



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 07:32 AM UTC

PDB ID : 5AA6 / pdb_00005aa6
Title : Homohexameric Structure of the second Vanadate-Dependent Bromoperoxidase (AnII) from *Ascophyllum nodosum*
Authors : Radlow, M.; Jeudy, A.; Dabin, J.; Delage, L.; Leblanc, C.; Hartung, J.; Czjzek, M.
Deposited on : 2015-07-23
Resolution : 2.26 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

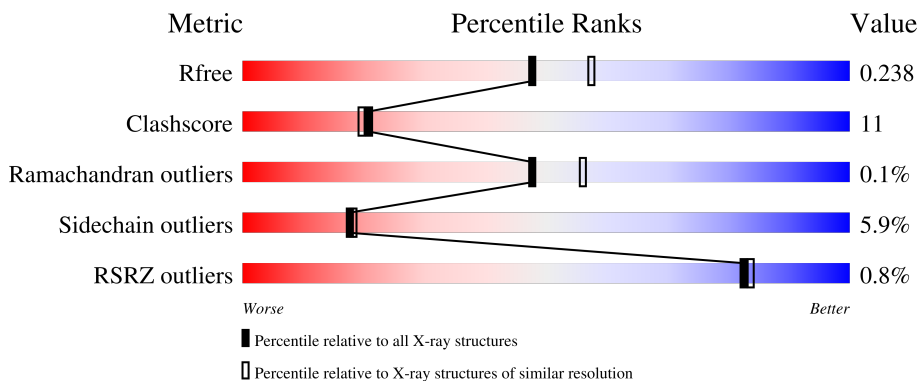
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.26 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	1898 (2.26-2.26)
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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	597	82% 15% ..
1	B	597	79% 18% .
1	C	597	77% 18% . .
1	D	597	79% 17% . .
1	E	597	81% 16% . .

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Mol	Chain	Length	Quality of chain
1	F	597	 81% 17% ..

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 29755 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 VANADIUM-DEPENDENT BROMOPEROXIDASE 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	594	4601	2906	786	878	31	0	11	0
1	B	595	4620	2912	791	885	32	4	11	0
1	C	594	4640	2930	790	887	33	0	17	0
1	D	594	4614	2912	786	883	33	0	13	0
1	E	594	4625	2924	786	882	33	0	16	0
1	F	594	4618	2914	785	888	31	0	13	0

There are 36 discrepancies between the modelled and reference sequences:

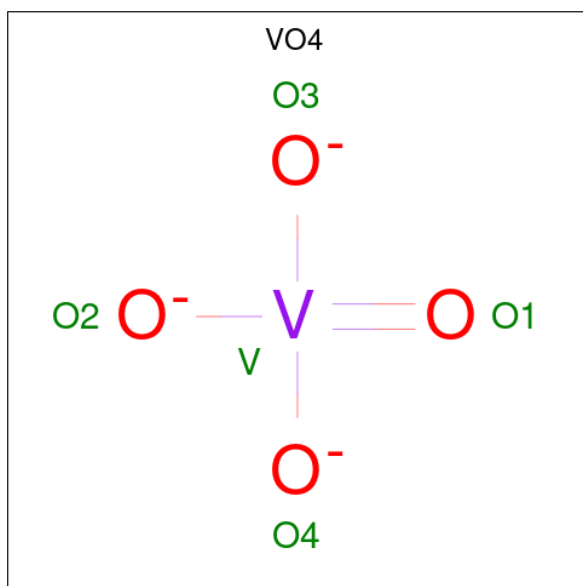
Chain	Residue	Modelled	Actual	Comment	Reference
A	68	VAL	ALA	conflict	UNP K7ZUA3
A	87	ILE	VAL	conflict	UNP K7ZUA3
A	103	MET	VAL	conflict	UNP K7ZUA3
A	203	VAL	ALA	conflict	UNP K7ZUA3
A	204	VAL	ALA	conflict	UNP K7ZUA3
A	327	MET	LEU	conflict	UNP K7ZUA3
B	68	VAL	ALA	conflict	UNP K7ZUA3
B	87	ILE	VAL	conflict	UNP K7ZUA3
B	103	MET	VAL	conflict	UNP K7ZUA3
B	203	VAL	ALA	conflict	UNP K7ZUA3
B	204	VAL	ALA	conflict	UNP K7ZUA3
B	327	MET	LEU	conflict	UNP K7ZUA3
C	68	VAL	ALA	conflict	UNP K7ZUA3
C	87	ILE	VAL	conflict	UNP K7ZUA3
C	103	MET	VAL	conflict	UNP K7ZUA3
C	203	VAL	ALA	conflict	UNP K7ZUA3
C	204	VAL	ALA	conflict	UNP K7ZUA3

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Chain	Residue	Modelled	Actual	Comment	Reference
C	327	MET	LEU	conflict	UNP K7ZUA3
D	68	VAL	ALA	conflict	UNP K7ZUA3
D	87	ILE	VAL	conflict	UNP K7ZUA3
D	103	MET	VAL	conflict	UNP K7ZUA3
D	203	VAL	ALA	conflict	UNP K7ZUA3
D	204	VAL	ALA	conflict	UNP K7ZUA3
D	327	MET	LEU	conflict	UNP K7ZUA3
E	68	VAL	ALA	conflict	UNP K7ZUA3
E	87	ILE	VAL	conflict	UNP K7ZUA3
E	103	MET	VAL	conflict	UNP K7ZUA3
E	203	VAL	ALA	conflict	UNP K7ZUA3
E	204	VAL	ALA	conflict	UNP K7ZUA3
E	327	MET	LEU	conflict	UNP K7ZUA3
F	68	VAL	ALA	conflict	UNP K7ZUA3
F	87	ILE	VAL	conflict	UNP K7ZUA3
F	103	MET	VAL	conflict	UNP K7ZUA3
F	203	VAL	ALA	conflict	UNP K7ZUA3
F	204	VAL	ALA	conflict	UNP K7ZUA3
F	327	MET	LEU	conflict	UNP K7ZUA3

- Molecule 2 is VANADATE ION (CCD ID: VO4) (formula: O₄V).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	O	V	0	0
			5	4	1		
2	D	1	Total	O	V	0	0
			5	4	1		
2	E	1	Total	O	V	0	0
			5	4	1		
2	F	1	Total	O	V	0	0
			5	4	1		

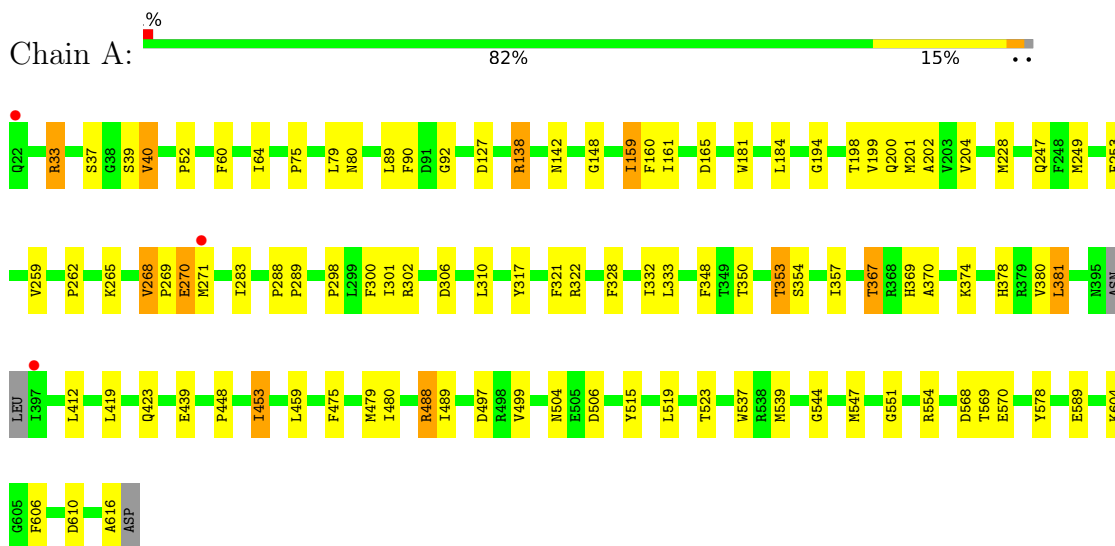
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	431	Total	O	0	0
			431	431		
3	B	338	Total	O	0	0
			338	338		
3	C	249	Total	O	0	0
			249	249		
3	D	355	Total	O	0	0
			355	355		
3	E	299	Total	O	0	0
			299	299		
3	F	335	Total	O	0	0
			335	335		

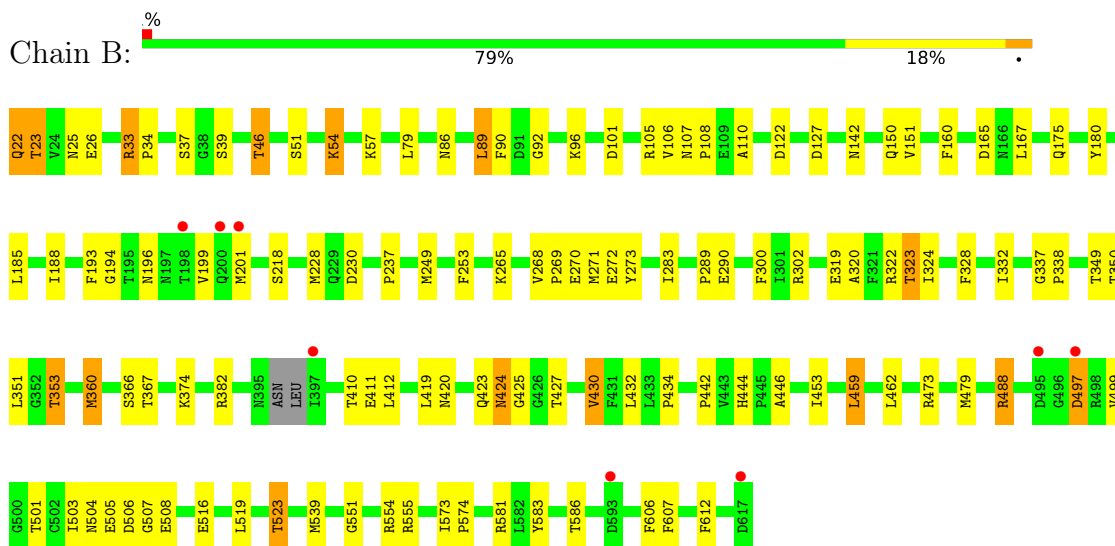
3 Residue-property plots i

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: VANADIUM-DEPENDENT BROMOPEROXIDASE 2

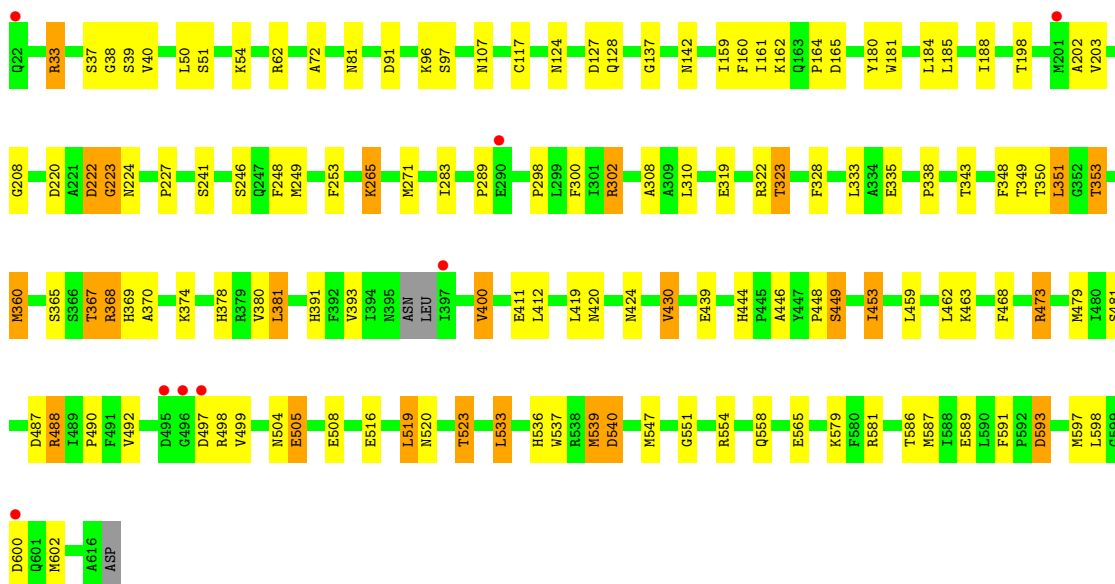


• Molecule 1: VANADIUM-DEPENDENT BROMOPEROXIDASE 2

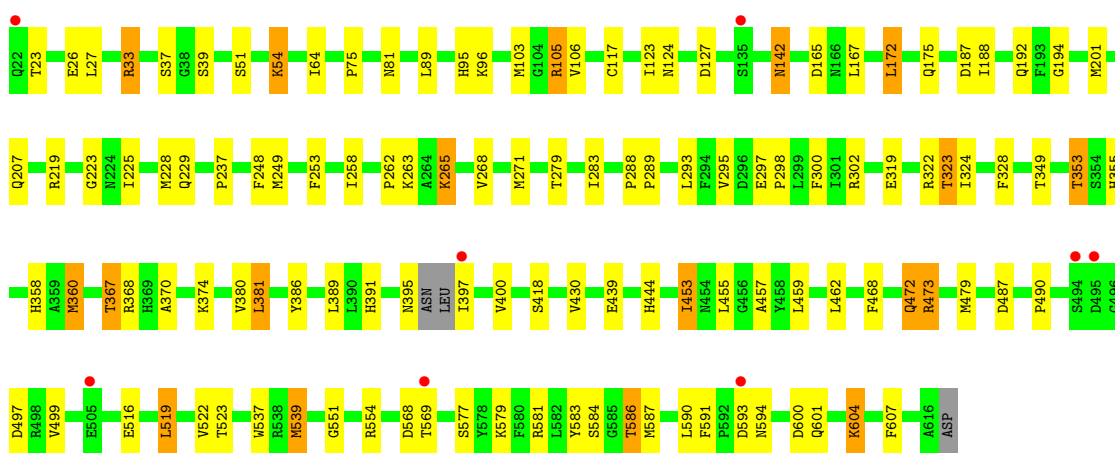
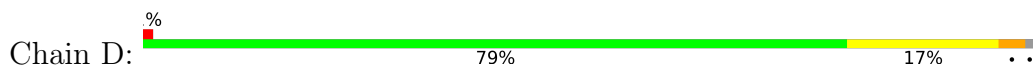


• Molecule 1: VANADIUM-DEPENDENT BROMOPEROXIDASE 2

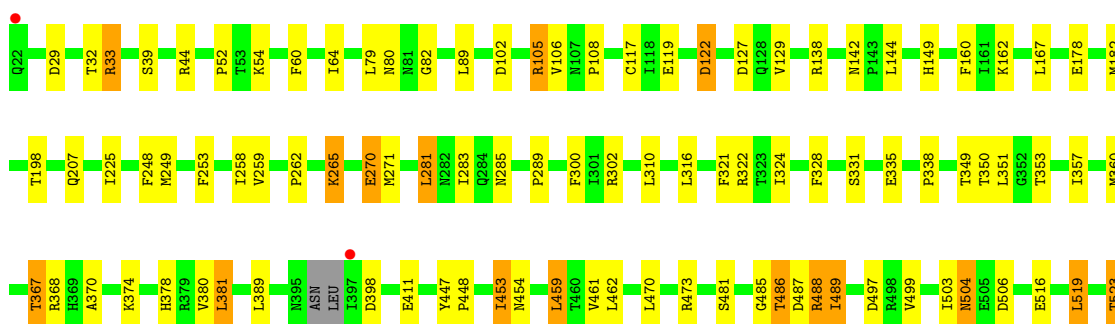
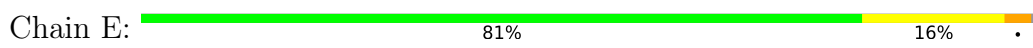




● Molecule 1: VANADIUM-DEPENDENT BROMOPEROXIDASE 2



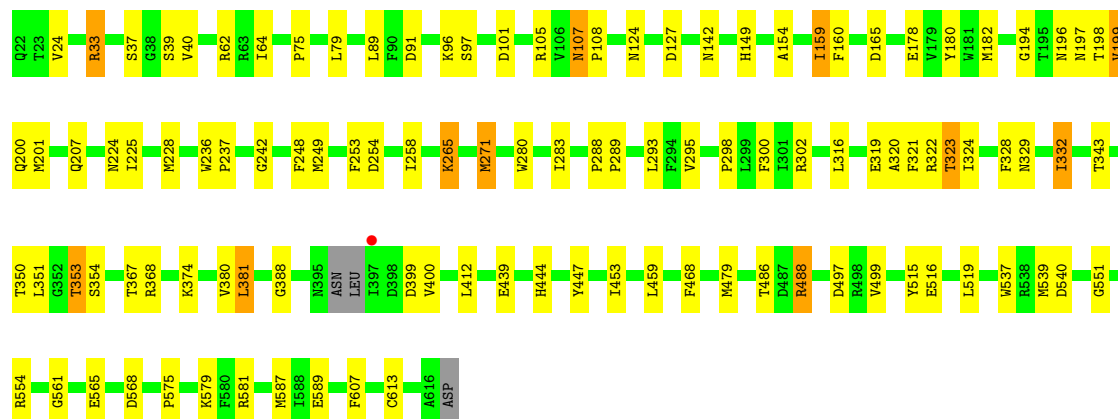
● Molecule 1: VANADIUM-DEPENDENT BROMOPEROXIDASE 2





• Molecule 1: VANADIUM-DEPENDENT BROMOPEROXIDASE 2

Chain F: 81% 17% ..



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	67.79Å 236.84Å 118.00Å 90.00° 93.74° 90.00°	Depositor
Resolution (Å)	70.00 – 2.26 70.00 – 2.26	Depositor EDS
% Data completeness (in resolution range)	98.6 (70.00-2.26) 98.6 (70.00-2.26)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.15 (at 2.27Å)	Xtrriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.170 , 0.236 0.172 , 0.238	Depositor DCC
R_{free} test set	8509 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	16.9	Xtrriage
Anisotropy	0.109	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 39.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	29755	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.03% 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: VO4

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	0.82	0/4734	0.98	3/6428 (0.0%)
1	B	0.80	1/4750 (0.0%)	1.00	5/6448 (0.1%)
1	C	0.79	0/4785	0.98	5/6497 (0.1%)
1	D	0.79	0/4753	1.01	11/6454 (0.2%)
1	E	0.80	1/4773 (0.0%)	0.98	6/6481 (0.1%)
1	F	0.81	1/4757 (0.0%)	1.02	7/6462 (0.1%)
All	All	0.80	3/28552 (0.0%)	0.99	37/38770 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	149	HIS	CG-CD2	5.28	1.41	1.35
1	B	505	GLU	CB-CG	-5.21	1.36	1.52
1	E	149	HIS	CG-CD2	5.03	1.41	1.35

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	188	ILE	N-CA-C	7.42	115.25	107.76
1	F	613	CYS	CA-C-N	-7.32	117.32	122.59
1	F	613	CYS	C-N-CA	-7.32	117.32	122.59
1	D	297	GLU	CA-C-N	6.80	126.78	119.78
1	D	297	GLU	C-N-CA	6.80	126.78	119.78

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	4601	0	4471	104	0
1	B	4620	0	4475	128	0
1	C	4640	0	4514	123	0
1	D	4614	0	4479	115	0
1	E	4625	0	4506	93	0
1	F	4618	0	4478	101	0
2	A	5	0	0	1	0
2	B	5	0	0	0	0
2	C	5	0	0	1	0
2	D	5	0	0	0	0
2	E	5	0	0	1	0
2	F	5	0	0	0	0
3	A	431	0	0	20	0
3	B	338	0	0	18	0
3	C	249	0	0	10	0
3	D	355	0	0	17	0
3	E	299	0	0	6	0
3	F	335	0	0	10	0
All	All	29755	0	26923	605	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 11.

The worst 5 of 605 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:E:33:ARG:HH11	1:E:33:ARG:CG	1.45	1.30
1:D:33:ARG:HH11	1:D:33:ARG:CG	1.40	1.30
1:A:551:GLY:HA3	3:A:2331:HOH:O	1.18	1.29
1:F:33:ARG:HH11	1:F:33:ARG:CG	1.49	1.25
1:C:33:ARG:HH11	1:C:33:ARG:CG	1.50	1.23

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	601/597 (101%)	586 (98%)	15 (2%)	0	100	100
1	B	602/597 (101%)	584 (97%)	17 (3%)	1 (0%)	43	50
1	C	607/597 (102%)	580 (96%)	26 (4%)	1 (0%)	43	50
1	D	603/597 (101%)	571 (95%)	32 (5%)	0	100	100
1	E	606/597 (102%)	588 (97%)	18 (3%)	0	100	100
1	F	603/597 (101%)	586 (97%)	17 (3%)	0	100	100
All	All	3622/3582 (101%)	3495 (96%)	125 (4%)	2 (0%)	48	56

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	89	LEU
1	C	223	GLY

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	498/495 (101%)	479 (96%)	19 (4%)	29	36
1	B	500/495 (101%)	476 (95%)	24 (5%)	23	25
1	C	505/495 (102%)	459 (91%)	46 (9%)	9	7
1	D	501/495 (101%)	460 (92%)	41 (8%)	10	9
1	E	503/495 (102%)	462 (92%)	41 (8%)	10	9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	502/495 (101%)	475 (95%)	27 (5%)	20	21
All	All	3009/2970 (101%)	2811 (93%)	198 (7%)	18	14

5 of 198 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	400	VAL
1	E	270	GLU
1	D	472	GLN
1	E	32	THR
1	E	411	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	142	ASN
1	F	207	GLN
1	F	423	GLN
1	C	213	ASN
1	C	124	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 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	VO4	C	800	-	0,4,4	-	-	-	-	-
2	VO4	E	800	-	0,4,4	-	-	-	-	-
2	VO4	D	800	-	0,4,4	-	-	-	-	-
2	VO4	F	800	-	0,4,4	-	-	-	-	-
2	VO4	A	800	-	0,4,4	-	-	-	-	-
2	VO4	B	800	-	0,4,4	-	-	-	-	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	800	VO4	1	0
2	E	800	VO4	1	0
2	A	800	VO4	1	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	594/597 (99%)	-0.58	3 (0%) 87 88	6, 15, 29, 56	24 (4%)
1	B	595/597 (99%)	-0.41	8 (1%) 75 76	8, 19, 34, 65	23 (3%)
1	C	594/597 (99%)	-0.24	8 (1%) 75 76	8, 21, 40, 74	24 (4%)
1	D	594/597 (99%)	-0.40	8 (1%) 75 76	6, 18, 32, 74	26 (4%)
1	E	594/597 (99%)	-0.50	2 (0%) 90 90	6, 17, 33, 62	22 (3%)
1	F	594/597 (99%)	-0.57	1 (0%) 91 92	6, 15, 29, 57	21 (3%)
All	All	3565/3582 (99%)	-0.45	30 (0%) 82 84	6, 17, 34, 74	140 (3%)

The worst 5 of 30 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	495	ASP	6.7
1	D	505	GLU	4.9
1	B	495	ASP	4.9
1	A	22	GLN	4.4
1	D	135	SER	4.4

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	VO4	C	800	5/5	0.97	0.07	27,27,28,31	0
2	VO4	D	800	5/5	0.98	0.06	23,23,24,26	0
2	VO4	A	800	5/5	0.99	0.04	16,16,16,19	0
2	VO4	B	800	5/5	0.99	0.06	25,26,27,29	0
2	VO4	E	800	5/5	0.99	0.07	18,18,19,20	2
2	VO4	F	800	5/5	0.99	0.05	21,22,23,23	0

6.5 Other polymers [i](#)

There are no such residues in this entry.