



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 01:04 PM UTC

PDB ID : 5M4O / pdb_00005m4o
Title : Crystal structure of hydroquinone 1,2-dioxygenase from *Sphingomonas* sp. TTNP3 in complex with 4-nitrophenol
Authors : Ferraroni, M.; Da Vela, S.; Scozzafava, A.; Kolvenbach, B.; Corvini, P.F.X.
Deposited on : 2016-10-18
Resolution : 2.10 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

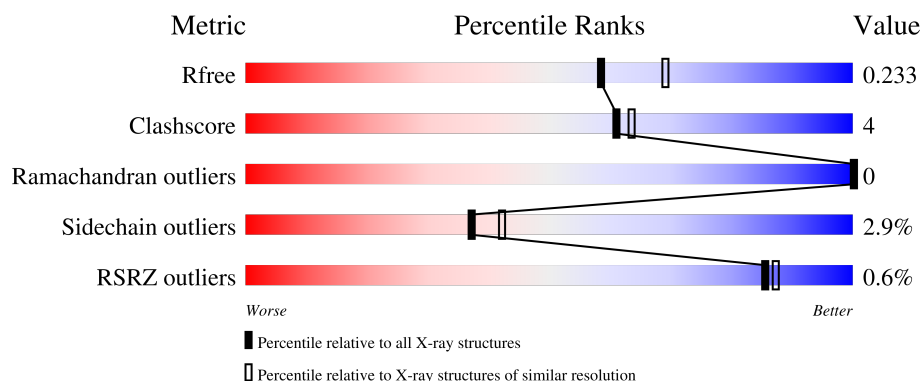
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

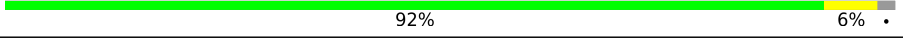
The reported resolution of this entry is 2.10 Å.

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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	
1	C	170	
1	E	170	
1	G	170	
2	B	341	

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Mol	Chain	Length	Quality of chain
2	D	341	% 86% 9%5%
2	F	341	87% 8%••
2	H	341	2% 89% 9%•

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 16487 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	166	Total	C	N	O	S	0	0	0
			1275	808	216	245	6			
1	C	167	Total	C	N	O	S	0	0	0
			1284	813	217	248	6			
1	E	167	Total	C	N	O	S	0	0	0
			1275	808	213	248	6			
1	G	164	Total	C	N	O	S	0	0	0
			1253	796	211	240	6			

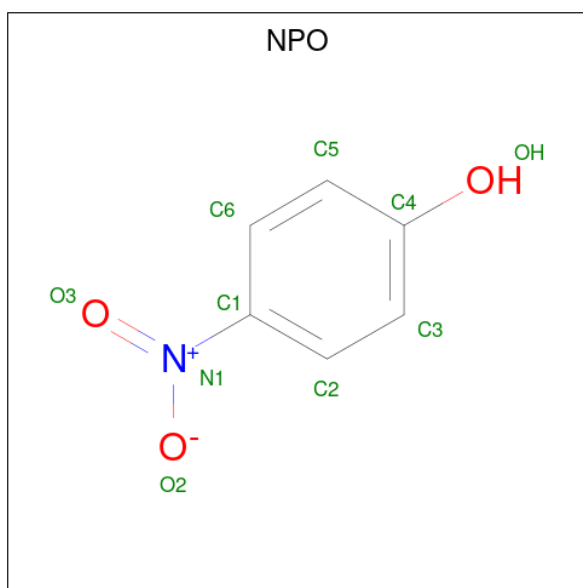
- Molecule 2 is a protein called Hydroquinone dioxygenase large subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	325	Total	C	N	O	S	0	2	0
			2573	1630	448	481	14			
2	D	324	Total	C	N	O	S	0	0	0
			2533	1603	441	475	14			
2	F	326	Total	C	N	O	S	0	4	0
			2579	1633	450	480	16			
2	H	332	Total	C	N	O	S	0	2	0
			2595	1642	453	486	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 P-NITROPHENOL (CCD ID: NPO) (formula: $C_6H_5NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			10	6	1	3		
4	D	1	Total	C	N	O	0	0
			10	6	1	3		
4	F	1	Total	C	N	O	0	0
			10	6	1	3		
4	H	1	Total	C	N	O	0	0
			10	6	1	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	88	Total	O	0	0
			88	88		
5	B	241	Total	O	0	0
			241	241		
5	C	101	Total	O	0	0
			101	101		
5	D	197	Total	O	0	0
			197	197		
5	E	71	Total	O	0	0
			71	71		
5	F	161	Total	O	0	0
			161	161		
5	G	37	Total	O	0	0
			37	37		

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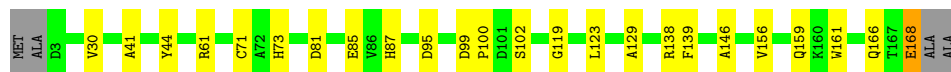
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	180	Total 180	O 180	0	0

3 Residue-property plots

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

Chain A: 



- Molecule 1: Hydroquinone dioxygenase small subunit

Chain C: 



- Molecule 1: Hydroquinone dioxygenase small subunit

Chain E: 



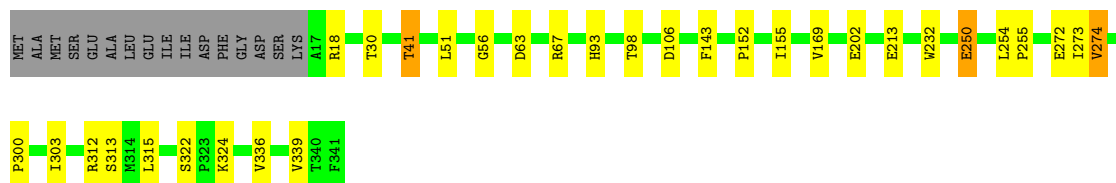
- Molecule 1: Hydroquinone dioxygenase small subunit

Chain G: 

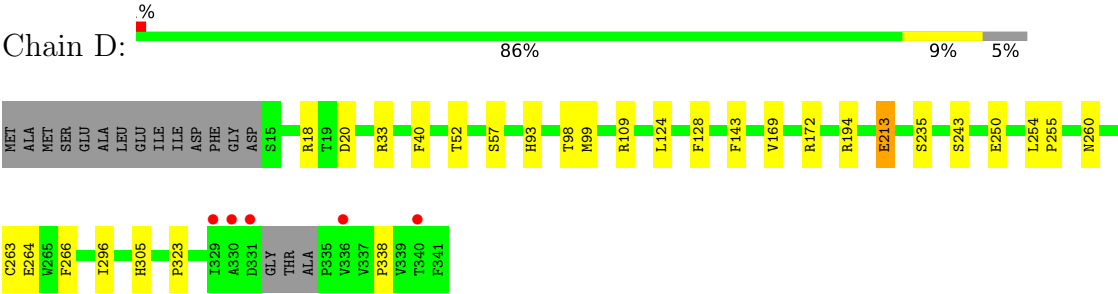


- Molecule 2: Hydroquinone dioxygenase large subunit

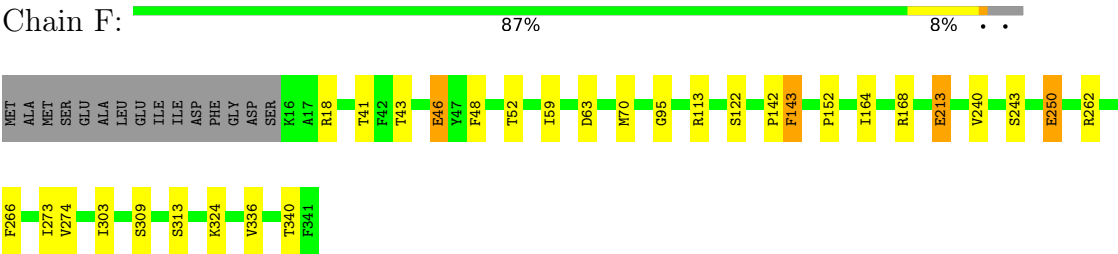
Chain B: 



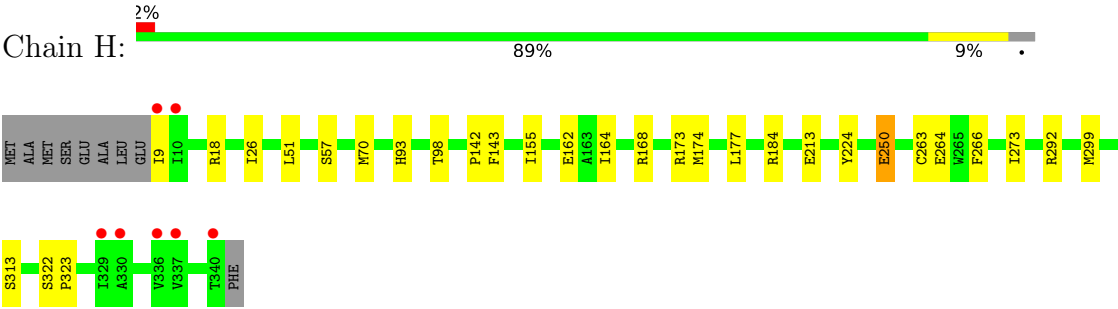
● Molecule 2: Hydroquinone dioxygenase large subunit



● Molecule 2: Hydroquinone dioxygenase large subunit



● Molecule 2: Hydroquinone dioxygenase large subunit



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	88.99Å 125.98Å 92.33Å 90.00° 105.14° 90.00°	Depositor
Resolution (Å)	29.70 – 2.10 29.70 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.3 (29.70-2.10) 99.0 (29.70-2.10)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.02 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.188 , 0.249 (Not available) , 0.233	Depositor DCC
R_{free} test set	6331 reflections (4.78%)	wwPDB-VP
Wilson B-factor (Å ²)	27.6	Xtriage
Anisotropy	0.637	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 44.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.028 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	16487	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.09% 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: NPO, FE

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	0.53	0/1302	0.79	0/1766
1	C	0.56	0/1311	0.88	3/1778 (0.2%)
1	E	0.51	0/1302	0.78	0/1768
1	G	0.51	0/1280	0.81	3/1737 (0.2%)
2	B	0.58	0/2652	0.84	3/3606 (0.1%)
2	D	0.58	0/2605	0.81	0/3543
2	F	0.53	0/2660	0.77	1/3615 (0.0%)
2	H	0.55	0/2674	0.80	0/3638
All	All	0.55	0/15786	0.81	10/21451 (0.0%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	22	ILE	N-CA-C	-7.26	104.65	111.48
1	C	99	ASP	CA-C-N	-6.89	113.70	120.52
1	C	99	ASP	C-N-CA	-6.89	113.70	120.52
2	B	272	GLU	N-CA-C	5.87	117.78	108.79
1	C	18	GLY	N-CA-C	5.68	118.25	110.69
1	G	151	SER	N-CA-C	5.32	115.06	108.19
2	F	95	GLY	N-CA-C	-5.14	107.77	113.79
2	B	56	GLY	N-CA-C	5.11	118.93	110.55
2	B	18	ARG	N-CA-C	5.04	117.03	110.43
1	G	119	GLY	N-CA-C	5.01	118.07	110.75

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	1275	0	1220	18	0
1	C	1284	0	1229	7	0
1	E	1275	0	1209	6	0
1	G	1253	0	1196	19	0
2	B	2573	0	2437	19	0
2	D	2533	0	2353	25	0
2	F	2579	0	2438	20	0
2	H	2595	0	2423	23	0
3	B	1	0	0	0	0
3	D	1	0	0	1	0
3	F	1	0	0	0	0
3	H	1	0	0	0	0
4	B	10	0	5	1	0
4	D	10	0	4	0	0
4	F	10	0	4	1	0
4	H	10	0	4	0	0
5	A	88	0	0	1	0
5	B	241	0	0	5	0
5	C	101	0	0	1	0
5	D	197	0	0	5	0
5	E	71	0	0	2	0
5	F	161	0	0	5	0
5	G	37	0	0	1	0
5	H	180	0	0	6	0
All	All	16487	0	14522	125	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 4.

All (125) 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:F:250[B]:GLU:OE1	2:F:313[B]:SER:HB2	1.37	1.21
2:D:172:ARG:HB2	5:D:676:HOH:O	1.48	1.10
1:G:58:GLU:OE2	1:G:157:THR:HG22	1.59	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:70[A]:MET:HE1	2:F:164:ILE:HA	1.44	0.98
2:D:99:MET:HE1	2:D:128:PHE:CZ	1.99	0.97
1:A:159:GLN:HE21	1:A:161:TRP:HE1	1.02	0.94
1:E:159:GLN:HE21	1:E:161:TRP:HE1	1.20	0.89
1:G:76:PHE:CD1	2:H:174:MET:HE3	2.08	0.89
2:H:250[B]:GLU:CD	2:H:273:ILE:HD11	1.99	0.88
2:D:305:HIS:HE1	5:D:526:HOH:O	1.57	0.87
2:F:41:THR:HG22	2:F:52:THR:OG1	1.75	0.87
2:H:70:MET:HE2	2:H:142:PRO:HG2	1.57	0.86
2:B:250[B]:GLU:OE2	2:B:313[B]:SER:HB2	1.77	0.84
2:D:99:MET:HE1	2:D:128:PHE:CE1	2.13	0.83
2:H:70:MET:HE1	2:H:164:ILE:HA	1.60	0.83
2:H:250[B]:GLU:OE1	2:H:313[B]:SER:OG	1.96	0.83
2:D:305:HIS:CE1	5:D:526:HOH:O	2.30	0.82
2:D:99:MET:CE	2:D:128:PHE:HZ	1.97	0.78
2:D:260:ASN:HB2	5:D:526:HOH:O	1.82	0.78
1:G:159:GLN:HE21	1:G:161:TRP:HE1	1.27	0.78
2:D:99:MET:CE	2:D:128:PHE:CZ	2.68	0.76
2:H:250[B]:GLU:CD	2:H:313[B]:SER:OG	2.29	0.74
1:G:76:PHE:CE1	2:H:174:MET:HE3	2.23	0.74
2:H:93:HIS:HE1	2:H:98:THR:OG1	1.71	0.73
2:F:250[B]:GLU:CD	2:F:273:ILE:HD11	2.14	0.72
1:G:89:LEU:HG	5:G:220:HOH:O	1.89	0.72
2:D:18:ARG:HD3	2:D:20:ASP:OD1	1.90	0.72
2:D:99:MET:HE1	2:D:128:PHE:HZ	1.53	0.71
1:A:100:PRO:HG3	2:D:323:PRO:HG2	1.73	0.70
1:C:159:GLN:HE21	1:C:161:TRP:HE1	1.40	0.69
2:B:93:HIS:HE1	2:B:98:THR:OG1	1.77	0.68
1:G:76:PHE:HD1	2:H:174:MET:HE3	1.59	0.68
2:H:263:CYS:HB3	5:H:570:HOH:O	1.93	0.68
2:B:202:GLU:HB2	5:B:663:HOH:O	1.95	0.67
2:H:250[B]:GLU:OE2	2:H:313[B]:SER:OG	2.11	0.67
1:G:143:GLN:HG3	1:G:144:PRO:HD2	1.78	0.66
2:D:264:GLU:OE1	3:D:401:FE:FE	1.49	0.66
1:E:87:HIS:HE1	5:E:821:HOH:O	1.80	0.64
1:A:95:ASP:OD2	2:D:323:PRO:HG3	1.99	0.62
2:D:99:MET:HE3	2:D:124:LEU:HD21	1.82	0.61
2:F:70[A]:MET:HE2	2:F:142:PRO:HG2	1.81	0.61
1:G:159:GLN:NE2	1:G:161:TRP:HE1	1.99	0.59
2:B:250[B]:GLU:CD	2:B:273:ILE:HD11	2.28	0.59
2:H:9:ILE:HA	5:H:659:HOH:O	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:168:GLU:HB3	5:C:284:HOH:O	2.03	0.59
2:F:41:THR:HG23	5:F:506:HOH:O	2.02	0.58
1:A:159:GLN:HE21	1:A:161:TRP:NE1	1.87	0.58
2:B:41:THR:HG22	5:B:521:HOH:O	2.03	0.58
1:G:159:GLN:HE21	1:G:161:TRP:NE1	1.99	0.57
2:F:240:VAL:HG13	2:F:243:SER:HB3	1.87	0.56
1:G:76:PHE:HD1	2:H:174:MET:CE	2.18	0.56
2:F:18:ARG:HD2	5:F:604:HOH:O	2.05	0.56
1:A:123:LEU:HD21	1:A:129:ALA:HB2	1.87	0.54
1:G:129:ALA:C	2:H:174:MET:HE1	2.33	0.54
2:B:322:SER:OG	2:B:324:LYS:HG2	2.06	0.54
2:H:184:ARG:HG3	2:H:224:TYR:CE1	2.43	0.54
1:E:87:HIS:HD2	5:E:866:HOH:O	1.90	0.53
2:H:250[B]:GLU:OE2	2:H:273:ILE:HD11	2.09	0.53
2:B:274:VAL:HG22	5:B:535:HOH:O	2.08	0.53
1:C:55:TYR:CD1	2:D:243:SER:HB2	2.44	0.53
2:F:168:ARG:HG2	5:F:650:HOH:O	2.08	0.52
1:A:156:VAL:HG12	5:A:230:HOH:O	2.10	0.52
1:C:83:GLN:HE21	1:C:124:ARG:HD2	1.74	0.52
2:D:263:CYS:SG	2:D:338:PRO:HD3	2.50	0.51
1:G:76:PHE:CD1	2:H:174:MET:CE	2.88	0.51
2:H:266:PHE:CE2	2:H:299:MET:HG3	2.45	0.51
1:A:81:ASP:HB3	1:A:146:ALA:H	1.76	0.50
1:A:87:HIS:ND1	1:A:138:ARG:NH1	2.60	0.50
2:F:113:ARG:HD2	5:F:631:HOH:O	2.11	0.50
1:G:15:ARG:O	2:H:292:ARG:HD2	2.11	0.50
1:E:25:ASP:OD1	1:E:26:PRO:HD2	2.11	0.50
2:B:41:THR:CG2	5:B:521:HOH:O	2.58	0.49
1:C:31:PHE:O	1:C:165:CYS:HA	2.12	0.49
2:H:184:ARG:HD3	5:H:653:HOH:O	2.11	0.49
2:B:232:TRP:HA	4:B:402:NPO:OH	2.12	0.49
1:G:153:GLU:HA	1:G:157:THR:HG21	1.93	0.49
2:D:93:HIS:HE1	2:D:98:THR:OG1	1.95	0.48
2:F:63:ASP:HB3	2:F:152:PRO:HG3	1.94	0.48
2:H:18:ARG:HD2	5:H:596:HOH:O	2.14	0.47
2:H:173:ARG:HD3	2:H:177:LEU:HD13	1.96	0.47
2:H:322:SER:HA	2:H:323:PRO:HD3	1.81	0.46
1:A:159:GLN:NE2	1:A:161:TRP:HE1	1.87	0.46
1:G:123:LEU:HD21	1:G:129:ALA:HB2	1.98	0.46
2:B:30:THR:HA	2:B:155:ILE:HG22	1.97	0.46
2:D:99:MET:HE2	2:D:128:PHE:HZ	1.76	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:64:GLY:O	1:G:140:TYR:HA	2.16	0.46
2:F:324:LYS:HA	5:F:651:HOH:O	2.16	0.45
2:F:48:PHE:HB3	2:F:59:ILE:HG23	1.97	0.45
2:F:250[B]:GLU:OE1	2:F:273:ILE:HD11	2.15	0.45
2:B:250[B]:GLU:OE2	2:B:273:ILE:HD11	2.17	0.45
1:G:14:TYR:OH	1:G:36:GLU:HG3	2.17	0.45
1:A:100:PRO:HG3	2:D:323:PRO:CG	2.45	0.45
2:D:213:GLU:H	2:D:213:GLU:CD	2.25	0.44
1:E:87:HIS:O	1:E:137:TYR:HA	2.18	0.44
2:F:274:VAL:CG2	5:H:504:HOH:O	2.64	0.44
1:A:119:GLY:HA2	5:B:558:HOH:O	2.16	0.44
1:A:161:TRP:CD2	2:B:339:VAL:HG11	2.52	0.44
2:B:250[A]:GLU:OE2	2:B:315:LEU:HD23	2.18	0.44
2:B:106:ASP:OD1	2:B:106:ASP:N	2.52	0.43
2:D:169:VAL:HG23	2:D:235:SER:OG	2.17	0.43
1:A:71:CYS:SG	1:A:73:HIS:CE1	3.11	0.43
2:F:213:GLU:H	2:F:213:GLU:CD	2.25	0.43
1:C:90:LYS:HB2	1:C:118:MET:HG3	2.00	0.43
2:F:46:GLU:HG3	5:H:508:HOH:O	2.19	0.43
1:A:166:GLN:HE21	1:A:168:GLU:HB2	1.84	0.43
1:C:100:PRO:C	1:C:102:SER:H	2.27	0.43
2:F:70[A]:MET:HE3	2:F:143:PHE:CD2	2.53	0.43
2:F:266:PHE:HZ	4:F:402:NPO:O3	2.01	0.42
2:B:67:ARG:HB3	2:B:255:PRO:HB3	2.00	0.42
2:D:40:PHE:HA	2:D:52:THR:O	2.20	0.42
2:B:300:PRO:O	2:B:303:ILE:HG13	2.21	0.41
1:A:85:GLU:O	1:A:139:PHE:HA	2.20	0.41
2:B:254:LEU:HA	2:B:255:PRO:HD3	1.90	0.41
1:G:58:GLU:OE2	1:G:157:THR:CG2	2.48	0.41
2:D:33:ARG:NE	5:D:509:HOH:O	2.54	0.41
2:F:303:ILE:C	2:F:303:ILE:HD12	2.46	0.41
1:E:46:ARG:NH1	1:E:137:TYR:OH	2.44	0.41
1:G:30:VAL:HG12	1:G:165:CYS:SG	2.60	0.41
2:B:63:ASP:HB3	2:B:152:PRO:HG3	2.02	0.40
2:D:254:LEU:HA	2:D:255:PRO:HD3	1.86	0.40
1:A:99:ASP:HB3	1:A:102:SER:HB3	2.03	0.40
1:A:41:ALA:O	1:A:61:ARG:NH1	2.47	0.40
1:A:44:TYR:CE1	1:A:139:PHE:HB2	2.56	0.40
2:D:266:PHE:O	2:D:296:ILE:HA	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	164/170 (96%)	157 (96%)	7 (4%)	0	100	100
1	C	165/170 (97%)	155 (94%)	10 (6%)	0	100	100
1	E	165/170 (97%)	159 (96%)	6 (4%)	0	100	100
1	G	162/170 (95%)	152 (94%)	10 (6%)	0	100	100
2	B	325/341 (95%)	310 (95%)	15 (5%)	0	100	100
2	D	320/341 (94%)	306 (96%)	14 (4%)	0	100	100
2	F	328/341 (96%)	311 (95%)	17 (5%)	0	100	100
2	H	332/341 (97%)	316 (95%)	16 (5%)	0	100	100
All	All	1961/2044 (96%)	1866 (95%)	95 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	128/131 (98%)	126 (98%)	2 (2%)	55	64
1	C	129/131 (98%)	126 (98%)	3 (2%)	44	51
1	E	127/131 (97%)	124 (98%)	3 (2%)	43	49
1	G	125/131 (95%)	122 (98%)	3 (2%)	43	49
2	B	271/284 (95%)	262 (97%)	9 (3%)	33	37
2	D	261/284 (92%)	255 (98%)	6 (2%)	44	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	F	269/284 (95%)	258 (96%)	11 (4%)	27	29
2	H	267/284 (94%)	256 (96%)	11 (4%)	27	29
All	All	1577/1660 (95%)	1529 (97%)	48 (3%)	37	41

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

Mol	Chain	Res	Type
1	A	30	VAL
1	A	168	GLU
2	B	41	THR
2	B	51	LEU
2	B	143	PHE
2	B	169	VAL
2	B	213	GLU
2	B	250[A]	GLU
2	B	250[B]	GLU
2	B	274	VAL
2	B	336	VAL
1	C	3	ASP
1	C	54	GLU
1	C	89	LEU
2	D	57	SER
2	D	109	ARG
2	D	143	PHE
2	D	194	ARG
2	D	213	GLU
2	D	250	GLU
1	E	7	GLU
1	E	12	THR
1	E	138	ARG
2	F	43	THR
2	F	46	GLU
2	F	122	SER
2	F	143	PHE
2	F	213	GLU
2	F	250[A]	GLU
2	F	250[B]	GLU
2	F	262	ARG
2	F	309	SER
2	F	336	VAL
2	F	340	THR

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Mol	Chain	Res	Type
1	G	4	VAL
1	G	30	VAL
1	G	143	GLN
2	H	26	ILE
2	H	51	LEU
2	H	57	SER
2	H	143	PHE
2	H	155	ILE
2	H	162	GLU
2	H	168	ARG
2	H	213	GLU
2	H	250[A]	GLU
2	H	250[B]	GLU
2	H	264	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	28	ASN
1	A	40	ASN
1	A	93	ASN
1	A	159	GLN
2	B	23	HIS
2	B	93	HIS
2	B	105	ASN
1	C	28	ASN
1	C	40	ASN
1	C	83	GLN
1	C	159	GLN
2	D	23	HIS
2	D	93	HIS
2	D	160	ASN
2	D	203	GLN
1	E	28	ASN
1	E	40	ASN
1	E	83	GLN
1	E	87	HIS
1	E	159	GLN
1	G	40	ASN
1	G	159	GLN
2	H	28	ASN
2	H	93	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	NPO	B	402	3	10,10,10	3.12	1 (10%)	11,13,13	0.82	1 (9%)
4	NPO	D	402	3	10,10,10	3.12	2 (20%)	11,13,13	1.15	1 (9%)
4	NPO	H	402	3	10,10,10	3.07	1 (10%)	11,13,13	0.94	1 (9%)
4	NPO	F	402	3	10,10,10	2.97	2 (20%)	11,13,13	0.89	1 (9%)

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	NPO	B	402	3	-	0/2/4/4	0/1/1/1
4	NPO	D	402	3	-	2/2/4/4	0/1/1/1
4	NPO	H	402	3	-	0/2/4/4	0/1/1/1
4	NPO	F	402	3	-	0/2/4/4	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	402	NPO	O3-N1	9.54	1.39	1.22
4	H	402	NPO	O3-N1	9.41	1.39	1.22
4	D	402	NPO	O3-N1	9.26	1.38	1.22
4	F	402	NPO	O3-N1	9.01	1.38	1.22
4	D	402	NPO	C1-N1	-3.08	1.37	1.45
4	F	402	NPO	C1-N1	-2.27	1.39	1.45

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	402	NPO	C2-C1-N1	2.68	121.68	119.34
4	F	402	NPO	O3-N1-C1	2.44	122.17	118.82
4	B	402	NPO	O3-N1-C1	2.32	122.01	118.82
4	D	402	NPO	C2-C1-N1	-2.02	117.58	119.34

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	402	NPO	C2-C1-N1-O3
4	D	402	NPO	C6-C1-N1-O3

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	402	NPO	1	0
4	F	402	NPO	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 ⓘ

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	166/170 (97%)	-0.37	0 100 100	22, 32, 45, 56	0
1	C	167/170 (98%)	-0.38	0 100 100	21, 31, 54, 72	0
1	E	167/170 (98%)	-0.27	0 100 100	23, 35, 51, 66	0
1	G	164/170 (96%)	0.07	0 100 100	29, 44, 63, 78	0
2	B	325/341 (95%)	-0.51	0 100 100	17, 27, 40, 55	2 (0%)
2	D	324/341 (95%)	-0.37	5 (1%) 72 74	19, 29, 50, 97	0
2	F	326/341 (95%)	-0.34	0 100 100	13, 32, 52, 69	4 (1%)
2	H	332/341 (97%)	-0.25	7 (2%) 63 66	17, 33, 64, 90	2 (0%)
All	All	1971/2044 (96%)	-0.32	12 (0%) 85 87	13, 31, 54, 97	8 (0%)

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	331	ASP	3.1
2	H	9	ILE	3.1
2	D	330	ALA	3.0
2	D	336	VAL	3.0
2	H	336	VAL	2.9
2	H	340	THR	2.9
2	D	329	ILE	2.8
2	H	337	VAL	2.8
2	D	340	THR	2.6
2	H	330	ALA	2.4
2	H	329	ILE	2.4
2	H	10	ILE	2.3

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	NPO	B	402	10/10	0.93	0.07	29,30,33,37	0
4	NPO	D	402	10/10	0.94	0.07	31,33,37,38	0
4	NPO	H	402	10/10	0.95	0.07	37,39,47,48	0
4	NPO	F	402	10/10	0.96	0.06	31,32,42,43	0
3	FE	B	401	1/1	0.99	0.02	25,25,25,25	0
3	FE	D	401	1/1	0.99	0.03	37,37,37,37	0
3	FE	F	401	1/1	0.99	0.02	32,32,32,32	0
3	FE	H	401	1/1	0.99	0.02	42,42,42,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.