



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 12:53 PM UTC

PDB ID : 5M26 / pdb_00005m26
Title : Crystal structure of hydroquinone 1,2-dioxygenase from *Sphingomonas* sp. TTNP3 in complex with methylhydroquinone
Authors : Ferraroni, M.; Da Vela, S.; Scozzafava, A.; Kolvenbach, B.; Corvini, P.F.X.
Deposited on : 2016-10-12
Resolution : 1.90 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

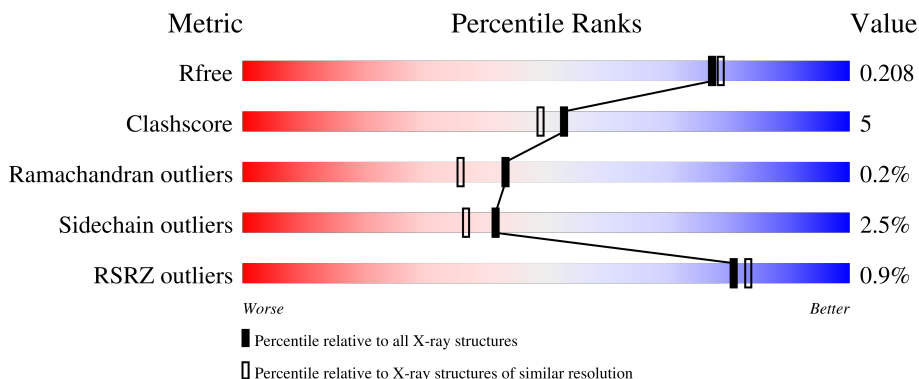
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	170	85% 12% ..
1	C	170	87% 8% 5%
1	E	170	86% 9% ..
1	G	170	86% 9% ..
2	B	341	89% 8% ..

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Mol	Chain	Length	Quality of chain
2	D	341	2% 86% 8% 6%
2	F	341	1% 84% 10% 5%
2	H	341	1% 87% 8% 4%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 17425 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 Hydroquinone dioxygenase small subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	167	Total	C	N	O	S	0	0	0
			1284	813	217	248	6			
1	C	161	Total	C	N	O	S	0	0	0
			1235	784	210	236	5			
1	E	164	Total	C	N	O	S	0	0	0
			1254	796	209	243	6			
1	G	165	Total	C	N	O	S	0	0	0
			1268	804	215	243	6			

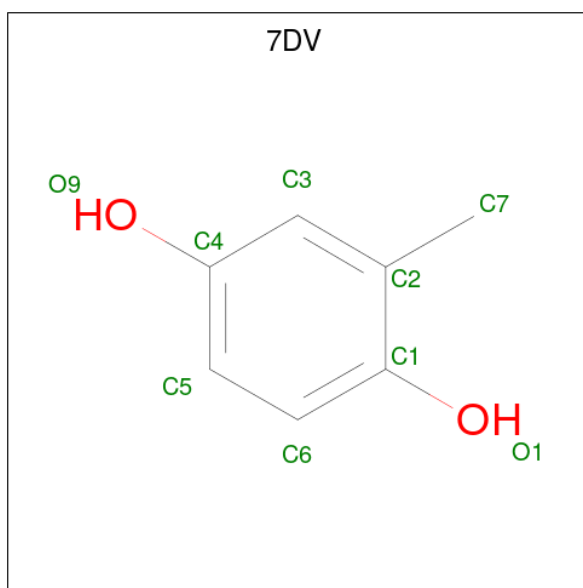
- Molecule 2 is a protein called Hydroquinone dioxygenase large subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	332	Total	C	N	O	S	0	3	0
			2620	1662	452	491	15			
2	D	321	Total	C	N	O	S	0	1	0
			2540	1607	446	473	14			
2	F	324	Total	C	N	O	S	0	1	0
			2551	1615	445	477	14			
2	H	329	Total	C	N	O	S	0	3	0
			2598	1648	453	483	14			

- Molecule 3 is FE (III) ION (CCD ID: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Fe	0	0
			1	1		
3	D	1	Total	Fe	0	0
			1	1		
3	F	1	Total	Fe	0	0
			1	1		
3	H	1	Total	Fe	0	0
			1	1		

- Molecule 4 is 2-methylbenzene-1,4-diol (CCD ID: 7DV) (formula: $C_7H_8O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			9	7	2		
4	D	1	Total	C	O	0	0
			9	7	2		
4	F	1	Total	C	O	1	0
			9	7	2		
4	H	1	Total	C	O	1	0
			9	7	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	145	Total	O	0	0
			145	145		
5	B	381	Total	O	0	0
			381	381		
5	C	160	Total	O	0	0
			160	160		
5	D	378	Total	O	0	0
			378	378		
5	E	155	Total	O	0	0
			155	155		
5	F	314	Total	O	0	0
			314	314		
5	G	149	Total	O	0	0
			149	149		

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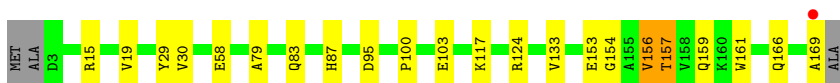
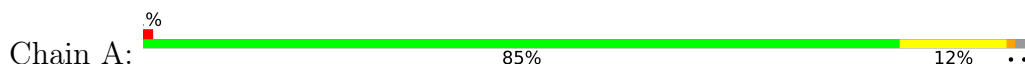
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	353	Total 353	O 353	0	0

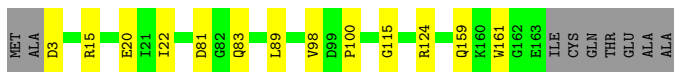
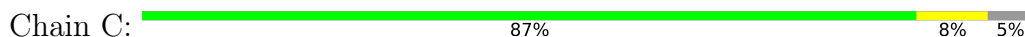
3 Residue-property plots [i](#)

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.

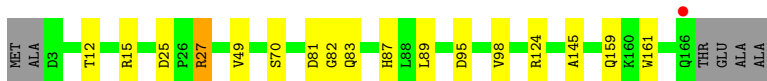
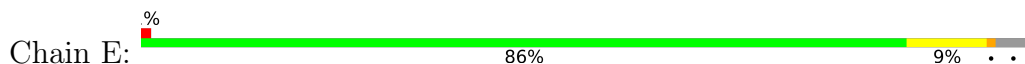
- Molecule 1: Hydroquinone dioxygenase small subunit



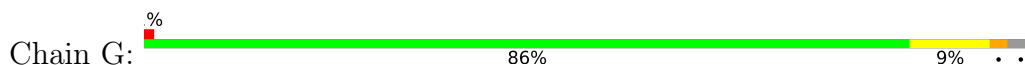
- Molecule 1: Hydroquinone dioxygenase small subunit



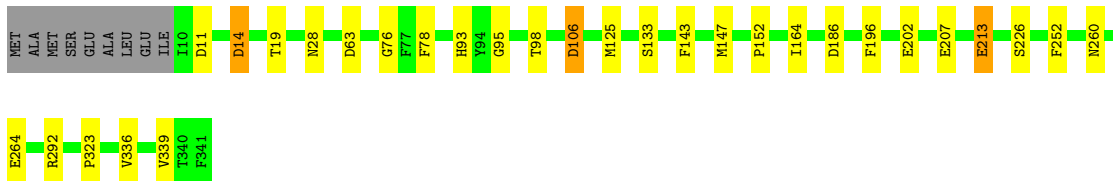
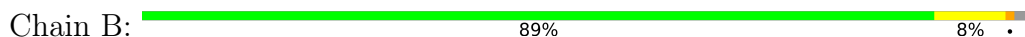
- Molecule 1: Hydroquinone dioxygenase small subunit



- Molecule 1: Hydroquinone dioxygenase small subunit

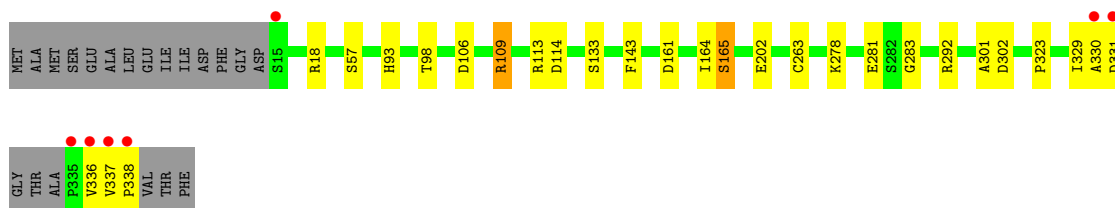


- Molecule 2: Hydroquinone dioxygenase large subunit



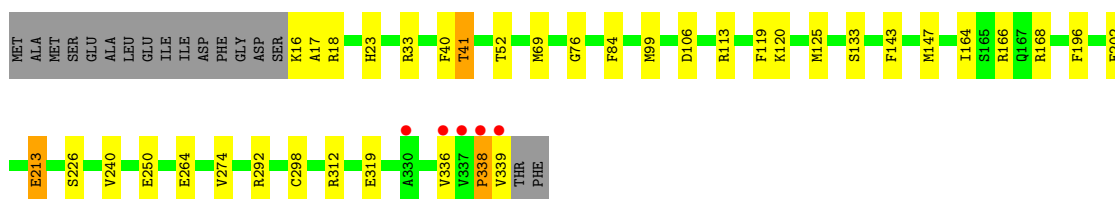
● Molecule 2: Hydroquinone dioxygenase large subunit

Chain D:  2% 86% 8% • 6%



● Molecule 2: Hydroquinone dioxygenase large subunit

Chain F:  % 84% 10% • 5%



● Molecule 2: Hydroquinone dioxygenase large subunit

Chain H:  % 87% 8% • •



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	88.41Å 125.23Å 91.35Å 90.00° 102.55° 90.00°	Depositor
Resolution (Å)	30.00 – 1.90 30.00 – 1.90	Depositor EDS
% Data completeness (in resolution range)	97.5 (30.00-1.90) 97.9 (30.00-1.90)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.53 (at 1.89Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.160 , 0.207 0.161 , 0.208	Depositor DCC
R_{free} test set	7454 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	18.3	Xtriage
Anisotropy	0.487	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 48.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.018 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	17425	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.52% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FE, 7DV

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	0.67	0/1311	0.88	1/1778 (0.1%)
1	C	0.70	0/1262	0.91	1/1712 (0.1%)
1	E	0.65	0/1281	0.84	1/1739 (0.1%)
1	G	0.62	0/1295	0.88	2/1756 (0.1%)
2	B	0.72	0/2703	0.88	1/3676 (0.0%)
2	D	0.74	0/2614	0.88	0/3551
2	F	0.66	0/2626	0.86	1/3570 (0.0%)
2	H	0.67	0/2679	0.86	1/3642 (0.0%)
All	All	0.69	0/15771	0.87	8/21424 (0.0%)

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	161	TRP	N-CA-C	6.62	118.49	111.28
1	G	22	ILE	N-CA-C	-6.45	106.02	111.56
2	H	339	VAL	N-CA-C	6.37	117.96	108.46
1	C	22	ILE	N-CA-C	-5.89	106.07	111.67
1	A	156	VAL	N-CA-CB	-5.25	106.44	112.21

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	1284	0	1229	22	0
1	C	1235	0	1181	12	0
1	E	1254	0	1189	15	0
1	G	1268	0	1216	13	0
2	B	2620	0	2473	20	0
2	D	2540	0	2399	22	0
2	F	2551	0	2410	26	0
2	H	2598	0	2452	29	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
3	F	1	0	0	0	0
3	H	1	0	0	0	0
4	B	9	0	0	2	0
4	D	9	0	0	0	0
4	F	9	0	0	0	0
4	H	9	0	0	0	0
5	A	145	0	0	7	0
5	B	381	0	0	4	1
5	C	160	0	0	2	1
5	D	378	0	0	8	0
5	E	155	0	0	5	0
5	F	314	0	0	10	0
5	G	149	0	0	2	0
5	H	353	0	0	10	0
All	All	17425	0	14549	150	1

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 5.

The worst 5 of 150 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)
2:H:70:MET:SD	5:H:754:HOH:O	1.93	1.21
1:A:87:HIS:HD2	5:A:314:HOH:O	1.32	1.11
2:B:147:MET:SD	5:B:764:HOH:O	2.12	1.06
2:H:70:MET:HE3	2:H:143:PHE:CD2	1.98	0.98
2:H:168[A]:ARG:CG	2:H:168[A]:ARG:HH11	1.77	0.98

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:515:HOH:O	5:C:201:HOH:O[1_655]	2.12	0.08

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	165/170 (97%)	158 (96%)	7 (4%)	0	100	100
1	C	159/170 (94%)	152 (96%)	6 (4%)	1 (1%)	21	13
1	E	162/170 (95%)	152 (94%)	10 (6%)	0	100	100
1	G	163/170 (96%)	154 (94%)	8 (5%)	1 (1%)	21	13
2	B	333/341 (98%)	320 (96%)	12 (4%)	1 (0%)	36	29
2	D	318/341 (93%)	302 (95%)	16 (5%)	0	100	100
2	F	323/341 (95%)	306 (95%)	16 (5%)	1 (0%)	36	29
2	H	328/341 (96%)	314 (96%)	14 (4%)	0	100	100
All	All	1951/2044 (96%)	1858 (95%)	89 (5%)	4 (0%)	43	36

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	81	ASP
1	C	81	ASP
2	B	252	PHE
2	F	338	PRO

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	129/131 (98%)	126 (98%)	3 (2%)	44	40
1	C	123/131 (94%)	122 (99%)	1 (1%)	73	75
1	E	125/131 (95%)	122 (98%)	3 (2%)	43	38
1	G	127/131 (97%)	120 (94%)	7 (6%)	19	11
2	B	275/284 (97%)	267 (97%)	8 (3%)	37	31
2	D	266/284 (94%)	261 (98%)	5 (2%)	50	47
2	F	266/284 (94%)	258 (97%)	8 (3%)	36	30
2	H	270/284 (95%)	260 (96%)	10 (4%)	30	22
All	All	1581/1660 (95%)	1536 (97%)	45 (3%)	42	32

5 of 45 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	4	VAL
2	H	57	SER
1	G	27	ARG
1	G	143	GLN
2	H	155	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	83	ASN
1	G	159	GLN
1	E	28	ASN
2	H	83	ASN
1	G	40	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

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
4	7DV	H	402	3	9,9,9	2.14	1 (11%)	12,12,12	0.79	0
4	7DV	B	402	3	9,9,9	0.64	0	12,12,12	1.36	1 (8%)
4	7DV	D	402	3	9,9,9	0.38	0	12,12,12	0.84	1 (8%)
4	7DV	F	402	3	9,9,9	1.05	0	12,12,12	0.93	1 (8%)

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
4	7DV	H	402	3	-	-	0/1/1/1
4	7DV	B	402	3	-	-	0/1/1/1
4	7DV	D	402	3	-	-	0/1/1/1
4	7DV	F	402	3	-	-	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	402	7DV	C7-C2	-5.97	1.39	1.51

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	402	7DV	C3-C2-C1	3.19	121.00	117.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	402	7DV	C3-C2-C1	2.31	120.06	117.64
4	F	402	7DV	O1-C1-C2	2.08	121.61	117.60

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	402	7DV	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 [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	167/170 (98%)	-0.48	1 (0%) 85 87	12, 19, 32, 47	0
1	C	161/170 (94%)	-0.49	0 100 100	11, 19, 32, 47	0
1	E	164/170 (96%)	-0.35	1 (0%) 85 87	13, 22, 39, 67	0
1	G	165/170 (97%)	-0.32	2 (1%) 76 79	14, 23, 41, 54	0
2	B	332/341 (97%)	-0.66	0 100 100	9, 16, 28, 55	3 (0%)
2	D	321/341 (94%)	-0.56	7 (2%) 62 66	10, 16, 32, 79	1 (0%)
2	F	324/341 (95%)	-0.46	5 (1%) 72 75	13, 19, 36, 73	1 (0%)
2	H	329/341 (96%)	-0.54	2 (0%) 85 87	11, 18, 32, 56	3 (0%)
All	All	1963/2044 (96%)	-0.51	18 (0%) 81 83	9, 18, 35, 79	8 (0%)

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	335	PRO	3.7
2	D	337	VAL	3.6
1	G	165	CYS	3.5
1	E	166	GLN	3.4
1	A	169	ALA	3.4

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($\text{\AA}^2$)	Q<0.9
4	7DV	D	402	9/9	0.92	0.10	20,21,22,24	0
4	7DV	B	402	9/9	0.94	0.10	19,20,21,23	0
4	7DV	F	402	9/9	0.94	0.10	24,25,27,36	1
4	7DV	H	402	9/9	0.94	0.09	20,25,26,26	1
3	FE	D	401	1/1	0.99	0.01	22,22,22,22	0
3	FE	H	401	1/1	0.99	0.02	24,24,24,24	0
3	FE	F	401	1/1	1.00	0.02	23,23,23,23	0
3	FE	B	401	1/1	1.00	0.02	19,19,19,19	0

6.5 Other polymers [i](#)

There are no such residues in this entry.