



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:03 PM UTC

PDB ID : 1QWT / pdb_00001qwt
Title : Auto-inhibitory interferon regulation factor-3 (IRF3) transactivation domain
Authors : Qin, B.Y.
Deposited on : 2003-09-03
Resolution : 2.10 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

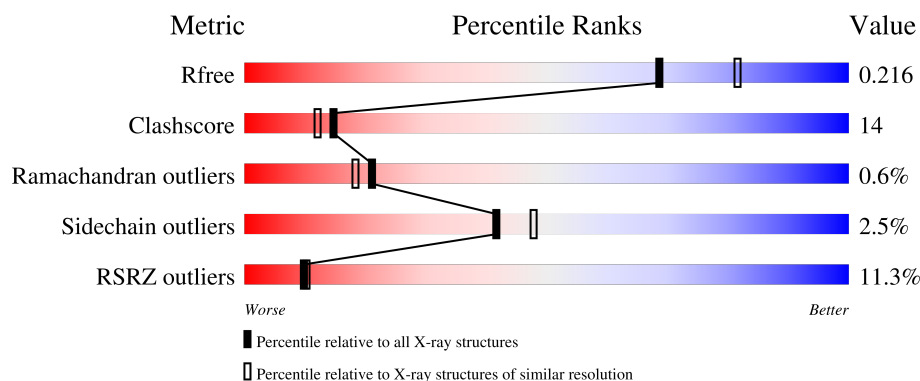
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	255	8% 69% 22% 6%
1	B	255	13% 72% 20% 6%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	PO4	A	602	-	-	X	-
2	PO4	B	605	-	-	X	-

2 Entry composition [i](#)

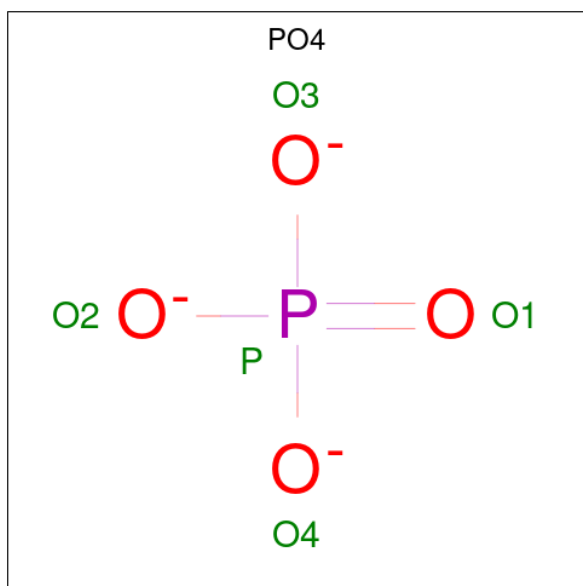
There are 3 unique types of molecules in this entry. The entry contains 4316 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Interferon regulatory factor 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	239	Total	C	N	O	S	0	0	0
			1869	1190	322	347	10			
1	B	239	Total	C	N	O	S	0	1	0
			1879	1199	323	347	10			

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		

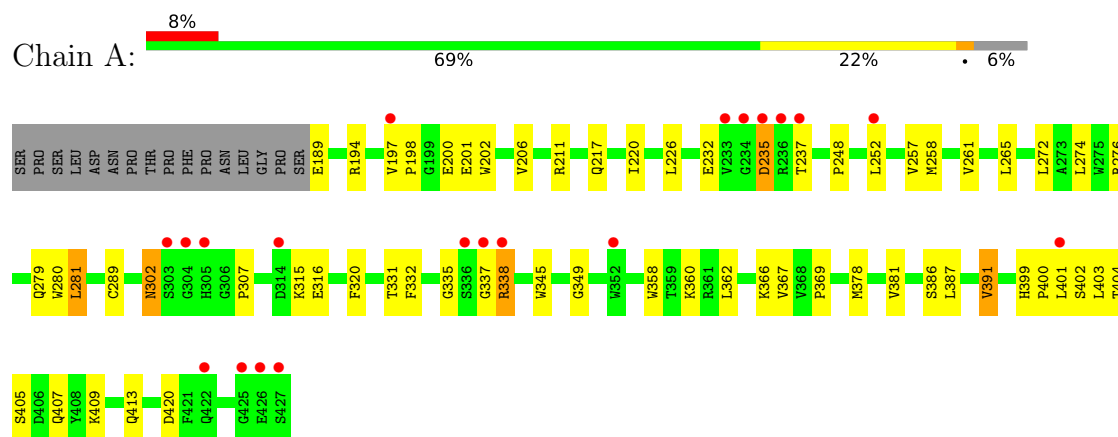
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	261	Total	O	0	0
			261	261		
3	B	267	Total	O	0	0
			267	267		

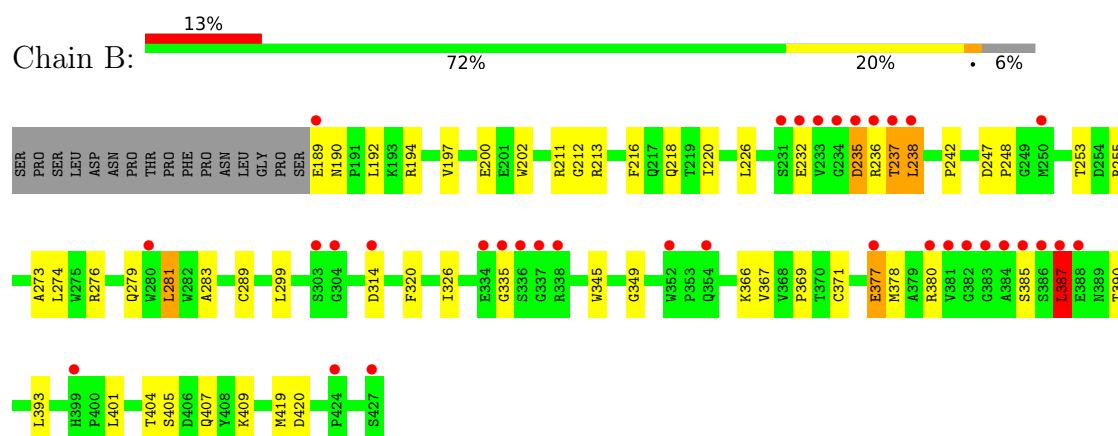
3 Residue-property plots [i](#)

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: Interferon regulatory factor 3



• Molecule 1: Interferon regulatory factor 3



4 Data and refinement statistics

Property	Value	Source
Space group	P 4 21 2	Depositor
Cell constants a, b, c, α , β , γ	135.54Å 135.54Å 68.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.00 – 2.10 95.84 – 2.10	Depositor EDS
% Data completeness (in resolution range)	(Not available) (100.00-2.10) 95.8 (95.84-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.87 (at 2.10Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.195 , 0.214 0.196 , 0.216	Depositor DCC
R_{free} test set	930 reflections (2.47%)	wwPDB-VP
Wilson B-factor (Å ²)	27.0	Xtriage
Anisotropy	0.067	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 70.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4316	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.68% 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: PO4

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	0.38	0/1923	0.86	1/2619 (0.0%)
1	B	0.36	0/1939	0.84	2/2642 (0.1%)
All	All	0.37	0/3862	0.85	3/5261 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	369	PRO	N-CA-C	-6.58	99.81	110.74
1	B	237	THR	N-CA-C	-6.15	106.10	113.97
1	A	369	PRO	N-CA-C	-5.80	100.53	112.47

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	1869	0	1808	52	0
1	B	1879	0	1814	53	0
2	A	15	0	0	3	0
2	B	25	0	0	3	0
3	A	261	0	0	10	0
3	B	267	0	0	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4316	0	3622	103	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 14.

All (103) 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:279:GLN:HE22	1:B:420:ASP:H	1.11	0.98
1:A:279:GLN:HE22	1:A:420:ASP:H	1.07	0.93
1:A:401:LEU:HD22	1:A:403:LEU:HG	1.63	0.80
1:A:201:GLU:HA	2:A:602:PO4:O1	1.82	0.80
1:B:377:GLU:CD	1:B:377:GLU:C	2.54	0.74
1:B:377:GLU:OE2	3:B:717:HOH:O	2.05	0.72
1:B:197:VAL:HG23	1:B:200:GLU:HB2	1.73	0.70
1:B:276:ARG:HB3	2:B:605:PO4:O3	1.90	0.70
1:B:255:ARG:NE	1:B:255:ARG:H	1.91	0.68
1:B:387:LEU:HD23	3:B:873:HOH:O	1.92	0.67
1:B:216:PHE:HZ	1:B:218:GLN:HE21	1.42	0.66
1:A:378:MET:SD	1:A:391:VAL:HG22	2.35	0.66
1:B:281:LEU:HB2	1:B:320:PHE:HB3	1.79	0.64
1:B:220:ILE:HD12	1:B:220:ILE:C	2.23	0.64
1:A:232:GLU:HA	1:A:235:ASP:OD1	2.00	0.62
1:B:335:GLY:HA2	3:B:712:HOH:O	2.01	0.61
1:A:252:LEU:HD12	1:A:258:MET:HE2	1.81	0.61
1:A:198:PRO:HA	3:A:604:HOH:O	2.00	0.61
1:A:404:THR:OG1	1:A:407:GLN:HG3	2.02	0.60
1:B:385:SER:HB2	1:B:387:LEU:HD11	1.83	0.59
3:A:762:HOH:O	1:B:213:ARG:HB2	2.03	0.58
1:B:387:LEU:HA	3:B:734:HOH:O	2.03	0.58
1:A:220:ILE:HD12	1:A:220:ILE:C	2.29	0.58
1:B:235:ASP:HB3	1:B:242:PRO:HG3	1.85	0.58
1:B:238:LEU:HD12	1:B:238:LEU:N	2.20	0.57
1:B:404:THR:OG1	1:B:407:GLN:HG3	2.03	0.57
1:A:401:LEU:HD23	1:A:402:SER:N	2.19	0.57
1:A:237:THR:HB	3:A:857:HOH:O	2.06	0.56
1:A:399:HIS:HB3	3:A:780:HOH:O	2.04	0.56
1:A:194:ARG:O	1:A:197:VAL:HG22	2.06	0.56
1:A:252:LEU:HD11	1:A:258:MET:HG3	1.88	0.56
1:B:194:ARG:O	1:B:197:VAL:HG22	2.06	0.55
1:B:405:SER:O	1:B:409:LYS:HG3	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:345:TRP:CZ2	1:B:366:LYS:HD3	2.42	0.55
1:A:252:LEU:CD1	1:A:258:MET:HE2	2.36	0.55
1:B:289:CYS:HB3	1:B:349:GLY:O	2.05	0.55
1:B:377:GLU:HB2	3:B:871:HOH:O	2.05	0.55
1:B:190:ASN:C	1:B:190:ASN:HD22	2.14	0.55
1:A:338:ARG:HG3	1:A:338:ARG:HH11	1.71	0.55
1:A:226:LEU:HD12	1:A:226:LEU:C	2.32	0.54
1:A:248:PRO:HB2	1:A:252:LEU:HD11	1.89	0.53
1:B:216:PHE:HZ	1:B:218:GLN:NE2	2.05	0.53
1:B:385:SER:CB	1:B:387:LEU:HD11	2.38	0.53
1:A:197:VAL:HG23	1:A:200:GLU:HB2	1.90	0.53
1:B:274:LEU:CD2	1:B:367:VAL:HG11	2.40	0.52
1:B:197:VAL:CG2	1:B:200:GLU:HB2	2.41	0.51
1:A:335:GLY:HA2	3:A:842:HOH:O	2.09	0.51
1:B:377:GLU:CD	1:B:378:MET:N	2.69	0.51
1:A:378:MET:SD	1:A:391:VAL:CG2	2.99	0.50
1:B:380:ARG:HA	3:B:814:HOH:O	2.11	0.50
1:B:255:ARG:H	1:B:255:ARG:CD	2.24	0.50
1:A:274:LEU:CD2	1:A:367:VAL:HG11	2.42	0.50
1:A:332:PHE:HA	1:A:337:GLY:O	2.11	0.50
1:B:387:LEU:HD12	1:B:387:LEU:N	2.27	0.50
1:B:237:THR:HB	1:B:238:LEU:HD12	1.93	0.50
1:B:371:CYS:HB3	1:B:393:LEU:O	2.11	0.50
1:A:189:GLU:HB2	3:A:829:HOH:O	2.12	0.49
1:A:331:THR:HG22	1:A:337:GLY:HA3	1.95	0.48
1:B:377:GLU:OE2	1:B:378:MET:HA	2.14	0.48
1:A:289:CYS:HB3	1:A:349:GLY:O	2.14	0.48
1:A:345:TRP:CZ2	1:A:366:LYS:HD3	2.49	0.48
1:B:255:ARG:CD	1:B:255:ARG:N	2.77	0.48
1:A:315:LYS:HD3	1:A:316:GLU:O	2.13	0.47
1:A:386:SER:HB2	3:B:709:HOH:O	2.14	0.47
1:A:360:LYS:HE2	1:A:362:LEU:HD11	1.95	0.47
1:A:338:ARG:N	1:A:338:ARG:NE	2.63	0.47
1:A:211:ARG:HD2	1:A:257:VAL:HG21	1.96	0.47
1:A:302:ASN:HD22	1:A:302:ASN:C	2.21	0.46
1:B:273:ALA:O	1:B:283:ALA:HA	2.15	0.46
1:A:281:LEU:HB2	1:A:320:PHE:HB3	1.96	0.46
1:A:272:LEU:C	1:A:272:LEU:HD13	2.40	0.46
1:B:190:ASN:ND2	1:B:192:LEU:H	2.14	0.46
1:A:194:ARG:NH2	3:A:811:HOH:O	2.49	0.45
1:A:280:TRP:HD1	3:A:751:HOH:O	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:391:VAL:O	1:A:400:PRO:HA	2.16	0.45
1:A:279:GLN:HE22	1:A:420:ASP:N	1.91	0.45
1:A:405:SER:O	1:A:409:LYS:HG3	2.16	0.45
1:B:314:ASP:HB2	3:B:715:HOH:O	2.15	0.45
1:A:206:VAL:O	1:A:217:GLN:HA	2.17	0.45
1:A:276:ARG:HB3	2:A:602:PO4:O4	2.17	0.45
1:B:390:THR:HA	1:B:401:LEU:O	2.17	0.45
1:A:189:GLU:N	3:A:854:HOH:O	2.50	0.44
1:A:381:VAL:HG12	1:B:299:LEU:HD23	2.00	0.44
1:A:202:TRP:HB2	2:A:602:PO4:O2	2.17	0.44
1:B:247:ASP:OD2	1:B:248:PRO:HD2	2.18	0.44
1:B:253:THR:O	1:B:255:ARG:HD3	2.18	0.44
1:B:226:LEU:C	1:B:226:LEU:HD12	2.43	0.43
1:B:377:GLU:HG3	3:B:749:HOH:O	2.19	0.43
1:A:302:ASN:ND2	1:A:302:ASN:H	2.16	0.42
1:A:338:ARG:HG3	1:A:338:ARG:NH1	2.34	0.42
1:B:387:LEU:CD1	1:B:387:LEU:C	2.93	0.42
1:A:261:VAL:O	1:A:265:LEU:HG	2.20	0.42
1:A:413:GLN:HG2	3:A:763:HOH:O	2.19	0.42
1:A:302:ASN:ND2	1:A:302:ASN:N	2.68	0.42
1:A:387:LEU:HD23	1:B:212:GLY:HA2	2.01	0.41
1:B:202:TRP:H	2:B:605:PO4:P	2.43	0.41
1:B:326:ILE:HG13	1:B:419:MET:HE1	2.02	0.41
1:A:307:PRO:HB3	1:A:358:TRP:CE3	2.56	0.41
1:B:232:GLU:HA	1:B:235:ASP:OD2	2.21	0.41
1:B:385:SER:HB3	1:B:387:LEU:HG	2.02	0.41
1:B:189:GLU:OE2	1:B:190:ASN:N	2.54	0.41
1:B:276:ARG:HE	2:B:605:PO4:P	2.44	0.41
1:B:377:GLU:OE2	1:B:378:MET:CA	2.69	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	237/255 (93%)	229 (97%)	8 (3%)	0	100	100
1	B	238/255 (93%)	229 (96%)	6 (2%)	3 (1%)	9	6
All	All	475/510 (93%)	458 (96%)	14 (3%)	3 (1%)	21	18

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	235	ASP
1	B	236	ARG
1	B	387	LEU

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	202/217 (93%)	197 (98%)	5 (2%)	42	48
1	B	203/217 (94%)	198 (98%)	5 (2%)	42	48
All	All	405/434 (93%)	395 (98%)	10 (2%)	42	48

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

Mol	Chain	Res	Type
1	A	235	ASP
1	A	281	LEU
1	A	302	ASN
1	A	338	ARG
1	A	391	VAL
1	B	211	ARG
1	B	238	LEU
1	B	281	LEU
1	B	377	GLU
1	B	387	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	279	GLN
1	A	284	GLN
1	A	288	HIS
1	A	302	ASN
1	A	305	HIS
1	A	394	HIS
1	B	190	ASN
1	B	218	GLN
1	B	279	GLN
1	B	284	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

8 ligands 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	PO4	B	604	-	4,4,4	1.70	1 (25%)	6,6,6	0.46	0
2	PO4	B	607	-	4,4,4	1.72	0	6,6,6	0.46	0
2	PO4	A	603	-	4,4,4	1.67	0	6,6,6	0.45	0
2	PO4	B	608	-	4,4,4	1.73	0	6,6,6	0.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PO4	B	605	-	4,4,4	1.92	3 (75%)	6,6,6	0.46	0
2	PO4	A	602	-	4,4,4	1.90	2 (50%)	6,6,6	0.46	0
2	PO4	A	601	-	4,4,4	1.73	0	6,6,6	0.46	0
2	PO4	B	606	-	4,4,4	1.71	0	6,6,6	0.45	0

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	605	PO4	P-O2	-2.28	1.48	1.54
2	A	602	PO4	P-O3	-2.21	1.48	1.54
2	B	605	PO4	P-O4	-2.10	1.48	1.54
2	A	602	PO4	P-O2	-2.08	1.48	1.54
2	B	605	PO4	P-O3	-2.06	1.48	1.54
2	B	604	PO4	P-O3	-2.05	1.48	1.54

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 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	605	PO4	3	0
2	A	602	PO4	3	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	239/255 (93%)	0.19	20 (8%) 17 18	18, 27, 69, 92	0
1	B	239/255 (93%)	0.45	34 (14%) 6 6	19, 30, 74, 100	1 (0%)
All	All	478/510 (93%)	0.32	54 (11%) 10 10	18, 28, 73, 100	1 (0%)

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	383	GLY	6.7
1	B	234	GLY	6.5
1	B	384	ALA	5.9
1	B	235	ASP	5.4
1	B	352	TRP	5.0
1	B	233	VAL	4.9
1	A	234	GLY	4.7
1	B	337	GLY	4.5
1	A	233	VAL	4.3
1	A	337	GLY	4.2
1	B	386	SER	4.0
1	B	381	VAL	4.0
1	A	425	GLY	4.0
1	B	336	SER	3.5
1	B	385	SER	3.5
1	A	427	SER	3.5
1	B	236	ARG	3.4
1	B	338	ARG	3.4
1	A	235	ASP	3.4
1	B	335	GLY	3.4
1	A	336	SER	3.2
1	B	382	GLY	3.1
1	A	338	ARG	3.1
1	B	380	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	377	GLU	3.0
1	B	387	LEU	2.9
1	B	250	MET	2.8
1	B	238	LEU	2.8
1	B	334	GLU	2.7
1	A	252	LEU	2.7
1	B	427	SER	2.7
1	B	231	SER	2.6
1	A	305	HIS	2.6
1	B	237	THR	2.6
1	B	354	GLN	2.6
1	B	232	GLU	2.6
1	A	303	SER	2.6
1	B	189	GLU	2.5
1	B	280[A]	TRP	2.5
1	A	304	GLY	2.5
1	A	422	GLN	2.4
1	A	426	GLU	2.4
1	A	401	LEU	2.4
1	B	399	HIS	2.3
1	A	352	TRP	2.3
1	B	303	SER	2.3
1	A	314	ASP	2.3
1	A	197	VAL	2.2
1	B	314	ASP	2.2
1	A	236	ARG	2.2
1	B	388	GLU	2.1
1	A	237	THR	2.0
1	B	424	PRO	2.0
1	B	304	GLY	2.0

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

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

6.3 Carbohydrates ⓘ

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($\text{\AA}^2$)	Q<0.9
2	PO4	B	607	5/5	0.76	0.14	93,98,99,100	0
2	PO4	B	606	5/5	0.80	0.17	82,84,84,85	0
2	PO4	A	603	5/5	0.83	0.15	78,80,81,83	0
2	PO4	B	608	5/5	0.89	0.13	97,97,98,98	0
2	PO4	B	604	5/5	0.94	0.12	50,53,54,55	0
2	PO4	A	601	5/5	0.96	0.09	38,44,45,46	0
2	PO4	B	605	5/5	0.98	0.19	7,37,38,38	5
2	PO4	A	602	5/5	0.98	0.14	1,28,28,32	5

6.5 Other polymers [i](#)

There are no such residues in this entry.