



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 27, 2017 – 06:04 PM EDT

PDB ID : 5GMP
Title : Crystal structure of EGFR 696-1022 T790M in complex with XTF-262
Authors : Yan, X.E.; Yun, C.H.
Deposited on : unknown
Resolution : 2.80 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20030345

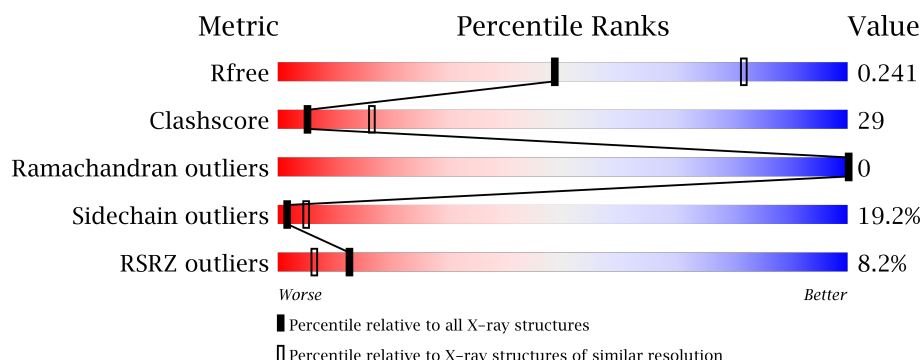
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	100719	2583 (2.80-2.80)
Clashscore	112137	3033 (2.80-2.80)
Ramachandran outliers	110173	2983 (2.80-2.80)
Sidechain outliers	110143	2985 (2.80-2.80)
RSRZ outliers	101464	2610 (2.80-2.80)

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	331	<div> <div>8%</div> <div>49%</div> <div>35%</div> <div>8%</div> <div>8%</div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2437 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.

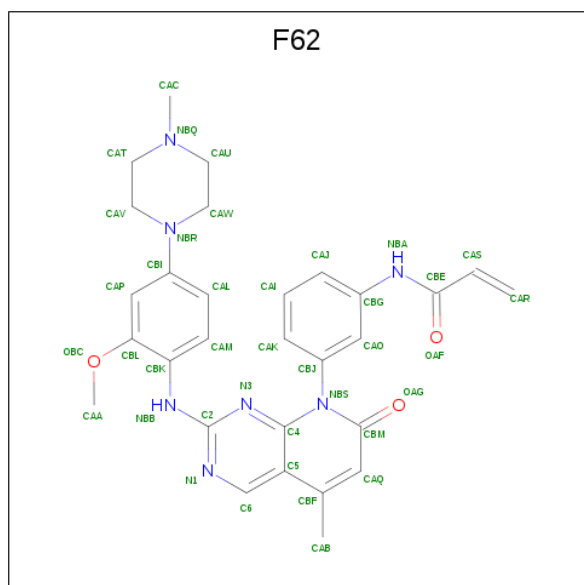
- Molecule 1 is a protein called Epidermal growth factor receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	305	2367	1522	397	429	19	0	1	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	692	GLY	-	expression tag	UNP P00533
A	693	ALA	-	expression tag	UNP P00533
A	694	MET	-	expression tag	UNP P00533
A	695	GLY	-	expression tag	UNP P00533
A	790	MET	THR	engineered mutation	UNP P00533

- Molecule 2 is N-[3-[2-[[2-methoxy-4-(4-methylpiperazin-1-yl)phenyl]amino]-5-methyl-7-oxidanylidene-pyrido[2,3-d]pyrimidin-8-yl]phenyl]prop-2-enamide (three-letter code: F62) (formula: C₂₉H₃₁N₇O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			39	29	7	3		

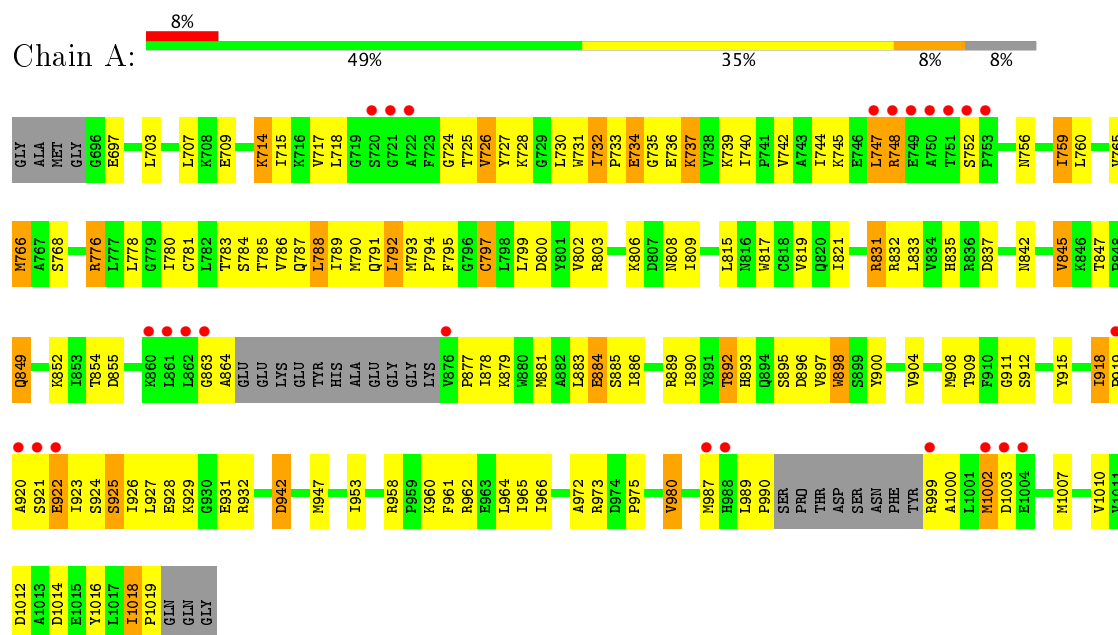
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	31	Total	O	0	0
			31	31		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Epidermal growth factor receptor



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 3	Depositor
Cell constants a, b, c, α , β , γ	145.34Å 145.34Å 145.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.96 – 2.80 45.96 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.4 (45.96-2.80) 99.5 (45.96-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.06 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.8.4 _1496	Depositor
R, R_{free}	0.212 , 0.241 0.212 , 0.241	Depositor DCC
R_{free} test set	621 reflections (4.88%)	DCC
Wilson B-factor (Å ²)	48.9	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 60.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.034 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	2437	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.27% 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: F62

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	0.55	0/2419	0.57	1/3283 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	797	CYS	N-CA-CB	-5.52	100.66	110.60

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	2367	0	2352	138	0
2	A	39	0	0	2	0
3	A	31	0	0	2	0
All	All	2437	0	2352	140	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 29.

All (140) 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:715:ILE:HG21	1:A:1003:ASP:CB	1.71	1.21
1:A:715:ILE:HD13	1:A:1003:ASP:CB	1.77	1.13
1:A:795:PHE:HB2	1:A:845:VAL:HG22	1.28	1.10
1:A:759:ILE:HD11	1:A:788:LEU:HD22	1.32	1.06
1:A:734:GLU:HA	1:A:734:GLU:OE2	1.53	1.05
1:A:780:ILE:CD1	1:A:788:LEU:HD12	1.88	1.04
1:A:780:ILE:HD13	1:A:788:LEU:HD12	1.40	0.98
1:A:877:PRO:O	1:A:881:MET:HG3	1.64	0.97
1:A:759:ILE:CD1	1:A:788:LEU:HD22	1.96	0.95
1:A:842:ASN:O	1:A:854:THR:HG22	1.66	0.94
1:A:739:LYS:HD2	1:A:1007:MET:CB	1.97	0.94
1:A:765:VAL:HG13	1:A:833:LEU:HD21	1.51	0.92
1:A:780:ILE:CD1	1:A:788:LEU:CD1	2.47	0.91
1:A:765:VAL:CG1	1:A:833:LEU:HD21	2.02	0.90
1:A:831:ARG:O	1:A:832:ARG:HG3	1.79	0.83
1:A:747:LEU:HD22	1:A:747:LEU:N	1.94	0.81
1:A:792:LEU:O	1:A:794:PRO:HD3	1.80	0.81
1:A:737:LYS:CG	1:A:737:LYS:O	2.30	0.79
1:A:795:PHE:HB2	1:A:845:VAL:CG2	2.10	0.78
1:A:734:GLU:CA	1:A:734:GLU:OE2	2.30	0.78
1:A:863:GLY:O	1:A:864:ALA:CB	2.30	0.77
1:A:835:HIS:CE1	1:A:837:ASP:O	2.38	0.76
1:A:715:ILE:CG2	1:A:1003:ASP:CB	2.61	0.74
1:A:1018:ILE:HD12	1:A:1019:PRO:HD2	1.71	0.72
1:A:799:LEU:O	1:A:803:ARG:HG3	1.90	0.71
1:A:926:ILE:HG22	1:A:931:GLU:HG2	1.72	0.70
2:A:1101:F62:OAF	2:A:1101:F62:CAJ	2.39	0.70
1:A:878:ILE:HG21	1:A:920:ALA:CB	2.20	0.69
1:A:747:LEU:N	1:A:747:LEU:CD2	2.56	0.68
1:A:883:LEU:HD13	1:A:927:LEU:HB2	1.76	0.68
1:A:765:VAL:HG13	1:A:833:LEU:CD2	2.22	0.68
1:A:863:GLY:O	1:A:864:ALA:HB2	1.95	0.67
1:A:1018:ILE:HD12	3:A:1229:HOH:O	1.95	0.66
1:A:737:LYS:HG3	1:A:737:LYS:O	1.95	0.66
2:A:1101:F62:N3	2:A:1101:F62:CAM	2.54	0.65
1:A:999:ARG:O	1:A:1000:ALA:HB3	1.96	0.65
1:A:795:PHE:CB	1:A:845:VAL:HG22	2.18	0.65
1:A:831:ARG:O	1:A:832:ARG:CG	2.43	0.65
1:A:878:ILE:HG21	1:A:920:ALA:HB1	1.78	0.64
1:A:961:PHE:O	1:A:965:ILE:HG13	1.98	0.64
1:A:780:ILE:CD1	1:A:788:LEU:HD11	2.27	0.64
1:A:926:ILE:CG2	1:A:931:GLU:HG2	2.27	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:904:VAL:HG12	1:A:947:MET:HE2	1.83	0.61
1:A:831:ARG:O	1:A:832:ARG:CB	2.49	0.60
1:A:747:LEU:H	1:A:747:LEU:CD2	2.14	0.60
1:A:731:TRP:HZ3	1:A:778:LEU:HD22	1.67	0.59
1:A:759:ILE:HD12	1:A:759:ILE:O	2.01	0.59
1:A:780:ILE:HD11	1:A:788:LEU:CD1	2.31	0.59
1:A:980:VAL:CG2	1:A:980:VAL:O	2.51	0.59
1:A:707:LEU:HD12	1:A:789:ILE:HD13	1.85	0.59
1:A:931:GLU:HG3	1:A:932:ARG:N	2.18	0.59
1:A:793:MET:HE2	1:A:852:LYS:HB2	1.84	0.58
1:A:919:PRO:O	1:A:922:GLU:HB2	2.03	0.58
1:A:765:VAL:HG11	1:A:833:LEU:HD21	1.84	0.58
1:A:879:LYS:HG2	1:A:915:TYR:HD2	1.68	0.58
1:A:780:ILE:HD11	1:A:788:LEU:HD11	1.86	0.57
1:A:724:GLY:HA2	1:A:748:ARG:H	1.69	0.57
1:A:759:ILE:CD1	1:A:788:LEU:CD2	2.76	0.57
1:A:845:VAL:O	1:A:845:VAL:HG22	2.03	0.57
1:A:879:LYS:HG2	1:A:915:TYR:CD2	2.41	0.56
1:A:715:ILE:CD1	1:A:1003:ASP:CB	2.69	0.56
1:A:739:LYS:CD	1:A:1007:MET:CB	2.78	0.55
1:A:878:ILE:HG21	1:A:920:ALA:HB2	1.87	0.55
1:A:898:TRP:CZ2	1:A:927:LEU:HD13	2.42	0.55
1:A:756:ASN:O	1:A:759:ILE:HG22	2.06	0.55
1:A:776:ARG:HH11	1:A:776:ARG:HB3	1.72	0.54
1:A:737:LYS:HG2	1:A:737:LYS:O	2.08	0.54
1:A:747:LEU:HD22	1:A:747:LEU:H	1.73	0.53
1:A:776:ARG:NE	1:A:1014:ASP:OD1	2.40	0.53
1:A:747:LEU:O	1:A:785:THR:HG21	2.09	0.53
1:A:890:ILE:O	1:A:890:ILE:HG22	2.09	0.52
1:A:893:HIS:O	1:A:896:ASP:HB2	2.09	0.52
1:A:920:ALA:HA	1:A:923:ILE:HG13	1.91	0.52
1:A:733:PRO:O	1:A:736:GLU:CG	2.59	0.51
1:A:728:LYS:NZ	1:A:1002:MET:HB2	2.25	0.50
1:A:1002:MET:SD	1:A:1002:MET:N	2.84	0.50
1:A:1018:ILE:O	1:A:1019:PRO:O	2.30	0.50
1:A:717:VAL:HG12	1:A:717:VAL:O	2.12	0.50
1:A:736:GLU:OE2	1:A:1016:TYR:OH	2.30	0.50
1:A:791:GLN:NE2	1:A:1012:ASP:OD2	2.44	0.49
1:A:835:HIS:HE1	1:A:837:ASP:O	1.90	0.49
1:A:999:ARG:O	1:A:1000:ALA:CB	2.61	0.49
1:A:845:VAL:O	1:A:845:VAL:CG2	2.59	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:731:TRP:CZ3	1:A:778:LEU:HD22	2.47	0.49
1:A:925:SER:O	1:A:929:LYS:N	2.42	0.49
1:A:714:LYS:HD2	1:A:727:TYR:CG	2.48	0.49
1:A:759:ILE:CG2	1:A:760:LEU:N	2.75	0.49
1:A:803:ARG:HG2	1:A:911:GLY:HA3	1.94	0.49
1:A:815:LEU:O	1:A:819:VAL:HG23	2.13	0.49
1:A:718:LEU:HD21	1:A:728:LYS:HB2	1.95	0.48
1:A:898:TRP:CD1	1:A:898:TRP:C	2.86	0.48
1:A:1002:MET:O	1:A:1003:ASP:CB	2.61	0.48
1:A:709:GLU:OE1	1:A:783:THR:HG21	2.13	0.48
1:A:863:GLY:O	1:A:864:ALA:HB3	2.11	0.48
1:A:884:GLU:OE2	1:A:958:ARG:CZ	2.61	0.48
1:A:972:ALA:O	1:A:975:PRO:HD3	2.14	0.47
1:A:878:ILE:HD11	1:A:886:ILE:HD13	1.96	0.47
1:A:766:MET:HE2	1:A:790:MET:HG2	1.95	0.47
1:A:733:PRO:HB2	1:A:736:GLU:HG3	1.96	0.47
1:A:797:CYS:HB3	1:A:800:ASP:HB2	1.97	0.47
1:A:831:ARG:C	1:A:832:ARG:CG	2.79	0.46
1:A:714:LYS:HD2	1:A:727:TYR:CD2	2.50	0.46
1:A:733:PRO:O	1:A:736:GLU:HG2	2.15	0.46
1:A:817:TRP:O	1:A:821:ILE:HD12	2.14	0.46
1:A:802:VAL:HA	1:A:809:ILE:CD1	2.44	0.46
1:A:926:ILE:HG22	1:A:931:GLU:CG	2.42	0.46
1:A:739:LYS:O	1:A:1010:VAL:HA	2.17	0.45
1:A:734:GLU:HB3	1:A:735:GLY:H	1.41	0.45
1:A:897:VAL:O	1:A:900:TYR:HB3	2.16	0.45
1:A:1018:ILE:CD1	3:A:1229:HOH:O	2.58	0.45
1:A:733:PRO:O	1:A:736:GLU:HG3	2.17	0.45
1:A:759:ILE:HA	1:A:759:ILE:HD13	1.77	0.45
1:A:881:MET:HE3	1:A:885:SER:HB3	1.98	0.44
1:A:740:ILE:HG22	1:A:742:VAL:HG13	1.99	0.44
1:A:898:TRP:CH2	1:A:927:LEU:HD13	2.52	0.44
1:A:736:GLU:HG2	1:A:736:GLU:H	1.52	0.44
1:A:877:PRO:O	1:A:881:MET:CG	2.52	0.44
1:A:781:CYS:HB3	1:A:787:GLN:HB2	1.99	0.44
1:A:908:MET:HG3	1:A:947:MET:HE1	2.00	0.44
1:A:759:ILE:HD12	1:A:788:LEU:CD2	2.47	0.43
1:A:980:VAL:HG22	1:A:980:VAL:O	2.19	0.43
1:A:1018:ILE:HA	1:A:1018:ILE:HD13	1.74	0.43
1:A:732:ILE:HD13	1:A:739:LYS:HG2	2.01	0.43
1:A:926:ILE:CG2	1:A:931:GLU:CG	2.94	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:961:PHE:HA	1:A:964:LEU:HD12	2.01	0.43
1:A:926:ILE:HG22	1:A:931:GLU:HB3	2.02	0.42
1:A:942:ASP:OD2	1:A:942:ASP:N	2.51	0.42
1:A:847:THR:OG1	1:A:849:GLN:HG2	2.20	0.42
1:A:726:VAL:HA	1:A:744:ILE:O	2.18	0.41
1:A:892:THR:OG1	1:A:893:HIS:N	2.53	0.41
1:A:922:GLU:OE1	1:A:922:GLU:HA	2.20	0.41
1:A:918:ILE:CD1	1:A:926:ILE:CD1	2.98	0.41
1:A:728:LYS:HZ2	1:A:1002:MET:HB2	1.86	0.41
1:A:884:GLU:H	1:A:884:GLU:HG3	1.26	0.41
1:A:831:ARG:HD2	1:A:831:ARG:HA	1.40	0.41
1:A:795:PHE:CB	1:A:845:VAL:CG2	2.92	0.40
1:A:776:ARG:HH11	1:A:776:ARG:CB	2.34	0.40
1:A:780:ILE:HD12	1:A:788:LEU:CD1	2.43	0.40
1:A:989:LEU:O	1:A:990:PRO:C	2.58	0.40
1:A:909:THR:HB	1:A:912:SER:HB2	2.03	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	300/331 (91%)	292 (97%)	8 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	251/288 (87%)	203 (81%)	48 (19%)	2 5

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	697	GLU
1	A	703	LEU
1	A	714	LYS
1	A	725	THR
1	A	726	VAL
1	A	730	LEU
1	A	732	ILE
1	A	734	GLU
1	A	737	LYS
1	A	745	LYS
1	A	747	LEU
1	A	748	ARG
1	A	752	SER
1	A	759	ILE
1	A	766	MET
1	A	768	SER
1	A	776	ARG
1	A	784	SER
1	A	786	VAL
1	A	788	LEU
1	A	792	LEU
1	A	806	LYS
1	A	808	ASN
1	A	831	ARG
1	A	845	VAL
1	A	849	GLN
1	A	855	ASP
1	A	884	GLU
1	A	889	ARG
1	A	892	THR
1	A	895	SER
1	A	898	TRP
1	A	918	ILE
1	A	921	SER
1	A	922	GLU

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Mol	Chain	Res	Type
1	A	924	SER
1	A	925	SER
1	A	928	GLU
1	A	942	ASP
1	A	953	ILE
1	A	960	LYS
1	A	962	ARG
1	A	966	ILE
1	A	973	ARG
1	A	980	VAL
1	A	987	MET
1	A	1002	MET
1	A	1018	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	771	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

1 ligand is 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	F62	A	1101	1	41,43,43	2.38	12 (29%)	49,61,61	3.02	13 (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	F62	A	1101	1	-	2/20/30/30	0/5/5/5

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1101	F62	CBJ-NBS	-9.20	1.32	1.46
2	A	1101	F62	CAB-CBF	-6.51	1.38	1.51
2	A	1101	F62	CBG-NBA	-4.51	1.32	1.41
2	A	1101	F62	C6-C5	-3.18	1.38	1.42
2	A	1101	F62	CBK-NBB	-3.04	1.31	1.39
2	A	1101	F62	CBM-NBS	-2.50	1.33	1.37
2	A	1101	F62	C5-C4	-2.44	1.38	1.41
2	A	1101	F62	C2-NBB	-2.13	1.32	1.36
2	A	1101	F62	CBI-NBR	-2.06	1.33	1.38
2	A	1101	F62	CAS-CBE	2.09	1.52	1.48
2	A	1101	F62	C6-N1	2.23	1.37	1.32
2	A	1101	F62	CAR-CAS	4.25	1.51	1.30

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	F62	CAR-CAS-CBE	-14.36	108.75	122.37
2	A	1101	F62	CBG-NBA-CBE	-7.67	116.56	128.27
2	A	1101	F62	N1-C2-N3	-5.48	121.18	126.65
2	A	1101	F62	CAA-OBC-CBL	-4.91	110.47	117.54
2	A	1101	F62	CAP-CBI-NBR	-2.97	118.03	121.34
2	A	1101	F62	CBK-NBB-C2	-2.71	120.27	129.51
2	A	1101	F62	C5-C4-N3	-2.57	120.40	123.64
2	A	1101	F62	CAO-CBJ-NBS	-2.18	115.43	119.24
2	A	1101	F62	N3-C4-NBS	2.10	120.15	114.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	F62	CBJ-CAO-CBG	2.71	121.42	118.50
2	A	1101	F62	C6-N1-C2	2.86	120.54	115.89
2	A	1101	F62	C2-N3-C4	4.80	120.58	115.11
2	A	1101	F62	CAV-NBR-CAW	4.94	122.05	111.57

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1101	F62	OAF-CBE-CAS-CAR
2	A	1101	F62	CAR-CAS-CBE-NBA

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1101	F62	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	305/331 (92%)	0.36	25 (8%) 12 6	12, 38, 102, 149	1 (0%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1003	ASP	7.8
1	A	750	ALA	7.2
1	A	748	ARG	5.0
1	A	922	GLU	4.5
1	A	753	PRO	4.2
1	A	751	THR	3.9
1	A	720	SER	3.2
1	A	862	LEU	3.0
1	A	1004	GLU	2.9
1	A	747	LEU	2.9
1	A	920	ALA	2.6
1	A	987	MET	2.5
1	A	921	SER	2.5
1	A	919	PRO	2.4
1	A	752	SER	2.4
1	A	721	GLY	2.4
1	A	1002	MET	2.2
1	A	860	LYS	2.2
1	A	749	GLU	2.2
1	A	863	GLY	2.2
1	A	861	LEU	2.1
1	A	876	VAL	2.1
1	A	999	ARG	2.1
1	A	722	ALA	2.0
1	A	988	HIS	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(\AA^2)	Q<0.9
2	F62	A	1101	39/39	0.94	0.27	1.44	26,43,70,77	0

6.5 Other polymers [i](#)

There are no such residues in this entry.