



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:20 PM GMT

PDB ID : 3WV5
Title : Complex structure of VinN with 3-methylaspartate
Authors : Miyanaga, A.; Cieslak, J.; Shinohara, Y.; Kudo, F.; Eguchi, T.
Deposited on : 2014-05-15
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

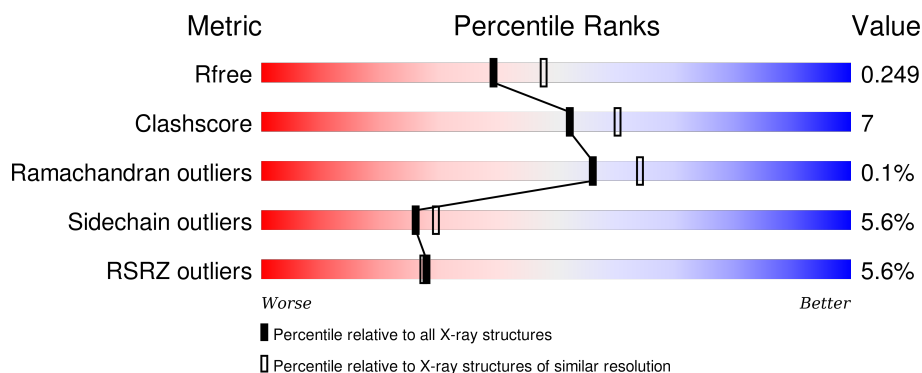
1 Overall quality at a glance

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	442	<div> <div>5%</div> <div> <div></div> <div>76%</div> <div>11%</div> <div>•</div> <div>12%</div> </div> </div>
1	B	442	<div> <div>5%</div> <div> <div></div> <div>67%</div> <div>12%</div> <div>•</div> <div>19%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5913 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 Non-ribosomal peptide synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	387	Total	C	N	O	S	0	0	0
			2948	1874	508	551	15			
1	B	359	Total	C	N	O	S	0	0	0
			2742	1744	473	510	15			

There are 126 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	MET	-	EXPRESSION TAG	UNP Q76KY2
A	-14	ASN	-	EXPRESSION TAG	UNP Q76KY2
A	-13	HIS	-	EXPRESSION TAG	UNP Q76KY2
A	-12	LYS	-	EXPRESSION TAG	UNP Q76KY2
A	-11	VAL	-	EXPRESSION TAG	UNP Q76KY2
A	-10	HIS	-	EXPRESSION TAG	UNP Q76KY2
A	-9	HIS	-	EXPRESSION TAG	UNP Q76KY2
A	-8	HIS	-	EXPRESSION TAG	UNP Q76KY2
A	-7	HIS	-	EXPRESSION TAG	UNP Q76KY2
A	-6	HIS	-	EXPRESSION TAG	UNP Q76KY2
A	-5	HIS	-	EXPRESSION TAG	UNP Q76KY2
A	-4	ILE	-	EXPRESSION TAG	UNP Q76KY2
A	-3	GLU	-	EXPRESSION TAG	UNP Q76KY2
A	-2	GLY	-	EXPRESSION TAG	UNP Q76KY2
A	-1	ARG	-	EXPRESSION TAG	UNP Q76KY2
A	0	HIS	-	EXPRESSION TAG	UNP Q76KY2
A	1	MET	-	EXPRESSION TAG	UNP Q76KY2
A	2	TYR	-	EXPRESSION TAG	UNP Q76KY2
A	3	SER	-	EXPRESSION TAG	UNP Q76KY2
A	4	PRO	-	EXPRESSION TAG	UNP Q76KY2
A	5	ASP	-	EXPRESSION TAG	UNP Q76KY2
A	6	ARG	-	EXPRESSION TAG	UNP Q76KY2
A	7	ARG	-	EXPRESSION TAG	UNP Q76KY2
A	8	ALA	-	EXPRESSION TAG	UNP Q76KY2
A	9	ALA	-	EXPRESSION TAG	UNP Q76KY2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	10	LEU	-	EXPRESSION TAG	UNP Q76KY2
A	11	ASN	-	EXPRESSION TAG	UNP Q76KY2
A	12	SER	-	EXPRESSION TAG	UNP Q76KY2
A	13	VAL	-	EXPRESSION TAG	UNP Q76KY2
A	14	ALA	-	EXPRESSION TAG	UNP Q76KY2
A	15	ASN	-	EXPRESSION TAG	UNP Q76KY2
A	16	MET	-	EXPRESSION TAG	UNP Q76KY2
A	17	VAL	-	EXPRESSION TAG	UNP Q76KY2
A	18	SER	-	EXPRESSION TAG	UNP Q76KY2
A	19	ASP	-	EXPRESSION TAG	UNP Q76KY2
A	20	ASN	-	EXPRESSION TAG	UNP Q76KY2
A	21	ALA	-	EXPRESSION TAG	UNP Q76KY2
A	22	ASP	-	EXPRESSION TAG	UNP Q76KY2
A	23	LYS	-	EXPRESSION TAG	UNP Q76KY2
A	24	ASP	-	EXPRESSION TAG	UNP Q76KY2
A	25	LEU	-	EXPRESSION TAG	UNP Q76KY2
A	26	ARG	-	EXPRESSION TAG	UNP Q76KY2
A	27	TYR	-	EXPRESSION TAG	UNP Q76KY2
A	28	GLY	-	EXPRESSION TAG	UNP Q76KY2
A	29	GLY	-	EXPRESSION TAG	UNP Q76KY2
A	30	LEU	-	EXPRESSION TAG	UNP Q76KY2
A	31	VAL	-	EXPRESSION TAG	UNP Q76KY2
A	32	HIS	-	EXPRESSION TAG	UNP Q76KY2
A	33	ASP	-	EXPRESSION TAG	UNP Q76KY2
A	34	LEU	-	EXPRESSION TAG	UNP Q76KY2
A	35	LEU	-	EXPRESSION TAG	UNP Q76KY2
A	36	ALA	-	EXPRESSION TAG	UNP Q76KY2
A	37	ASP	-	EXPRESSION TAG	UNP Q76KY2
A	38	SER	-	EXPRESSION TAG	UNP Q76KY2
A	39	GLY	-	EXPRESSION TAG	UNP Q76KY2
A	40	LYS	-	EXPRESSION TAG	UNP Q76KY2
A	41	ALA	-	EXPRESSION TAG	UNP Q76KY2
A	42	THR	-	EXPRESSION TAG	UNP Q76KY2
A	43	PRO	-	EXPRESSION TAG	UNP Q76KY2
A	44	ASN	-	EXPRESSION TAG	UNP Q76KY2
A	45	SER	-	EXPRESSION TAG	UNP Q76KY2
A	46	ASP	-	EXPRESSION TAG	UNP Q76KY2
A	47	ALA	-	EXPRESSION TAG	UNP Q76KY2
B	-15	MET	-	EXPRESSION TAG	UNP Q76KY2
B	-14	ASN	-	EXPRESSION TAG	UNP Q76KY2
B	-13	HIS	-	EXPRESSION TAG	UNP Q76KY2
B	-12	LYS	-	EXPRESSION TAG	UNP Q76KY2

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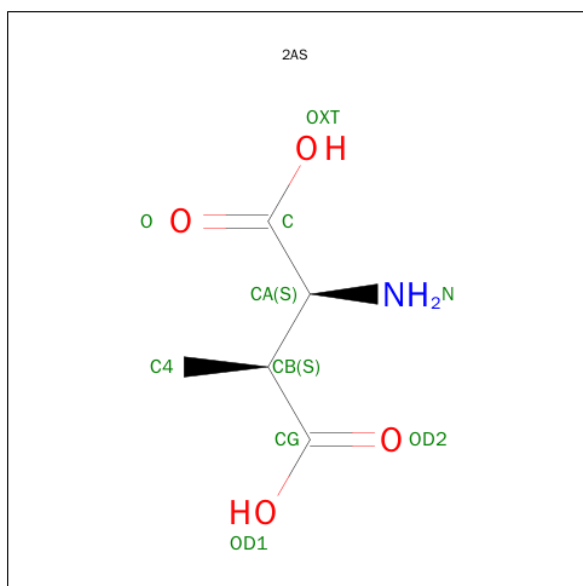
Chain	Residue	Modelled	Actual	Comment	Reference
B	-11	VAL	-	EXPRESSION TAG	UNP Q76KY2
B	-10	HIS	-	EXPRESSION TAG	UNP Q76KY2
B	-9	HIS	-	EXPRESSION TAG	UNP Q76KY2
B	-8	HIS	-	EXPRESSION TAG	UNP Q76KY2
B	-7	HIS	-	EXPRESSION TAG	UNP Q76KY2
B	-6	HIS	-	EXPRESSION TAG	UNP Q76KY2
B	-5	HIS	-	EXPRESSION TAG	UNP Q76KY2
B	-4	ILE	-	EXPRESSION TAG	UNP Q76KY2
B	-3	GLU	-	EXPRESSION TAG	UNP Q76KY2
B	-2	GLY	-	EXPRESSION TAG	UNP Q76KY2
B	-1	ARG	-	EXPRESSION TAG	UNP Q76KY2
B	0	HIS	-	EXPRESSION TAG	UNP Q76KY2
B	1	MET	-	EXPRESSION TAG	UNP Q76KY2
B	2	TYR	-	EXPRESSION TAG	UNP Q76KY2
B	3	SER	-	EXPRESSION TAG	UNP Q76KY2
B	4	PRO	-	EXPRESSION TAG	UNP Q76KY2
B	5	ASP	-	EXPRESSION TAG	UNP Q76KY2
B	6	ARG	-	EXPRESSION TAG	UNP Q76KY2
B	7	ARG	-	EXPRESSION TAG	UNP Q76KY2
B	8	ALA	-	EXPRESSION TAG	UNP Q76KY2
B	9	ALA	-	EXPRESSION TAG	UNP Q76KY2
B	10	LEU	-	EXPRESSION TAG	UNP Q76KY2
B	11	ASN	-	EXPRESSION TAG	UNP Q76KY2
B	12	SER	-	EXPRESSION TAG	UNP Q76KY2
B	13	VAL	-	EXPRESSION TAG	UNP Q76KY2
B	14	ALA	-	EXPRESSION TAG	UNP Q76KY2
B	15	ASN	-	EXPRESSION TAG	UNP Q76KY2
B	16	MET	-	EXPRESSION TAG	UNP Q76KY2
B	17	VAL	-	EXPRESSION TAG	UNP Q76KY2
B	18	SER	-	EXPRESSION TAG	UNP Q76KY2
B	19	ASP	-	EXPRESSION TAG	UNP Q76KY2
B	20	ASN	-	EXPRESSION TAG	UNP Q76KY2
B	21	ALA	-	EXPRESSION TAG	UNP Q76KY2
B	22	ASP	-	EXPRESSION TAG	UNP Q76KY2
B	23	LYS	-	EXPRESSION TAG	UNP Q76KY2
B	24	ASP	-	EXPRESSION TAG	UNP Q76KY2
B	25	LEU	-	EXPRESSION TAG	UNP Q76KY2
B	26	ARG	-	EXPRESSION TAG	UNP Q76KY2
B	27	TYR	-	EXPRESSION TAG	UNP Q76KY2
B	28	GLY	-	EXPRESSION TAG	UNP Q76KY2
B	29	GLY	-	EXPRESSION TAG	UNP Q76KY2
B	30	LEU	-	EXPRESSION TAG	UNP Q76KY2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	31	VAL	-	EXPRESSION TAG	UNP Q76KY2
B	32	HIS	-	EXPRESSION TAG	UNP Q76KY2
B	33	ASP	-	EXPRESSION TAG	UNP Q76KY2
B	34	LEU	-	EXPRESSION TAG	UNP Q76KY2
B	35	LEU	-	EXPRESSION TAG	UNP Q76KY2
B	36	ALA	-	EXPRESSION TAG	UNP Q76KY2
B	37	ASP	-	EXPRESSION TAG	UNP Q76KY2
B	38	SER	-	EXPRESSION TAG	UNP Q76KY2
B	39	GLY	-	EXPRESSION TAG	UNP Q76KY2
B	40	LYS	-	EXPRESSION TAG	UNP Q76KY2
B	41	ALA	-	EXPRESSION TAG	UNP Q76KY2
B	42	THR	-	EXPRESSION TAG	UNP Q76KY2
B	43	PRO	-	EXPRESSION TAG	UNP Q76KY2
B	44	ASN	-	EXPRESSION TAG	UNP Q76KY2
B	45	SER	-	EXPRESSION TAG	UNP Q76KY2
B	46	ASP	-	EXPRESSION TAG	UNP Q76KY2
B	47	ALA	-	EXPRESSION TAG	UNP Q76KY2

- Molecule 2 is (2S,3S)-3-METHYL-ASPARTIC ACID (three-letter code: 2AS) (formula: $C_5H_9NO_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 10	C 5	N 1	O 4	0	0
2	B	1	Total 10	C 5	N 1	O 4	0	0

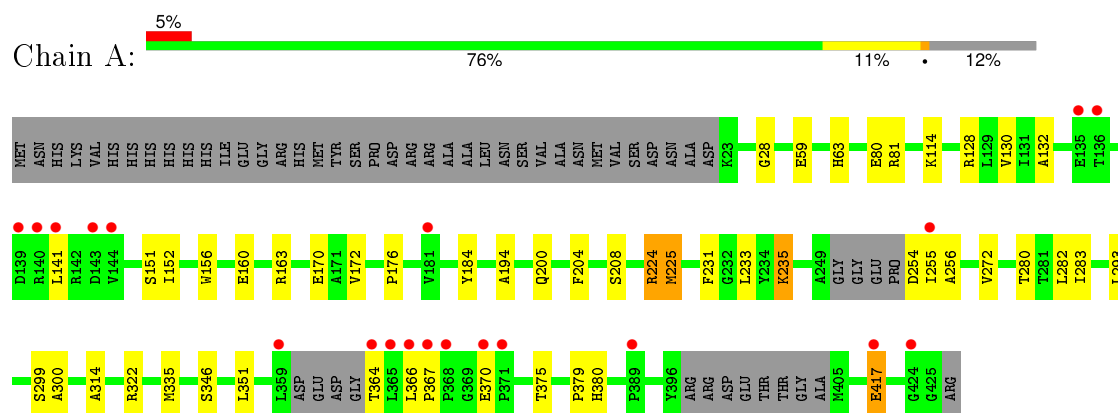
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	96	Total 96	O 96	0	0
3	B	107	Total 107	O 107	0	0

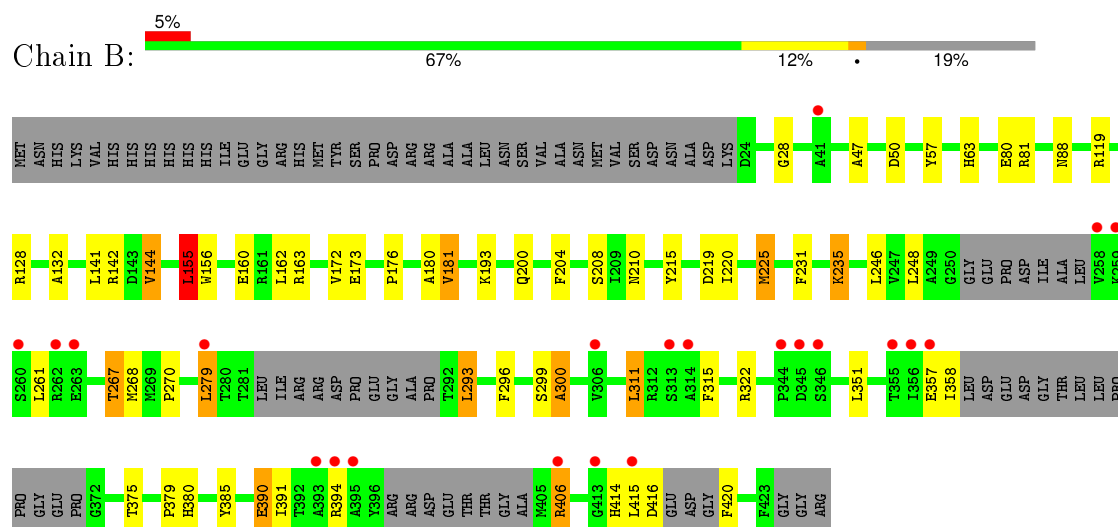
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Non-ribosomal peptide synthetase



- Molecule 1: Non-ribosomal peptide synthetase



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	80.66Å 109.41Å 200.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.44 – 2.20 37.41 – 2.20	Depositor EDS
% Data completeness (in resolution range)	97.6 (37.44-2.20) 97.7 (37.41-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.13 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.205 , 0.245 0.212 , 0.249	Depositor DCC
R_{free} test set	2233 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	36.3	Xtriage
Anisotropy	0.314	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 39.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 44288 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5913	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.94% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 2AS

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	0.80	0/3014	0.90	4/4106 (0.1%)
1	B	0.78	0/2801	0.92	7/3811 (0.2%)
All	All	0.79	0/5815	0.91	11/7917 (0.1%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	322	ARG	NE-CZ-NH1	9.02	124.81	120.30
1	B	322	ARG	NE-CZ-NH1	8.76	124.68	120.30
1	B	155	LEU	CA-CB-CG	7.98	133.66	115.30
1	A	322	ARG	NE-CZ-NH2	-7.62	116.49	120.30
1	B	322	ARG	NE-CZ-NH2	-7.11	116.75	120.30
1	B	235	LYS	CD-CE-NZ	6.86	127.49	111.70
1	A	235	LYS	CD-CE-NZ	6.25	126.08	111.70
1	B	311	LEU	CA-CB-CG	5.55	128.06	115.30
1	B	142	ARG	NE-CZ-NH1	5.34	122.97	120.30
1	B	50	ASP	CB-CG-OD1	5.16	122.95	118.30
1	A	293	LEU	CB-CG-CD2	5.12	119.71	111.00

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	2948	0	2934	31	0
1	B	2742	0	2722	45	0
2	A	10	0	7	0	0
2	B	10	0	7	0	0
3	A	96	0	0	2	0
3	B	107	0	0	0	0
All	All	5913	0	5670	76	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 7.

All (76) 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:358:ILE:HD13	1:B:414:HIS:HA	1.68	0.76
1:B:375:THR:CG2	1:B:406:ARG:HD3	2.19	0.71
1:B:28:GLY:HA2	1:B:200:GLN:HE21	1.56	0.70
1:B:246:LEU:HG	1:B:248:LEU:HD12	1.77	0.67
1:A:28:GLY:HA2	1:A:200:GLN:HE21	1.59	0.67
1:A:366:LEU:HD23	1:A:370:GLU:HB3	1.76	0.66
1:B:219:ASP:OD1	1:B:267:THR:HG21	1.96	0.65
1:B:375:THR:CG2	1:B:406:ARG:CD	2.76	0.64
1:B:293:LEU:HD23	1:B:296:PHE:CZ	2.33	0.63
1:A:132:ALA:HB2	1:A:141:LEU:HD22	1.81	0.62
1:A:272:VAL:HG13	3:A:787:HOH:O	2.00	0.62
1:B:358:ILE:HD11	1:B:415:LEU:HG	1.83	0.61
1:A:280:THR:O	1:A:283:ILE:HG22	2.00	0.59
1:B:225:MET:HE2	1:B:270:PRO:HB2	1.84	0.59
1:B:357:GLU:O	1:B:375:THR:HB	2.02	0.59
1:A:225:MET:HE2	1:A:225:MET:N	2.18	0.58
1:B:219:ASP:HA	1:B:267:THR:HG21	1.86	0.57
1:B:193:LYS:HE3	1:B:391:ILE:HG21	1.87	0.56
1:B:267:THR:HG23	1:B:268:MET:HG2	1.88	0.56
1:B:416:ASP:OD1	1:B:416:ASP:C	2.44	0.56
1:B:220:ILE:H	1:B:267:THR:HG22	1.72	0.55
1:A:225:MET:HE1	3:A:701:HOH:O	2.07	0.55
1:B:358:ILE:CD1	1:B:414:HIS:HA	2.37	0.54
1:B:219:ASP:OD1	1:B:267:THR:CG2	2.55	0.54
1:A:225:MET:CE	1:A:225:MET:N	2.71	0.54
1:A:63:HIS:CE1	1:A:163:ARG:HH11	2.27	0.53
1:B:128:ARG:HG3	1:B:128:ARG:HH11	1.73	0.53
1:A:224:ARG:NH2	1:A:254:ASP:OD2	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:204:PHE:CZ	1:A:379:PRO:HG2	2.44	0.52
1:A:255:ILE:HD12	1:A:256:ALA:N	2.25	0.52
1:A:366:LEU:HD23	1:A:370:GLU:CB	2.39	0.51
1:B:204:PHE:CZ	1:B:379:PRO:HG2	2.46	0.51
1:B:63:HIS:CE1	1:B:163:ARG:HH11	2.31	0.49
1:B:210:ASN:ND2	1:B:215:TYR:HB2	2.28	0.49
1:B:390:GLU:H	1:B:390:GLU:CD	2.17	0.49
1:B:155:LEU:C	1:B:155:LEU:HD23	2.33	0.48
1:A:156:TRP:O	1:A:160:GLU:HG3	2.13	0.48
1:A:417:GLU:OE2	1:A:417:GLU:N	2.47	0.48
1:A:283:ILE:HG12	1:A:314:ALA:HB1	1.95	0.47
1:B:375:THR:HG22	1:B:406:ARG:HD3	1.96	0.47
1:A:80:GLU:CD	1:A:128:ARG:HH11	2.18	0.46
1:B:156:TRP:O	1:B:160:GLU:HG3	2.15	0.46
1:A:130:VAL:CG1	1:A:141:LEU:HD23	2.46	0.46
1:B:80:GLU:HB3	1:B:128:ARG:HG2	1.97	0.46
1:A:272:VAL:HG22	1:A:300:ALA:HB3	1.99	0.45
1:B:225:MET:CE	1:B:270:PRO:HB2	2.46	0.45
1:B:358:ILE:HD11	1:B:415:LEU:N	2.31	0.44
1:A:176:PRO:O	1:A:200:GLN:HG3	2.18	0.44
1:A:225:MET:H	1:A:225:MET:CE	2.31	0.44
1:A:152:ILE:O	1:A:156:TRP:HB2	2.17	0.44
1:A:130:VAL:HG11	1:A:141:LEU:HD23	1.99	0.43
1:B:415:LEU:HA	1:B:420:PHE:O	2.18	0.43
1:A:59:GLU:O	1:A:63:HIS:HD2	2.01	0.43
1:B:132:ALA:HB2	1:B:141:LEU:HD12	2.01	0.43
1:B:208:SER:OG	1:B:351:LEU:HB3	2.19	0.43
1:A:225:MET:H	1:A:225:MET:HE3	1.84	0.43
1:B:210:ASN:HD21	1:B:215:TYR:HB2	1.84	0.43
1:B:299:SER:O	1:B:300:ALA:HB3	2.19	0.43
1:A:299:SER:O	1:A:300:ALA:HB3	2.19	0.43
1:B:80:GLU:HB3	1:B:128:ARG:CG	2.49	0.42
1:B:193:LYS:HE2	1:B:385:TYR:CE1	2.54	0.42
1:B:267:THR:CG2	1:B:268:MET:HG2	2.49	0.42
1:A:184:TYR:CE1	1:A:194:ALA:HB2	2.54	0.42
1:B:375:THR:HG21	1:B:406:ARG:CD	2.50	0.42
1:B:88:ASN:HB3	1:B:248:LEU:HB3	2.00	0.42
1:B:176:PRO:O	1:B:200:GLN:HG3	2.19	0.41
1:B:119:ARG:HA	1:B:144:VAL:HG13	2.02	0.41
1:B:279:LEU:HD11	1:B:315:PHE:CE2	2.56	0.41
1:B:180:ALA:C	1:B:181:VAL:HG12	2.41	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:208:SER:OG	1:A:351:LEU:HB3	2.21	0.41
1:B:128:ARG:CG	1:B:128:ARG:HH11	2.33	0.40
1:A:335:MET:HE1	1:A:346:SER:HB3	2.04	0.40
1:B:47:ALA:HB2	1:B:57:TYR:CD1	2.56	0.40
1:A:367:PRO:HG2	1:A:370:GLU:HG3	2.03	0.40
1:A:335:MET:CE	1:A:346:SER:HB3	2.51	0.40
1:B:375:THR:HG21	1:B:406:ARG:HD2	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	379/442 (86%)	375 (99%)	4 (1%)	0	100	100
1	B	347/442 (78%)	344 (99%)	2 (1%)	1 (0%)	46	50
All	All	726/884 (82%)	719 (99%)	6 (1%)	1 (0%)	56	64

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	300	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	312/357 (87%)	297 (95%)	15 (5%)	31	37
1	B	290/357 (81%)	271 (93%)	19 (7%)	21	22
All	All	602/714 (84%)	568 (94%)	34 (6%)	26	29

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	81	ARG
1	A	114	LYS
1	A	151	SER
1	A	170	GLU
1	A	172	VAL
1	A	224	ARG
1	A	225	MET
1	A	231	PHE
1	A	233	LEU
1	A	235	LYS
1	A	282	LEU
1	A	364	THR
1	A	375	THR
1	A	380	HIS
1	A	417	GLU
1	B	81	ARG
1	B	144	VAL
1	B	155	LEU
1	B	162	LEU
1	B	172	VAL
1	B	173	GLU
1	B	181	VAL
1	B	225	MET
1	B	231	PHE
1	B	235	LYS
1	B	261	LEU
1	B	267	THR
1	B	279	LEU
1	B	293	LEU
1	B	311	LEU
1	B	380	HIS
1	B	390	GLU
1	B	394	ARG
1	B	406	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	58	GLN
1	A	63	HIS
1	A	200	GLN
1	B	58	GLN
1	B	63	HIS
1	B	88	ASN
1	B	110	ASN
1	B	200	GLN
1	B	210	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

2 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	2AS	A	601	-	3,9,9	2.22	1 (33%)	3,12,12	2.67	1 (33%)
2	2AS	B	601	-	3,9,9	1.42	1 (33%)	3,12,12	1.20	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	2AS	A	601	-	-	0/4/12/12	0/0/0/0
2	2AS	B	601	-	-	0/4/12/12	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	2AS	CB-CA	-3.22	1.52	1.54
2	B	601	2AS	CB-CA	2.09	1.56	1.54

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	2AS	C4-CB-CA	-4.58	107.05	111.88

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	387/442 (87%)	0.05	20 (5%) 31 30	23, 39, 67, 84	0
1	B	359/442 (81%)	0.23	22 (6%) 25 24	24, 45, 80, 90	0
All	All	746/884 (84%)	0.14	42 (5%) 28 27	23, 42, 76, 90	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	365	LEU	5.9
1	B	258	VAL	5.8
1	B	344	PRO	4.7
1	B	259	LYS	4.5
1	A	144	VAL	4.1
1	A	367	PRO	4.0
1	A	359	LEU	3.7
1	B	262	ARG	3.4
1	A	140	ARG	3.1
1	B	279	LEU	3.0
1	A	364	THR	3.0
1	B	345	ASP	2.9
1	B	394	ARG	2.9
1	A	366	LEU	2.9
1	A	135	GLU	2.9
1	B	314	ALA	2.8
1	B	415	LEU	2.8
1	A	389	PRO	2.8
1	A	255	ILE	2.7
1	A	417	GLU	2.7
1	B	356	ILE	2.7
1	A	141	LEU	2.6
1	B	395	ALA	2.6
1	B	313	SER	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	306	VAL	2.6
1	B	260	SER	2.6
1	A	368	PRO	2.5
1	B	357	GLU	2.5
1	A	143	ASP	2.5
1	A	139	ASP	2.4
1	A	136	THR	2.3
1	B	41	ALA	2.3
1	B	393	ALA	2.3
1	B	413	GLY	2.3
1	B	263	GLU	2.3
1	A	371	PRO	2.2
1	B	406	ARG	2.2
1	A	424	GLY	2.1
1	A	370	GLU	2.1
1	B	346	SER	2.0
1	A	181	VAL	2.0
1	B	355	THR	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	2AS	A	601	10/10	0.96	0.17	0.93	25,29,35,41	0
2	2AS	B	601	10/10	0.94	0.15	0.70	32,35,40,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.