



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:05 AM GMT

PDB ID : 2FJN
Title : The structure of phosphotyrosine phosphatase 1B in complex with compound 2
Authors : Asante-Appiah, E.; Patel, S.; Despons, C.; Taylor, J.M.; Lau, C.; Dufresne, C.; Therien, M.; Friesen, R.; Becker, J.W.; Leblanc, Y.; Kennedy, B.P.; Scapin, G.
Deposited on : 2006-01-03
Resolution : 2.20 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
<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

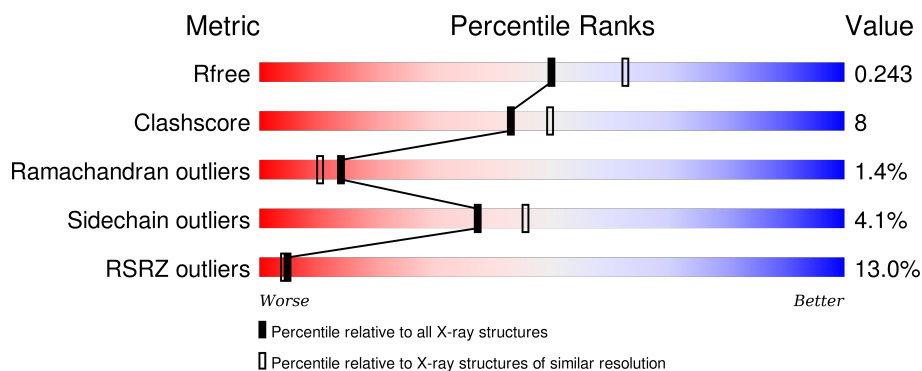
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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	310	
1	B	310	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5150 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 Tyrosine-protein phosphatase, non-receptor type 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	289	Total	C	N	O	S	0	0	0
			2346	1488	404	439	15			
1	B	289	Total	C	N	O	S	0	0	0
			2349	1490	404	439	16			

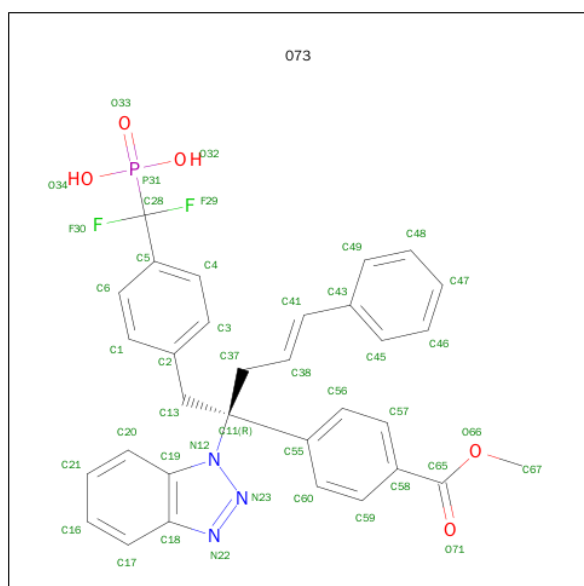
There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	489	MET	-	CLONING ARTIFACT	UNP P18031
A	490	ASP	-	CLONING ARTIFACT	UNP P18031
A	491	TYR	-	CLONING ARTIFACT	UNP P18031
A	492	LYS	-	CLONING ARTIFACT	UNP P18031
A	493	ASP	-	CLONING ARTIFACT	UNP P18031
A	494	ASP	-	CLONING ARTIFACT	UNP P18031
A	495	ASP	-	CLONING ARTIFACT	UNP P18031
A	496	ASP	-	CLONING ARTIFACT	UNP P18031
A	497	LYS	-	CLONING ARTIFACT	UNP P18031
A	498	LEU	-	CLONING ARTIFACT	UNP P18031
A	499	GLU	-	CLONING ARTIFACT	UNP P18031
A	500	PHE	-	CLONING ARTIFACT	UNP P18031
B	489	MET	-	CLONING ARTIFACT	UNP P18031
B	490	ASP	-	CLONING ARTIFACT	UNP P18031
B	491	TYR	-	CLONING ARTIFACT	UNP P18031
B	492	LYS	-	CLONING ARTIFACT	UNP P18031
B	493	ASP	-	CLONING ARTIFACT	UNP P18031
B	494	ASP	-	CLONING ARTIFACT	UNP P18031
B	495	ASP	-	CLONING ARTIFACT	UNP P18031
B	496	ASP	-	CLONING ARTIFACT	UNP P18031
B	497	LYS	-	CLONING ARTIFACT	UNP P18031
B	498	LEU	-	CLONING ARTIFACT	UNP P18031
B	499	GLU	-	CLONING ARTIFACT	UNP P18031
B	500	PHE	-	CLONING ARTIFACT	UNP P18031

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Cl 1 1	0	0
2	A	1	Total Cl 1 1	0	0

- Molecule 3 is (4-{(2S,4E)-2-(1H-1,2,3-BENZOTRIAZOL-1-YL)-2-[4-(METHOXYCARBONYL)PHENYL]-5-PHENYLPENT-4-ENYL}PHENYL)(DIFLUORO)METHYLPHOSPHONIC ACID (three-letter code: 073) (formula: C₃₂H₂₈F₂N₃O₅P).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	F	N	O	P	0	0
			43	32	2	3	5	1		
3	B	1	Total	C	F	N	O	P	0	0
			43	32	2	3	5	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	168	Total O 168 168	0	0
4	B	199	Total O 199 199	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	87.43Å 85.62Å 137.27Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	13.00 – 2.20 29.44 – 1.94	Depositor EDS
% Data completeness (in resolution range)	96.7 (13.00-2.20) 91.5 (29.44-1.94)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.42 (at 1.93Å)	Xtriage
Refinement program	CNX	Depositor
R, R_{free}	0.208 , 0.244 0.207 , 0.243	Depositor DCC
R_{free} test set	2603 reflections (5.38%)	DCC
Wilson B-factor (Å ²)	30.5	Xtriage
Anisotropy	0.052	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 54.9	EDS
Estimated twinning fraction	0.035 for k,h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 70406 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5150	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.23% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 073, CL

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	0.41	0/2399	0.62	0/3234
1	B	0.44	0/2402	0.62	0/3237
All	All	0.43	0/4801	0.62	0/6471

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

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	2346	0	2299	34	0
1	B	2349	0	2306	43	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	43	0	26	1	0
3	B	43	0	26	2	0
4	A	168	0	0	1	0
4	B	199	0	0	1	0
All	All	5150	0	4657	77	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 (77) 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:500:PHE:HB3	1:B:779:LYS:NZ	1.98	0.78
1:B:697:LYS:HA	1:B:697:LYS:HE2	1.67	0.75
1:B:504:GLU:O	1:B:508:GLU:HG3	1.89	0.72
1:B:500:PHE:HB3	1:B:779:LYS:HZ3	1.54	0.70
1:B:778:ALA:O	1:B:782:MET:HG2	1.96	0.66
1:A:661:GLU:HG3	1:A:668:THR:HG22	1.79	0.65
1:B:781:ILE:HG13	1:B:782:MET:H	1.64	0.62
1:A:611:ASN:O	1:A:675:HIS:HE1	1.83	0.61
1:B:605:ARG:HH21	1:B:669:ARG:HD3	1.64	0.61
1:B:781:ILE:HG13	1:B:782:MET:N	2.15	0.59
1:A:613:VAL:HA	1:A:621:CYS:HB3	1.87	0.57
1:A:526:GLU:HG3	3:B:402:073:H21	1.86	0.57
1:A:696:PHE:O	1:A:700:GLU:HG3	2.05	0.56
1:B:510:ILE:HG22	1:B:510:ILE:O	2.05	0.56
1:A:679:TRP:CE2	1:A:721:ARG:HG2	2.39	0.56
1:B:753:MET:HB3	1:B:760:LEU:HD23	1.86	0.55
1:B:650:LYS:HD2	1:B:653:TYR:CZ	2.42	0.55
1:B:561:GLN:HB3	4:B:184:HOH:O	2.07	0.54
1:B:697:LYS:HE2	1:B:697:LYS:CA	2.37	0.54
1:B:500:PHE:HZ	1:B:782:MET:HG3	1.72	0.53
1:A:781:ILE:HG13	1:A:782:MET:HG2	1.90	0.53
1:B:640:LEU:HD23	1:B:662:ASN:HA	1.92	0.52
1:A:506:GLU:O	1:A:510:ILE:HG13	2.10	0.52
1:A:572:ILE:HG13	1:A:756:PHE:HB2	1.92	0.51
1:A:633:MET:C	1:A:634:ILE:HD12	2.31	0.51
1:A:546:TYR:HB3	3:A:401:073:N23	2.25	0.51
1:B:614:MET:O	1:B:620:LYS:HB3	2.10	0.50
1:A:497:LYS:C	1:A:499:GLU:H	2.14	0.50
1:A:504:GLU:OE2	1:A:779:LYS:HE3	2.12	0.50
1:A:572:ILE:HD13	1:A:583:LEU:HD13	1.94	0.49
1:A:629:GLU:N	1:A:629:GLU:OE1	2.36	0.49
1:B:612:ARG:HH11	1:B:677:THR:HG22	1.77	0.49
1:A:532:CYS:O	1:A:536:LYS:HG2	2.13	0.49
1:B:546:TYR:HB3	3:B:402:073:N23	2.28	0.48
1:B:523:ILE:HD13	1:B:750:LEU:HD23	1.95	0.48
1:B:696:PHE:O	1:B:700:GLU:HG3	2.14	0.47
1:B:579:ARG:CZ	1:B:733:LEU:HD11	2.44	0.47
1:B:500:PHE:HB3	1:B:779:LYS:HZ2	1.79	0.47
1:A:739:LYS:O	1:A:741:PRO:HD3	2.15	0.46
1:B:634:ILE:HD12	1:B:634:ILE:N	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:679:TRP:NE1	1:A:721:ARG:HG2	2.30	0.45
1:B:605:ARG:NH2	1:B:669:ARG:HD3	2.31	0.45
1:A:611:ASN:O	1:A:675:HIS:CE1	2.66	0.45
1:A:577:ALA:O	1:A:578:GLN:HB2	2.16	0.45
1:B:597:GLU:OE2	1:B:601:GLU:OE2	2.35	0.45
1:A:640:LEU:HD23	1:A:662:ASN:HA	1.98	0.45
1:B:502:GLU:O	1:B:505:LYS:HB2	2.17	0.45
1:B:602:GLN:O	1:B:709:GLY:HA3	2.16	0.44
1:B:661:GLU:HB2	1:B:668:THR:HG22	1.99	0.44
1:B:503:MET:HE3	1:B:775:ILE:HA	1.99	0.44
1:A:737:LYS:HG3	1:A:738:ARG:N	2.33	0.44
1:B:504:GLU:OE2	1:B:779:LYS:HE3	2.17	0.44
1:B:546:TYR:OH	1:B:619:LEU:HA	2.17	0.44
1:B:705:SER:HA	1:B:706:PRO:HD3	1.87	0.44
1:B:597:GLU:HA	1:B:640:LEU:HD11	1.99	0.43
1:A:583:LEU:HD12	1:A:583:LEU:N	2.33	0.43
1:B:633:MET:C	1:B:634:ILE:HD12	2.39	0.43
1:A:656:ARG:HG3	4:A:196:HOH:O	2.17	0.43
1:B:719:ILE:O	1:B:760:LEU:HA	2.18	0.43
1:B:563:ASP:OD1	1:B:563:ASP:N	2.51	0.43
1:A:644:LEU:HA	1:A:658:LEU:HD23	2.01	0.42
1:A:605:ARG:HA	1:A:605:ARG:HD3	1.68	0.42
1:A:602:GLN:O	1:A:709:GLY:HA3	2.20	0.42
1:A:674:PHE:CG	1:A:698:VAL:HG22	2.55	0.42
1:B:537:LEU:HD13	1:B:539:LYS:HE2	2.02	0.41
1:B:737:LYS:HD3	1:B:737:LYS:O	2.20	0.41
1:A:561:GLN:NE2	1:A:597:GLU:OE1	2.53	0.41
1:B:777:GLY:O	1:B:781:ILE:HG12	2.21	0.41
1:B:579:ARG:HG3	1:B:580:SER:N	2.36	0.41
1:B:702:GLY:O	1:B:705:SER:HB3	2.20	0.41
1:A:634:ILE:N	1:A:634:ILE:HD12	2.35	0.41
1:B:662:ASN:OD1	1:B:664:THR:HB	2.21	0.41
1:A:499:GLU:HG2	1:A:499:GLU:O	2.21	0.41
1:A:732:LEU:HD23	1:A:732:LEU:HA	1.92	0.41
1:A:661:GLU:CG	1:A:668:THR:HG22	2.49	0.41
1:B:532:CYS:O	1:B:536:LYS:HG2	2.21	0.40
1:A:613:VAL:HG13	1:A:621:CYS:O	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	A	287/310 (93%)	270 (94%)	12 (4%)	5 (2%)	11	7
1	B	287/310 (93%)	271 (94%)	13 (4%)	3 (1%)	19	16
All	All	574/620 (93%)	541 (94%)	25 (4%)	8 (1%)	14	10

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	615	GLU
1	A	563	ASP
1	A	616	LYS
1	B	563	ASP
1	B	784	ASP
1	A	498	LEU
1	B	761	ILE
1	A	761	ILE

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	258/283 (91%)	247 (96%)	11 (4%)	35	43
1	B	259/283 (92%)	249 (96%)	10 (4%)	39	48
All	All	517/566 (91%)	496 (96%)	21 (4%)	37	45

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	500	PHE
1	A	505	LYS
1	A	511	ASP
1	A	563	ASP
1	A	579	ARG
1	A	616	LYS
1	A	619	LEU
1	A	639	ASN
1	A	651	SER
1	A	737	LYS
1	A	760	LEU
1	B	509	GLN
1	B	605	ARG
1	B	615	GLU
1	B	631	LYS
1	B	644	LEU
1	B	686	GLU
1	B	697	LYS
1	B	737	LYS
1	B	760	LEU
1	B	765	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	554	HIS
1	A	561	GLN
1	A	639	ASN
1	A	657	GLN
1	A	675	HIS
1	B	509	GLN
1	B	578	GLN
1	B	693	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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$
3	073	A	401	-	39,47,47	2.06	12 (30%)	50,69,69	2.01	9 (18%)
3	073	B	402	-	39,47,47	2.00	11 (28%)	50,69,69	2.00	10 (20%)

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	073	A	401	-	-	0/30/45/45	0/5/5/5
3	073	B	402	-	-	0/30/45/45	0/5/5/5

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	401	073	C17-C18	-2.36	1.37	1.41
3	B	402	073	P31-O33	-2.29	1.46	1.50
3	A	401	073	C16-C17	2.01	1.41	1.36
3	B	402	073	C4-C5	2.05	1.42	1.39
3	A	401	073	C46-C45	2.06	1.43	1.38
3	B	402	073	C19-C18	2.08	1.44	1.40
3	B	402	073	C16-C17	2.14	1.41	1.36
3	B	402	073	C59-C58	2.17	1.43	1.39
3	A	401	073	C19-C18	2.17	1.44	1.40
3	A	401	073	C6-C5	2.18	1.42	1.39
3	A	401	073	C21-C20	2.30	1.41	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	401	073	C45-C43	2.32	1.43	1.39
3	A	401	073	C4-C5	2.36	1.42	1.39
3	B	402	073	C21-C20	2.56	1.42	1.36
3	B	402	073	C56-C55	2.84	1.43	1.39
3	B	402	073	C60-C55	2.91	1.43	1.39
3	A	401	073	C60-C55	2.96	1.43	1.39
3	A	401	073	C56-C55	3.03	1.44	1.39
3	B	402	073	C6-C5	3.04	1.44	1.39
3	B	402	073	C13-C11	3.62	1.59	1.55
3	A	401	073	C13-C11	4.76	1.61	1.55
3	A	401	073	C11-C55	6.45	1.60	1.52
3	B	402	073	C11-C55	6.73	1.60	1.52

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	402	073	C19-C18-N22	-3.65	103.84	108.55
3	A	401	073	C19-C18-N22	-3.34	104.24	108.55
3	A	401	073	C56-C55-C11	-2.55	116.18	121.06
3	B	402	073	C20-C19-C18	-2.51	117.14	121.36
3	B	402	073	C56-C55-C11	-2.48	116.32	121.06
3	A	401	073	C20-C19-C18	-2.40	117.34	121.36
3	B	402	073	C17-C18-N22	2.12	133.80	130.22
3	B	402	073	F29-C28-F30	2.28	109.52	106.56
3	A	401	073	F29-C28-F30	2.39	109.66	106.56
3	A	401	073	P31-C28-C5	2.89	117.62	108.95
3	B	402	073	P31-C28-C5	2.99	117.94	108.95
3	B	402	073	C60-C55-C11	3.00	126.78	121.06
3	A	401	073	C60-C55-C11	3.03	126.85	121.06
3	B	402	073	C11-C13-C2	4.54	125.20	115.90
3	B	402	073	C55-C11-N12	4.72	117.21	108.91
3	A	401	073	C11-C13-C2	4.78	125.69	115.90
3	A	401	073	C55-C11-N12	5.99	119.46	108.91
3	A	401	073	C20-C19-N12	8.74	140.50	131.97
3	B	402	073	C20-C19-N12	8.93	140.68	131.97

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	401	073	1	0
3	B	402	073	2	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	A	289/310 (93%)	0.56	40 (13%) 4 3	20, 34, 59, 67	0
1	B	289/310 (93%)	0.33	35 (12%) 6 5	17, 31, 56, 68	0
All	All	578/620 (93%)	0.45	75 (12%) 5 4	17, 32, 58, 68	0

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	498	LEU	7.8
1	B	501	MET	6.6
1	B	498	LEU	6.5
1	B	784	ASP	6.5
1	A	500	PHE	5.7
1	B	500	PHE	5.7
1	A	784	ASP	5.6
1	A	615	GLU	5.4
1	A	505	LYS	5.2
1	A	652	TYR	4.9
1	B	785	SER	4.7
1	B	562	GLU	4.6
1	A	783	GLY	4.5
1	B	502	GLU	4.4
1	A	502	GLU	4.3
1	A	562	GLU	4.3
1	B	497	LYS	4.3
1	A	785	SER	4.2
1	B	509	GLN	4.1
1	B	782	MET	4.1
1	A	616	LYS	4.0
1	B	783	GLY	3.9
1	A	563	ASP	3.9
1	A	713	VAL	3.9

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Mol	Chain	Res	Type	RSRZ
1	B	739	LYS	3.7
1	B	505	LYS	3.7
1	A	499	GLU	3.7
1	A	608	VAL	3.6
1	A	712	VAL	3.6
1	B	652	TYR	3.5
1	A	707	GLU	3.4
1	B	780	PHE	3.4
1	A	607	VAL	3.3
1	A	584	THR	3.2
1	B	781	ILE	3.2
1	A	614	MET	3.2
1	B	707	GLU	3.1
1	A	725	PHE	3.1
1	A	726	CYS	3.1
1	A	595	PHE	3.1
1	A	583	LEU	3.0
1	A	708	HIS	3.0
1	A	781	ILE	3.0
1	B	510	ILE	3.0
1	B	615	GLU	2.9
1	B	499	GLU	2.9
1	A	501	MET	2.8
1	A	561	GLN	2.8
1	B	563	ASP	2.8
1	B	616	LYS	2.7
1	A	497	LYS	2.7
1	B	664	THR	2.6
1	A	618	SER	2.5
1	B	608	VAL	2.5
1	A	617	GLY	2.5
1	B	607	VAL	2.4
1	B	713	VAL	2.4
1	A	508	GLU	2.3
1	A	705	SER	2.3
1	B	578	GLN	2.3
1	B	508	GLU	2.2
1	B	726	CYS	2.2
1	A	780	PHE	2.2
1	B	740	ASP	2.2
1	A	728	ALA	2.2
1	B	583	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	782	MET	2.1
1	B	584	THR	2.1
1	A	686	GLU	2.1
1	B	712	VAL	2.1
1	B	737	LYS	2.1
1	A	714	HIS	2.1
1	A	723	GLY	2.0
1	A	663	LEU	2.0
1	B	569	ALA	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 carbohydrates 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. 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
2	CL	A	799	1/1	0.99	0.13	-0.19	25,25,25,25	0
3	073	A	401	43/43	0.96	0.11	-0.51	20,24,31,38	0
3	073	B	402	43/43	0.96	0.11	-0.62	19,23,28,31	0
2	CL	B	799	1/1	1.00	0.09	-1.33	25,25,25,25	0

6.5 Other polymers [i](#)

There are no such residues in this entry.