-DIPENTYL AMINE)



• Molecule 2: ACE-FORMYL PHOSPHOTYR-GLU-(N,N-DIPENTYL AMINE)



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	51.40Å 65.40Å 74.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 2.00 6.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	95.0 (6.00-2.00) 91.4 (6.00-2.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.80 (at 1.91Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.198 , (Not available) 0.462 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	31.5	Xtriage
Anisotropy	0.318	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.78 , 120.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.71	EDS
Total number of atoms	2734	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.54% 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: DIP, ACE, PTH

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	1.11	4/860 (0.5%)	1.44	10/1160 (0.9%)
1	B	1.23	8/832 (1.0%)	1.43	9/1121 (0.8%)
2	C	0.71	0/8	1.08	0/9
2	D	0.84	0/8	0.62	0/9
All	All	1.17	12/1708 (0.7%)	1.43	19/2299 (0.8%)

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
1	A	0	1
1	B	0	1
All	All	0	2

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	166	LEU	C-N	10.08	1.44	1.33
1	B	169	GLU	C-N	7.83	1.45	1.33
1	A	204	HIS	CD2-NE2	-7.61	1.29	1.37
1	A	242	HIS	CD2-NE2	-7.06	1.30	1.37
1	B	217	ILE	C-N	6.66	1.42	1.33
1	B	204	HIS	CD2-NE2	-6.52	1.30	1.37
1	B	236	HIS	CG-ND1	-5.75	1.31	1.38
1	A	236	HIS	CD2-NE2	-5.65	1.31	1.37
1	B	230	VAL	CA-CB	5.61	1.60	1.54
1	B	242	HIS	CD2-NE2	-5.54	1.31	1.37
1	A	216	TYR	CA-CB	5.17	1.62	1.53
1	B	236	HIS	CD2-NE2	-5.15	1.32	1.37

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	195	ASP	CA-CB-CG	7.36	119.96	112.60
1	B	204	HIS	CB-CG-CD2	-7.17	121.89	131.20
1	B	166	LEU	CA-C-N	-7.11	113.26	122.79
1	B	166	LEU	C-N-CA	-7.11	113.26	122.79
1	A	204	HIS	CB-CG-CD2	-7.07	122.01	131.20
1	B	242	HIS	CB-CG-CD2	-6.49	122.76	131.20
1	A	204	HIS	CB-CG-ND1	5.73	131.30	122.70
1	A	217	ILE	N-CA-C	-5.67	107.36	112.12
1	A	227	GLN	OE1-CD-NE2	-5.58	117.02	122.60
1	A	236	HIS	CB-CG-CD2	-5.36	124.23	131.20
1	B	151	TRP	CE2-CD2-CG	-5.35	100.78	107.20
1	A	222	GLN	OE1-CD-NE2	-5.30	117.30	122.60
1	B	238	ASP	CA-CB-CG	5.27	117.87	112.60
1	A	168	ALA	N-CA-C	5.22	119.13	112.34
1	B	151	TRP	CB-CG-CD1	-5.15	119.18	126.90
1	A	151	TRP	CE2-CD2-CG	-5.08	101.10	107.20
1	A	151	TRP	CG-CD2-CE3	5.04	138.94	133.90
1	A	151	TRP	CB-CG-CD1	-5.03	119.35	126.90
1	B	243	ARG	CB-CG-CD	-5.02	99.75	111.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	176	LEU	Mainchain
1	B	169	GLU	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	A	843	205	810	9	3
1	B	815	201	792	8	11
2	C	41	3	38	1	0
2	D	41	3	39	1	0
3	A	113	226	0	2	10

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	76	152	0	2	2
3	C	3	6	0	0	0
3	D	2	4	0	0	0
All	All	1934	800	1679	18	13

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (18) 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:B:163:ARG:O	1:B:167:ASN:HB2	1.86	0.74
1:A:242:HIS:HD2	1:A:243:ARG:O	1.80	0.65
1:A:204:HIS:HB3	2:C:101:PTH:OF	1.97	0.64
1:A:174:THR:HA	1:A:246:THR:O	2.02	0.58
1:B:163:ARG:HG3	3:B:675:HOH:O	2.04	0.58
1:A:176:LEU:HD12	1:A:176:LEU:C	2.30	0.56
1:A:206:LYS:NZ	3:A:657:HOH:O	2.41	0.52
1:A:203:LYS:HD2	1:A:241:CYS:HB3	1.92	0.52
2:D:101:PTH:HF2	2:D:101:PTH:O2P	2.13	0.49
1:B:152:TYR:CZ	1:B:154:GLY:HA2	2.49	0.48
1:B:174:THR:HA	1:B:246:THR:O	2.13	0.48
1:B:158:ARG:O	1:B:162:GLU:HG3	2.14	0.48
1:A:206:LYS:HB2	1:A:206:LYS:HE2	1.73	0.46
1:B:183:THR:HG21	1:B:208:ARG:NH1	2.31	0.45
1:B:206:LYS:HE3	1:B:208:ARG:NH2	2.32	0.45
1:B:148:ALA:N	3:B:585:HOH:O	2.54	0.41
1:A:242:HIS:CD2	1:A:243:ARG:O	2.67	0.40
1:A:220:ARG:HD3	3:A:523:HOH:O	2.22	0.40

All (13) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:224:ASN:HD22	3:A:529:HOH:O[4_456]	0.67	0.93
1:B:224:ASN:ND2	3:A:529:HOH:O[4_456]	1.40	0.80
1:B:159:ARG:HH12	3:A:503:HOH:H1[3_745]	0.91	0.69
1:A:169:GLU:O	1:B:172:ARG:HH22[4_456]	0.97	0.63
3:A:665:HOH:O	3:B:589:HOH:O[3_755]	1.65	0.55
1:B:224:ASN:HD22	3:A:529:HOH:H1[4_456]	1.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:GLU:O	1:B:172:ARG:NH2[4_456]	1.86	0.34
1:A:219:SER:O	1:B:208:ARG:HE[2_654]	1.26	0.34
1:B:159:ARG:HH12	3:A:503:HOH:O[3_745]	1.35	0.25
1:B:216:TYR:OH	3:A:521:HOH:O[2_655]	1.98	0.22
3:A:693:HOH:O	3:B:538:HOH:O[4_556]	2.15	0.05
1:B:216:TYR:OH	3:A:521:HOH:H1[2_655]	1.56	0.04
1:B:224:ASN:O	3:A:544:HOH:H2[4_456]	1.57	0.03

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	104/107 (97%)	102 (98%)	1 (1%)	1 (1%)	12	8
1	B	100/107 (94%)	96 (96%)	3 (3%)	1 (1%)	12	8
2	C	1/4 (25%)	1 (100%)	0	0	100	100
2	D	1/4 (25%)	1 (100%)	0	0	100	100
All	All	206/222 (93%)	200 (97%)	4 (2%)	2 (1%)	12	8

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	168	ALA
1	A	197	ALA

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	89/94 (95%)	88 (99%)	1 (1%)	65	73
1	B	86/94 (92%)	86 (100%)	0	100	100
2	C	1/1 (100%)	1 (100%)	0	100	100
2	D	1/1 (100%)	1 (100%)	0	100	100
All	All	177/190 (93%)	176 (99%)	1 (1%)	78	85

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	146	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	222	GLN
1	A	228	GLN
1	A	242	HIS
1	B	170	ASN
1	B	228	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
2	PTH	C	101	2	17,18,19	2.37	3 (17%)	19,25,27	2.05	6 (31%)
2	PTH	D	101	2	17,18,19	2.59	4 (23%)	19,25,27	1.74	5 (26%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PTH	C	101	2	-	1/12/13/15	0/1/1/1
2	PTH	D	101	2	-	3/12/13/15	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	101	PTH	P-OH	8.22	1.75	1.59
2	D	101	PTH	P-OH	7.25	1.73	1.59
2	D	101	PTH	CF-CE1	-5.30	1.38	1.51
2	D	101	PTH	OF-CF	-3.86	1.25	1.41
2	C	101	PTH	P-O1P	-2.88	1.41	1.50
2	D	101	PTH	P-O1P	-2.35	1.43	1.50
2	C	101	PTH	P-O3P	-2.12	1.46	1.54

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	101	PTH	CF-CE1-CZ	5.03	128.08	119.18
2	D	101	PTH	O3P-P-OH	-4.61	91.69	105.32
2	C	101	PTH	CD1-CE1-CZ	-4.07	113.80	118.26
2	C	101	PTH	CE1-CD1-CG	2.88	126.27	121.76
2	D	101	PTH	OF-CF-CE1	2.66	119.36	111.94
2	C	101	PTH	P-OH-CZ	-2.65	113.92	123.84
2	C	101	PTH	O3P-P-OH	-2.53	97.85	105.32
2	C	101	PTH	O3P-P-O2P	2.51	117.23	107.80
2	D	101	PTH	CF-CE1-CZ	-2.50	114.74	119.18
2	D	101	PTH	O3P-P-O1P	2.42	120.26	110.83
2	D	101	PTH	CF-CE1-CD1	2.30	125.71	120.60

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	101	PTH	CE1-CZ-OH-P
2	D	101	PTH	CE2-CZ-OH-P
2	D	101	PTH	CZ-OH-P-O2P
2	C	101	PTH	CZ-CE1-CF-OF

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	101	PTH	1	0
2	D	101	PTH	1	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

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	106/107 (99%)	2.32	65 (61%)  	15, 26, 50, 60	0
1	B	102/107 (95%)	2.81	74 (72%)  	17, 25, 49, 60	0
2	C	1/4 (25%)	0.29	0  	30, 30, 30, 30	0
2	D	1/4 (25%)	1.73	0  	30, 30, 30, 30	0
All	All	210/222 (94%)	2.55	139 (66%)  	15, 26, 51, 60	0

All (139) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	239	GLY	6.6
1	B	184	LYS	6.4
1	B	182	THR	6.2
1	B	148	ALA	5.9
1	A	199	GLY	5.2
1	A	224	ASN	5.1
1	B	200	LEU	4.9
1	B	180	SER	4.9
1	B	188	SER	4.9
1	A	196	ASN	4.9
1	B	231	ALA	4.8
1	B	151	TRP	4.4
1	B	167	ASN	4.4
1	A	243	ARG	4.3
1	A	211	ASP	4.2
1	B	194	PHE	4.2
1	B	193	ASP	4.1
1	B	220	ARG	4.1
1	B	214	GLY	4.1
1	A	184	LYS	4.1
1	B	237	ALA	4.1

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Mol	Chain	Res	Type	RSRZ
1	B	211	ASP	4.1
1	B	196	ASN	4.1
1	B	175	PHE	4.1
1	A	238	ASP	4.1
1	B	213	GLY	4.0
1	B	216	TYR	4.0
1	B	183	THR	3.9
1	B	199	GLY	3.9
1	B	241	CYS	3.9
1	B	245	THR	3.8
1	A	212	SER	3.8
1	B	205	TYR	3.8
1	B	223	PHE	3.7
1	A	149	GLU	3.7
1	A	167	ASN	3.7
1	B	195	ASP	3.7
1	B	171	PRO	3.7
1	B	240	LEU	3.6
1	A	180	SER	3.6
1	B	210	LEU	3.5
1	B	207	ILE	3.5
1	A	246	THR	3.5
1	A	148	ALA	3.4
1	B	156	ILE	3.4
1	A	200	LEU	3.4
1	A	187	TYR	3.3
1	A	213	GLY	3.3
1	B	152	TYR	3.3
1	B	164	LEU	3.2
1	A	241	CYS	3.2
1	B	170	ASN	3.2
1	A	244	LEU	3.2
1	A	161	SER	3.2
1	A	169	GLU	3.1
1	B	191	VAL	3.1
1	B	244	LEU	3.1
1	B	187	TYR	3.0
1	B	169	GLU	3.0
1	A	183	THR	3.0
1	B	232	TYR	3.0
1	A	198	LYS	3.0
1	B	238	ASP	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	198	LYS	3.0
1	B	186	ALA	3.0
1	A	164	LEU	3.0
1	A	166	LEU	3.0
1	B	247	VAL	3.0
1	A	182	THR	2.9
1	B	236	HIS	2.9
1	B	197	ALA	2.8
1	B	166	LEU	2.8
1	B	212	SER	2.8
1	A	245	THR	2.8
1	B	153	PHE	2.7
1	A	230	VAL	2.7
1	B	242	HIS	2.7
1	A	207	ILE	2.7
1	A	220	ARG	2.7
1	A	194	PHE	2.7
1	B	225	SER	2.7
1	B	248	CYS	2.7
1	B	157	THR	2.6
1	B	229	LEU	2.6
1	B	201	ASN	2.6
1	B	246	THR	2.6
1	A	188	SER	2.6
1	A	235	LYS	2.6
1	A	191	VAL	2.6
1	A	249	PRO	2.6
1	A	225	SER	2.6
1	B	160	GLU	2.5
1	A	160	GLU	2.5
1	A	151	TRP	2.5
1	A	204	HIS	2.5
1	B	178	ARG	2.5
1	B	217	ILE	2.5
1	A	170	ASN	2.5
1	A	168	ALA	2.5
1	B	222	GLN	2.4
1	A	205	TYR	2.4
1	A	195	ASP	2.4
1	A	145	SER	2.4
1	A	192	SER	2.4
1	B	209	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	176	LEU	2.4
1	A	189	LEU	2.4
1	B	172	ARG	2.4
1	B	174	THR	2.4
1	A	147	GLN	2.3
1	A	242	HIS	2.3
1	A	173	GLY	2.3
1	B	249	PRO	2.3
1	A	226	LEU	2.3
1	B	149	GLU	2.2
1	A	234	SER	2.2
1	B	161	SER	2.2
1	B	228	GLN	2.2
1	A	217	ILE	2.2
1	A	171	PRO	2.2
1	B	202	VAL	2.2
1	B	230	VAL	2.2
1	A	172	ARG	2.2
1	B	168	ALA	2.2
1	A	158	ARG	2.2
1	A	162	GLU	2.2
1	A	216	TYR	2.2
1	A	157	THR	2.2
1	A	153	PHE	2.1
1	B	221	THR	2.1
1	A	156	ILE	2.1
1	B	185	GLY	2.1
1	A	201	ASN	2.1
1	A	163	ARG	2.1
1	A	239	GLY	2.1
1	B	208	ARG	2.1
1	A	206	LYS	2.1
1	B	243	ARG	2.0
1	A	146	ILE	2.0

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

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
2	PTH	C	101	18/19	0.64	0.16	0,35,44,59	0
2	PTH	D	101	18/19	0.76	0.15	0,41,47,55	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.