



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 03:46 PM UTC

PDB ID : 3JS2 / pdb_00003js2
Title : Crystal structure of minimal kinase domain of fibroblast growth factor receptor 1 in complex with 5-(2-thienyl)nicotinic acid
Authors : Bae, J.H.; Ravindranathan, K.P.; Mandiyan, V.; Ekkati, A.R.; Schlessinger, J.; Jorgensen, W.L.
Deposited on : 2009-09-09
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

<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

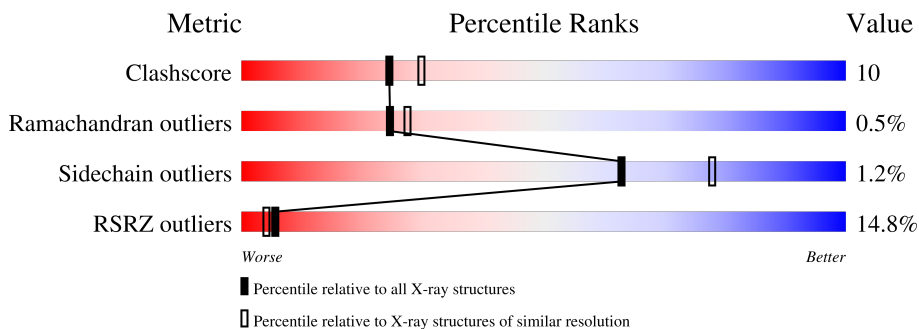
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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))
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (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 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	317	
1	B	317	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4796 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.

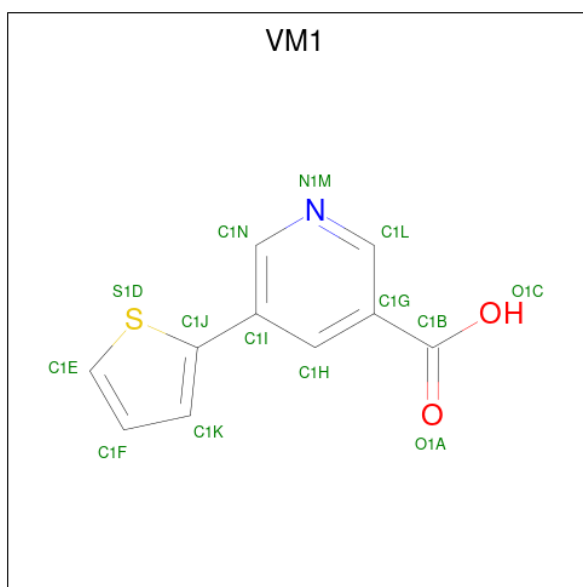
- Molecule 1 is a protein called Basic fibroblast growth factor receptor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	295	2316	1477	405	417	17	0	0	0
1	B	291	2300	1467	400	416	17	0	0	0

There are 22 discrepancies between the modelled and reference sequences:

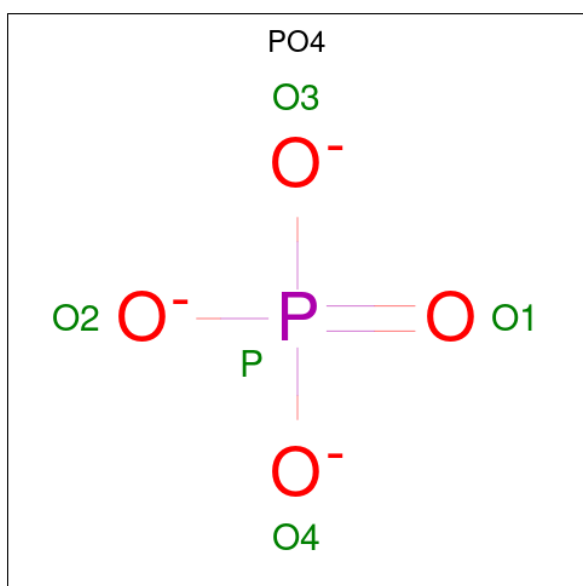
Chain	Residue	Modelled	Actual	Comment	Reference
A	449	MET	-	expression tag	UNP P11362
A	450	GLY	-	expression tag	UNP P11362
A	451	HIS	-	expression tag	UNP P11362
A	452	HIS	-	expression tag	UNP P11362
A	453	HIS	-	expression tag	UNP P11362
A	454	HIS	-	expression tag	UNP P11362
A	455	HIS	-	expression tag	UNP P11362
A	456	HIS	-	expression tag	UNP P11362
A	457	MET	-	expression tag	UNP P11362
A	488	ALA	CYS	engineered mutation	UNP P11362
A	584	SER	CYS	engineered mutation	UNP P11362
B	449	MET	-	expression tag	UNP P11362
B	450	GLY	-	expression tag	UNP P11362
B	451	HIS	-	expression tag	UNP P11362
B	452	HIS	-	expression tag	UNP P11362
B	453	HIS	-	expression tag	UNP P11362
B	454	HIS	-	expression tag	UNP P11362
B	455	HIS	-	expression tag	UNP P11362
B	456	HIS	-	expression tag	UNP P11362
B	457	MET	-	expression tag	UNP P11362
B	488	ALA	CYS	engineered mutation	UNP P11362
B	584	SER	CYS	engineered mutation	UNP P11362

- Molecule 2 is 5-(2-thienyl)nicotinic acid (CCD ID: VM1) (formula: C₁₀H₇NO₂S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	14	10	1	2	1	0	0
2	B	1	14	10	1	2	1	0	0

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



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

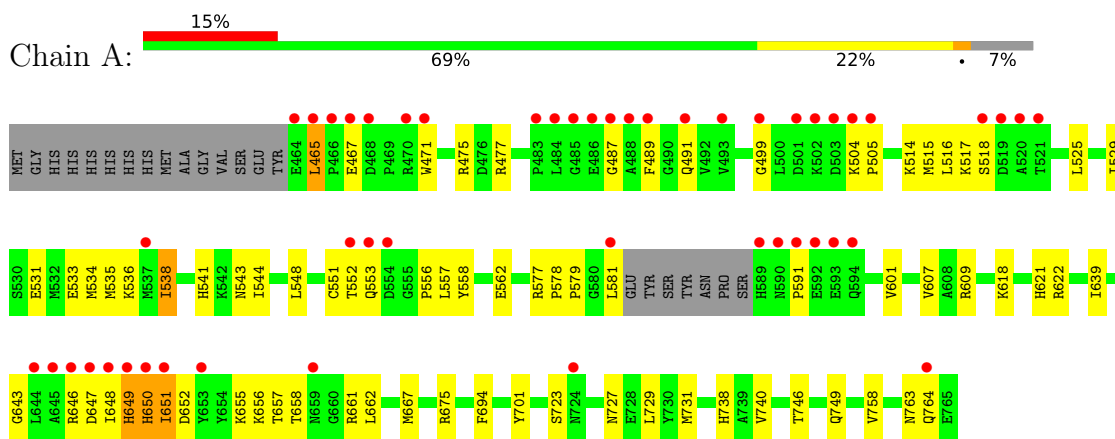
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	77	Total 77	O 77	0	0
4	B	65	Total 65	O 65	0	0

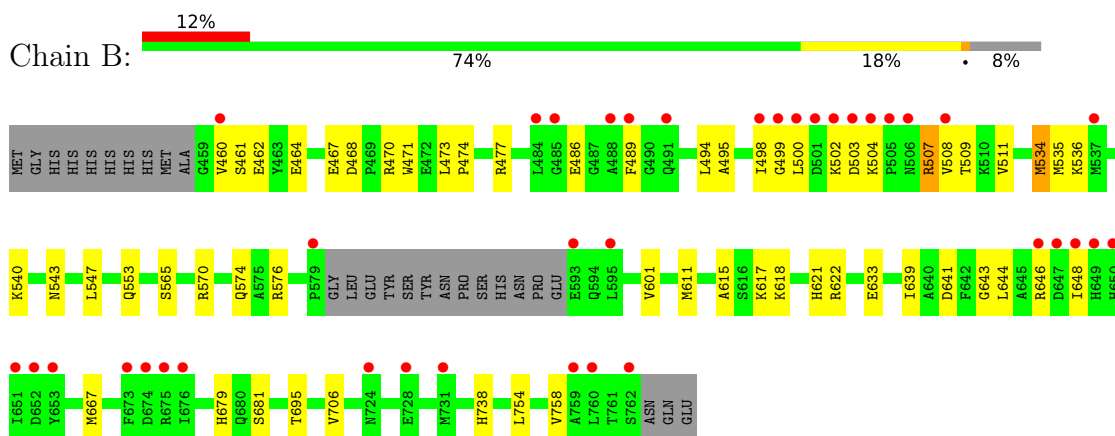
3 Residue-property plots i

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: Basic fibroblast growth factor receptor 1



- Molecule 1: Basic fibroblast growth factor receptor 1



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	207.80Å 58.30Å 66.25Å 90.00° 107.36° 90.00°	Depositor
Resolution (Å)	50.00 – 2.20 50.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.6 (50.00-2.20) 95.6 (50.00-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.39 (at 2.20Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.216 , 0.259 0.216 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	38.6	Xtrriage
Anisotropy	0.487	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 38.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.019 for -h-2*1,-k,l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4796	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.53% 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: VM1, 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	0.57	0/2365	0.98	10/3199 (0.3%)
1	B	0.55	0/2349	0.94	5/3176 (0.2%)
All	All	0.56	0/4714	0.96	15/6375 (0.2%)

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	650	HIS	N-CA-C	-8.97	102.89	113.21
1	B	695	THR	N-CA-C	-6.67	104.27	112.88
1	A	543	ASN	N-CA-C	6.38	119.78	112.57
1	B	667	MET	N-CA-C	5.88	119.10	109.76
1	A	701	TYR	CA-C-N	-5.57	114.19	119.76
1	A	701	TYR	C-N-CA	-5.57	114.19	119.76
1	A	723	SER	N-CA-C	-5.52	103.24	110.53
1	B	540	LYS	N-CA-C	5.37	118.43	110.48
1	A	465	LEU	CA-C-N	5.22	124.98	119.76
1	A	465	LEU	C-N-CA	5.22	124.98	119.76
1	A	763	ASN	N-CA-C	-5.22	106.67	112.57
1	B	543	ASN	N-CA-C	5.07	118.30	112.57
1	A	667	MET	N-CA-C	5.05	117.85	109.46
1	B	681	SER	N-CA-C	-5.04	105.88	112.23
1	A	538	ILE	N-CA-C	5.01	115.73	110.62

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	2316	0	2326	58	0
1	B	2300	0	2317	35	0
2	A	14	0	6	0	0
2	B	14	0	6	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	77	0	0	2	0
4	B	65	0	0	2	0
All	All	4796	0	4655	92	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 10.

All (92) 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:504:LYS:HB3	1:B:507:ARG:HB2	1.57	0.86
1:A:622:ARG:CZ	1:A:646:ARG:HG3	2.11	0.81
1:A:531:GLU:HG2	1:A:535:MET:HE2	1.64	0.80
1:B:601:VAL:HG12	1:B:758:VAL:HG22	1.64	0.79
1:B:500:LEU:HD11	1:B:511:VAL:HG11	1.65	0.78
1:A:487:GLY:HA2	1:A:658:THR:HG21	1.67	0.77
1:A:551:CYS:HB2	1:A:558:TYR:HB2	1.74	0.70
1:B:534:MET:HE3	1:B:643:GLY:HA2	1.74	0.68
1:A:525:LEU:O	1:A:529:ILE:HG13	1.94	0.67
1:A:471:TRP:CD1	1:A:536:LYS:HD3	2.32	0.65
1:B:601:VAL:HG12	1:B:758:VAL:CG2	2.25	0.65
1:A:649:HIS:C	1:A:651:ILE:H	2.04	0.63
1:B:644:LEU:HD23	1:B:646:ARG:HE	1.64	0.63
1:A:477:ARG:NE	1:A:477:ARG:HA	2.14	0.63
1:A:621:HIS:O	1:A:622:ARG:HB2	2.00	0.62
1:B:500:LEU:HD12	1:B:509:THR:HB	1.82	0.62
1:B:621:HIS:O	1:B:622:ARG:HB2	2.00	0.62
1:A:646:ARG:HD3	1:A:647:ASP:H	1.66	0.61
1:A:516:LEU:HD11	1:A:525:LEU:HD13	1.81	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:517:LYS:HG2	1:A:518:SER:H	1.66	0.60
1:A:487:GLY:C	1:A:489:PHE:H	2.09	0.59
1:A:649:HIS:HA	1:A:651:ILE:HG13	1.85	0.59
1:A:694:PHE:CZ	1:A:729:LEU:HD13	2.39	0.58
1:A:646:ARG:CD	1:A:647:ASP:H	2.17	0.58
1:A:475:ARG:NH2	1:A:556:PRO:O	2.34	0.57
1:A:646:ARG:HD3	1:A:647:ASP:N	2.18	0.57
1:B:565:SER:OG	1:B:633:GLU:HG2	2.06	0.56
1:A:646:ARG:CG	1:A:647:ASP:H	2.18	0.55
1:A:505:PRO:HD2	4:A:117:HOH:O	2.07	0.54
1:B:570:ARG:O	1:B:574:GLN:HG3	2.08	0.54
1:A:607:VAL:HG13	1:A:639:ILE:HD11	1.91	0.53
1:B:502:LYS:HG2	1:B:503:ASP:OD2	2.08	0.53
1:A:577:ARG:O	1:A:591:PRO:HG3	2.08	0.52
1:A:764:GLN:O	1:B:679:HIS:HB2	2.08	0.52
1:A:738:HIS:HD2	1:A:740:VAL:H	1.55	0.52
1:A:467:GLU:HG2	1:A:553:GLN:CD	2.35	0.52
1:A:491:GLN:HE21	1:A:515:MET:HG3	1.74	0.51
1:B:611:MET:SD	1:B:639:ILE:HD13	2.50	0.51
1:B:502:LYS:O	1:B:503:ASP:HB2	2.11	0.51
1:A:548:LEU:HD21	1:A:562:GLU:HG3	1.93	0.51
1:A:647:ASP:C	1:A:649:HIS:H	2.19	0.50
1:A:477:ARG:NE	1:A:477:ARG:CA	2.75	0.49
1:A:656:LYS:HD3	1:A:662:LEU:CD2	2.43	0.49
1:B:468:ASP:OD1	1:B:470:ARG:HG2	2.12	0.49
1:B:461:SER:HA	1:B:464:GLU:O	2.12	0.49
1:B:489:PHE:HB3	4:B:104:HOH:O	2.12	0.49
1:A:534:MET:HG2	1:A:643:GLY:HA2	1.96	0.48
1:A:552:THR:HG22	1:A:557:LEU:CD1	2.43	0.48
1:A:581:LEU:N	1:A:581:LEU:HD22	2.29	0.48
1:B:535:MET:HE3	1:B:547:LEU:HD13	1.96	0.48
1:A:649:HIS:C	1:A:651:ILE:N	2.72	0.47
1:A:648:ILE:C	1:A:650:HIS:H	2.23	0.47
1:B:615:ALA:HA	1:B:679:HIS:CE1	2.49	0.47
1:A:534:MET:HG2	1:A:643:GLY:CA	2.45	0.47
1:A:499:GLY:HA2	1:A:504:LYS:O	2.14	0.46
1:A:534:MET:HG3	1:A:538:ILE:HD12	1.98	0.46
1:A:657:THR:HG23	1:A:661:ARG:O	2.16	0.46
1:A:727:ASN:O	1:A:731:MET:HG2	2.15	0.46
1:A:622:ARG:NH1	1:A:646:ARG:HG3	2.31	0.46
1:B:502:LYS:HB3	1:B:502:LYS:HE2	1.76	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:754:LEU:O	1:B:758:VAL:HG23	2.17	0.45
1:A:487:GLY:C	1:A:489:PHE:N	2.74	0.45
1:A:529:ILE:O	1:A:533:GLU:HG2	2.16	0.45
1:A:746:THR:HG1	1:A:749:GLN:HG3	1.82	0.44
1:A:534:MET:HE3	1:A:643:GLY:HA2	2.00	0.44
1:B:494:LEU:HD12	1:B:495:ALA:H	1.82	0.44
1:A:622:ARG:NE	1:A:646:ARG:HG3	2.32	0.44
1:B:473:LEU:HD12	1:B:474:PRO:HD2	2.01	0.42
1:A:465:LEU:N	1:A:465:LEU:HD12	2.34	0.42
1:A:517:LYS:HG2	1:A:518:SER:N	2.32	0.42
1:A:601:VAL:HG12	1:A:758:VAL:CG2	2.50	0.42
1:B:601:VAL:CG1	1:B:758:VAL:HG22	2.44	0.42
1:B:498:ILE:HG12	1:B:508:VAL:HG12	2.02	0.42
1:B:576:ARG:HG3	1:B:576:ARG:HH11	1.84	0.42
1:A:514:LYS:HE2	1:A:514:LYS:HB3	1.96	0.42
1:B:502:LYS:O	1:B:503:ASP:CB	2.68	0.42
1:A:578:PRO:HA	1:A:579:PRO:HD3	1.92	0.41
1:B:471:TRP:CD1	1:B:536:LYS:HE2	2.55	0.41
1:A:541:HIS:HB3	1:A:544:ILE:HG12	2.02	0.41
1:B:467:GLU:HG2	1:B:553:GLN:CD	2.46	0.41
1:A:579:PRO:O	1:A:581:LEU:HD22	2.20	0.41
1:B:477:ARG:NH1	1:B:499:GLY:O	2.54	0.41
1:B:641:ASP:HB3	1:B:646:ARG:NH2	2.35	0.41
1:B:460:VAL:C	1:B:462:GLU:H	2.27	0.41
1:B:706:VAL:HG23	4:B:56:HOH:O	2.21	0.41
1:A:601:VAL:HG12	1:A:758:VAL:HG22	2.03	0.40
1:A:609:ARG:NH1	4:A:48:HOH:O	2.54	0.40
1:A:651:ILE:HG22	1:A:652:ASP:N	2.36	0.40
1:B:617:LYS:O	1:B:618:LYS:HB2	2.20	0.40
1:A:618:LYS:N	1:A:618:LYS:HD2	2.37	0.40
1:A:646:ARG:CG	1:A:647:ASP:N	2.84	0.40
1:B:500:LEU:HD12	1:B:509:THR:CB	2.51	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	291/317 (92%)	278 (96%)	11 (4%)	2 (1%)	18	19
1	B	287/317 (90%)	273 (95%)	13 (4%)	1 (0%)	36	42
All	All	578/634 (91%)	551 (95%)	24 (4%)	3 (0%)	24	27

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	651	ILE
1	A	649	HIS
1	B	648	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	247/277 (89%)	245 (99%)	2 (1%)	73	85
1	B	248/277 (90%)	244 (98%)	4 (2%)	55	71
All	All	495/554 (89%)	489 (99%)	6 (1%)	63	78

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	655	LYS
1	A	675	ARG
1	B	486	GLU
1	B	507	ARG
1	B	534	MET
1	B	738	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	543	ASN
1	A	738	HIS
1	A	743	GLN
1	B	594	GLN
1	B	679	HIS
1	B	680	GLN
1	B	717	HIS

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](#)

4 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	$\# Z > 2$
3	PO4	B	2	-	4,4,4	1.85	2 (50%)	6,6,6	0.45	0
2	VM1	A	801	-	15,15,15	1.37	1 (6%)	20,20,20	1.46	3 (15%)
2	VM1	B	801	-	15,15,15	1.40	1 (6%)	20,20,20	1.46	2 (10%)
3	PO4	A	1	-	4,4,4	1.70	0	6,6,6	0.50	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
2	VM1	A	801	-	-	0/8/8/8	0/2/2/2
2	VM1	B	801	-	-	0/8/8/8	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	VM1	C1I-C1J	-4.10	1.39	1.47
2	A	801	VM1	C1I-C1J	-3.94	1.39	1.47
3	B	2	PO4	P-O4	-2.16	1.48	1.54
3	B	2	PO4	P-O2	-2.15	1.48	1.54

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	801	VM1	C1N-N1M-C1L	3.15	121.79	117.51
2	A	801	VM1	C1N-N1M-C1L	3.12	121.74	117.51
2	A	801	VM1	C1F-C1E-S1D	-2.85	106.04	113.02
2	B	801	VM1	C1F-C1E-S1D	-2.67	106.49	113.02
2	A	801	VM1	C1G-C1L-N1M	-2.06	120.44	123.50

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	295/317 (93%)	0.83	49 (16%) 4 3	23, 41, 83, 111	0
1	B	291/317 (91%)	0.86	38 (13%) 7 5	27, 44, 86, 108	0
All	All	586/634 (92%)	0.85	87 (14%) 5 4	23, 42, 84, 111	0

All (87) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	489	PHE	7.9
1	A	764	GLN	6.9
1	A	648	ILE	6.7
1	B	648	ILE	6.6
1	A	503	ASP	6.5
1	A	649	HIS	5.5
1	A	464	GLU	5.1
1	A	485	GLY	4.9
1	B	500	LEU	4.5
1	A	487	GLY	4.5
1	B	460	VAL	4.4
1	B	485	GLY	4.1
1	B	488	ALA	4.0
1	B	649	HIS	3.9
1	A	647	ASP	3.8
1	A	502	LYS	3.8
1	A	465	LEU	3.8
1	A	650	HIS	3.8
1	A	501	ASP	3.8
1	B	674	ASP	3.8
1	A	489	PHE	3.7
1	B	759	ALA	3.6
1	A	491	GLN	3.6
1	B	498	ILE	3.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	519	ASP	3.5
1	A	488	ALA	3.4
1	A	467	GLU	3.4
1	B	579	PRO	3.4
1	A	645	ALA	3.3
1	A	518	SER	3.3
1	A	537	MET	3.3
1	B	505	PRO	3.2
1	A	644	LEU	3.2
1	B	731	MET	3.2
1	A	466	PRO	3.1
1	A	646	ARG	3.1
1	B	650	HIS	3.1
1	B	593	GLU	3.1
1	A	724	ASN	3.1
1	A	653	TYR	3.1
1	B	502	LYS	3.1
1	B	647	ASP	3.1
1	B	651	ILE	3.0
1	B	653	TYR	3.0
1	B	501	ASP	3.0
1	A	651	ILE	3.0
1	A	470	ARG	2.9
1	B	503	ASP	2.9
1	B	673	PHE	2.8
1	A	591	PRO	2.8
1	A	581	LEU	2.8
1	A	505	PRO	2.7
1	A	504	LYS	2.7
1	A	520	ALA	2.7
1	A	594	GLN	2.6
1	B	499	GLY	2.6
1	A	589	HIS	2.6
1	B	760	LEU	2.6
1	B	504	LYS	2.6
1	A	592	GLU	2.6
1	A	483	PRO	2.6
1	B	652	ASP	2.6
1	B	724	ASN	2.5
1	A	486	GLU	2.4
1	A	521	THR	2.4
1	A	593	GLU	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	762	SER	2.4
1	B	508	VAL	2.4
1	B	646	ARG	2.4
1	B	537	MET	2.3
1	A	493	VAL	2.3
1	B	675	ARG	2.3
1	A	484	LEU	2.2
1	A	552	THR	2.2
1	A	554	ASP	2.2
1	B	676	ILE	2.2
1	B	728	GLU	2.2
1	A	499	GLY	2.2
1	B	484	LEU	2.1
1	B	506	ASN	2.1
1	A	468	ASP	2.1
1	A	659	ASN	2.1
1	A	471	TRP	2.1
1	A	553	GLN	2.0
1	B	491	GLN	2.0
1	A	590	ASN	2.0
1	B	595	LEU	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 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(Å ²)	Q<0.9
2	VM1	B	801	14/14	0.87	0.15	70,75,77,78	0
2	VM1	A	801	14/14	0.89	0.17	59,63,69,69	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	PO4	A	1	5/5	0.92	0.14	62,62,64,65	0
3	PO4	B	2	5/5	0.96	0.09	52,52,54,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.