



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 04:26 pm GMT

PDB ID : 1W1J
Title : STRUCTURE OF THE OCTAMERIC FLAVOENZYME VANILLYL-ALCOHOL OXIDASE: THE505SER MUTANT
Authors : Van Den Heuvel, R.H.
Deposited on : 2004-06-22
Resolution : 2.70 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 : trunk28620
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) : recalc28949

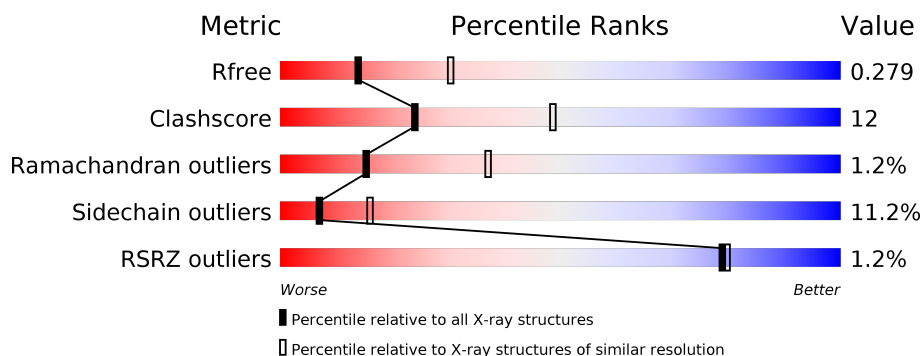
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.70 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	2259 (2.70-2.70)
Clashscore	112137	2590 (2.70-2.70)
Ramachandran outliers	110173	2550 (2.70-2.70)
Sidechain outliers	110143	2550 (2.70-2.70)
RSRZ outliers	101464	2275 (2.70-2.70)

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	560	
1	B	560	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	EUG	B	1562	-	-	-	X

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 8828 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.

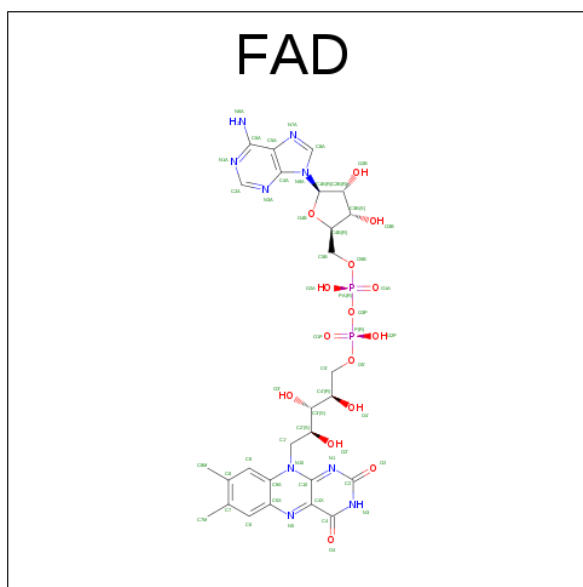
- Molecule 1 is a protein called VANILLYL-ALCOHOL OXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	550	Total	C	N	O	S	0	0	0
			4350	2792	744	790	24			
1	B	550	Total	C	N	O	S	0	0	0
			4350	2792	744	790	24			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	505	SER	THR	ENGINEERED MUTATION	UNP P56216
B	505	SER	THR	ENGINEERED MUTATION	UNP P56216

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



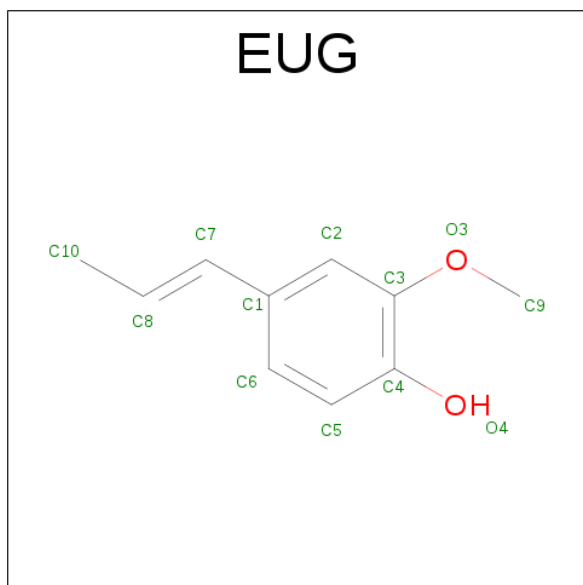
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 3 is 2-METHOXY-4-VINYL-PHENOL (three-letter code: EUG) (formula: $C_{10}H_{12}O_2$).

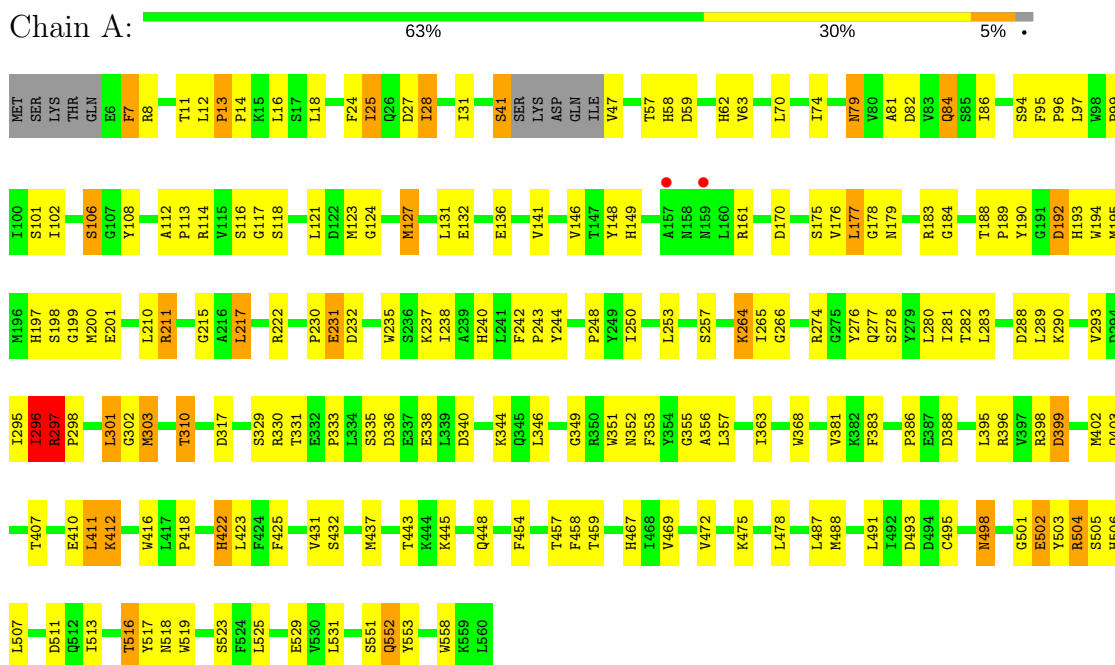


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			11	9	2		
3	B	1	Total	C	O	0	0
			11	9	2		

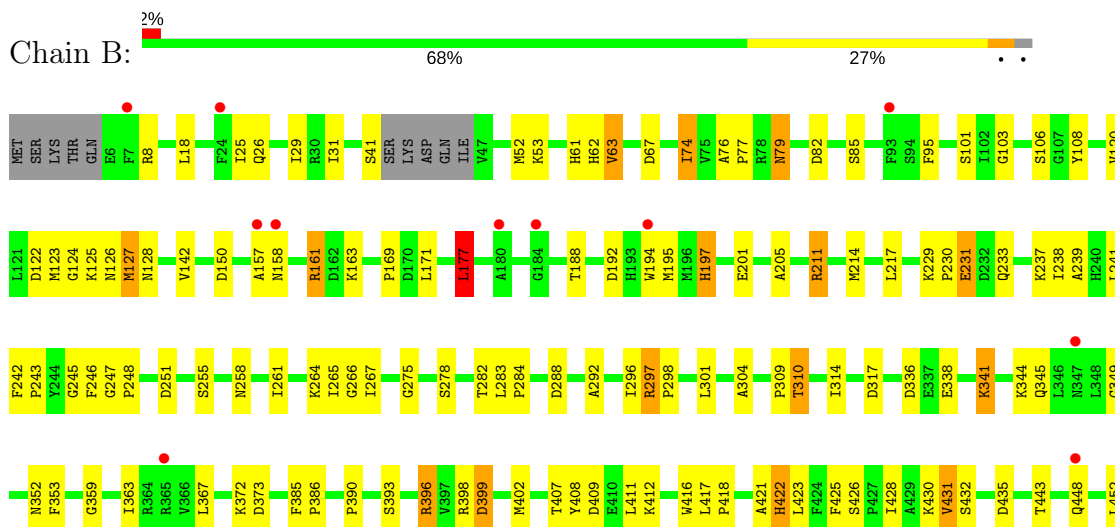
3 Residue-property plots

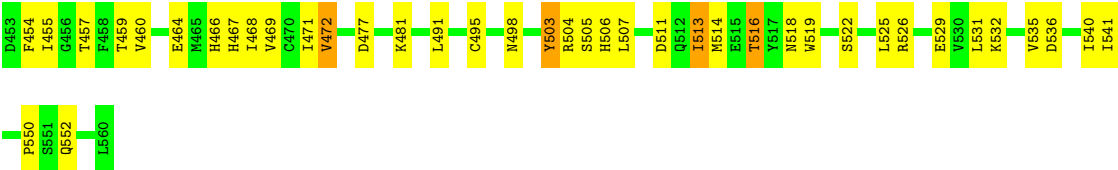
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: VANILLYL-ALCOHOL OXIDASE



• Molecule 1: VANILLYL-ALCOHOL OXIDASE





4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α , β , γ	129.52Å 129.52Å 133.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.70 42.02 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.9 (40.00-2.70) 97.9 (42.02-2.70)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.61 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.1.27	Depositor
R, R_{free}	0.207 , 0.292 0.205 , 0.279	Depositor DCC
R_{free} test set	1501 reflections (5.36%)	DCC
Wilson B-factor (Å ²)	56.2	Xtriage
Anisotropy	0.533	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 36.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.008 for l,-k,h 0.023 for -l,-k,-h 0.023 for -h,-l,-k 0.008 for -h,l,k 0.038 for -h,k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8828	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.16% 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: EUG, FAD

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	0.71	0/4469	0.89	9/6073 (0.1%)
1	B	0.51	0/4469	0.80	13/6073 (0.2%)
All	All	0.62	0/8938	0.85	22/12146 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	251	ASP	CB-CG-OD2	6.97	124.58	118.30
1	A	317	ASP	CB-CG-OD2	6.39	124.05	118.30
1	A	192	ASP	CB-CG-OD2	6.30	123.97	118.30
1	B	288	ASP	CB-CG-OD2	6.30	123.97	118.30
1	B	317	ASP	CB-CG-OD2	6.21	123.89	118.30
1	B	511	ASP	CB-CG-OD2	6.09	123.78	118.30
1	A	388	ASP	CB-CG-OD2	6.04	123.74	118.30
1	A	288	ASP	CB-CG-OD2	5.98	123.68	118.30
1	B	122	ASP	CB-CG-OD2	5.67	123.40	118.30
1	A	340	ASP	CB-CG-OD2	5.66	123.39	118.30
1	B	177	LEU	CA-CB-CG	5.61	128.21	115.30
1	B	409	ASP	CB-CG-OD2	5.50	123.25	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	192	ASP	CB-CG-OD2	5.47	123.22	118.30
1	A	27	ASP	CB-CG-OD2	5.45	123.21	118.30
1	A	399	ASP	CB-CG-OD2	5.39	123.15	118.30
1	A	232	ASP	CB-CG-OD2	5.38	123.14	118.30
1	B	477	ASP	CB-CG-OD2	5.31	123.08	118.30
1	B	435	ASP	CB-CG-OD2	5.17	122.95	118.30
1	A	493	ASP	CB-CG-OD2	5.16	122.95	118.30
1	B	399	ASP	CB-CG-OD2	5.13	122.92	118.30
1	B	67	ASP	CB-CG-OD2	5.07	122.86	118.30
1	B	150	ASP	CB-CG-OD2	5.04	122.84	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	127	MET	Peptide
1	B	127	MET	Peptide

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	4350	0	4286	136	0
1	B	4350	0	4286	97	0
2	A	53	0	29	0	0
2	B	53	0	29	2	0
3	A	11	0	7	1	0
3	B	11	0	7	1	0
All	All	8828	0	8644	218	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 12.

All (218) 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:513:ILE:O	1:A:516:THR:HB	1.64	0.97
1:A:552:GLN:H	1:A:552:GLN:HE21	0.99	0.93
1:A:552:GLN:H	1:A:552:GLN:NE2	1.71	0.86
1:B:550:PRO:HB2	1:B:552:GLN:NE2	1.91	0.86
1:A:79:ASN:ND2	1:A:82:ASP:H	1.77	0.82
1:B:513:ILE:O	1:B:516:THR:HB	1.81	0.80
1:B:550:PRO:HB2	1:B:552:GLN:HE22	1.48	0.79
1:A:114:ARG:NH2	1:A:511:ASP:OD2	2.15	0.77
1:B:310:THR:HG22	1:B:459:THR:HG22	1.66	0.76
1:B:74:ILE:HG13	1:B:120:VAL:HB	1.68	0.76
1:A:552:GLN:HE21	1:A:552:GLN:N	1.82	0.74
1:A:330:ARG:NH2	1:A:333:PRO:O	2.21	0.73
1:A:519:TRP:CZ3	1:B:211:ARG:HG2	2.22	0.73
1:B:292:ALA:O	1:B:296:ILE:HG13	1.91	0.71
1:A:211:ARG:HG3	1:B:519:TRP:CZ3	2.24	0.71
1:A:28:ILE:HD11	1:A:86:ILE:HG23	1.72	0.70
1:B:275:GLY:HA3	1:B:359:GLY:O	1.91	0.70
1:A:82:ASP:O	1:A:86:ILE:HG13	1.93	0.68
1:A:179:ASN:OD1	1:A:184:GLY:HA3	1.93	0.68
1:A:443:THR:HG21	1:A:469:VAL:HG21	1.73	0.68
1:B:349:GLY:H	1:B:352:ASN:HD21	1.41	0.67
1:A:277:GLN:HB3	1:A:357:LEU:HD12	1.78	0.66
1:A:282:THR:HG22	1:A:352:ASN:HD22	1.61	0.65
1:A:443:THR:HA	1:A:491:LEU:HD21	1.78	0.65
1:B:177:LEU:HB2	1:B:265:ILE:HG21	1.80	0.64
1:A:136:GLU:HA	1:B:297:ARG:HH21	1.63	0.64
1:B:31:ILE:HD13	1:B:85:SER:HB3	1.79	0.64
1:A:8:ARG:O	1:A:41:SER:HB3	1.97	0.64
1:A:81:ALA:HA	1:A:84:GLN:HG3	1.80	0.64
1:A:63:VAL:HG11	1:A:423:LEU:HD22	1.79	0.64
1:B:443:THR:HA	1:B:491:LEU:HD21	1.80	0.64
1:A:201:GLU:OE2	1:A:211:ARG:HD3	1.98	0.64
1:A:330:ARG:NH1	1:A:338:GLU:OE1	2.31	0.63
1:A:281:ILE:HG12	1:A:383:PHE:HD1	1.64	0.63
1:A:108:TYR:CZ	1:A:504:ARG:HG2	2.34	0.62
1:A:177:LEU:HB2	1:A:265:ILE:HG21	1.82	0.62
1:A:79:ASN:HD21	1:A:82:ASP:H	1.46	0.62
1:A:297:ARG:HB3	1:A:298:PRO:HD3	1.81	0.62
1:A:502:GLU:N	1:A:502:GLU:OE1	2.33	0.61
1:A:250:ILE:O	1:A:253:LEU:HB2	2.00	0.61
1:A:59:ASP:OD2	1:A:62:HIS:HA	2.00	0.61
1:A:355:GLY:O	1:A:402:MET:CE	2.49	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:177:LEU:HB2	1:B:265:ILE:CG2	2.32	0.60
1:A:47:VAL:O	1:A:58:HIS:HE1	1.86	0.59
1:A:425:PHE:HD1	1:A:488:MET:CE	2.16	0.58
1:A:201:GLU:OE1	1:A:264:LYS:NZ	2.32	0.58
1:A:13:PRO:HD3	1:A:117:GLY:O	2.04	0.58
1:B:201:GLU:HB3	1:B:264:LYS:HB2	1.85	0.58
1:A:106:SER:HB3	1:A:422:HIS:HE1	1.70	0.57
1:A:194:TRP:O	1:A:197:HIS:HD2	1.87	0.57
1:A:487:LEU:CD1	1:A:491:LEU:HD12	2.35	0.56
1:A:425:PHE:HD1	1:A:488:MET:HE1	1.71	0.56
1:B:106:SER:HB3	1:B:422:HIS:HE1	1.70	0.56
1:B:464:GLU:OE1	1:B:466:HIS:ND1	2.38	0.56
1:A:302:GLY:O	1:A:303:MET:HB2	2.05	0.55
1:A:238:ILE:O	1:A:238:ILE:HG22	2.06	0.55
1:B:525:LEU:O	1:B:529:GLU:HG3	2.07	0.55
1:A:211:ARG:HG3	1:B:519:TRP:CH2	2.41	0.54
1:A:281:ILE:HG12	1:A:383:PHE:CD1	2.42	0.54
1:B:282:THR:HG22	1:B:352:ASN:HD22	1.71	0.54
1:A:101:SER:O	1:A:124:GLY:HA3	2.07	0.54
1:A:297:ARG:O	1:A:301:LEU:HB2	2.08	0.54
1:B:214:MET:HB2	1:B:239:ALA:HA	1.88	0.54
1:B:79:ASN:HD22	1:B:79:ASN:C	2.11	0.53
1:A:79:ASN:HD22	1:A:79:ASN:C	2.12	0.53
1:A:242:PHE:CZ	1:A:244:TYR:HB2	2.44	0.53
1:B:431:VAL:HG12	1:B:431:VAL:O	2.09	0.53
1:A:454:PHE:C	1:A:454:PHE:CD2	2.82	0.53
1:B:230:PRO:HA	1:B:233:GLN:NE2	2.24	0.53
1:A:349:GLY:H	1:A:352:ASN:HD21	1.57	0.53
1:A:297:ARG:HB3	1:A:298:PRO:CD	2.39	0.52
1:A:96:PRO:HG3	1:A:553:TYR:OH	2.09	0.52
1:A:519:TRP:CE3	1:B:211:ARG:HG2	2.44	0.52
1:A:201:GLU:HB3	1:A:264:LYS:HG3	1.91	0.52
1:A:531:LEU:HD22	1:B:531:LEU:HD22	1.93	0.52
1:A:211:ARG:CG	1:B:519:TRP:CZ3	2.92	0.51
1:A:188:THR:HB	1:A:189:PRO:CD	2.41	0.51
1:A:501:GLY:C	1:A:502:GLU:OE1	2.48	0.51
1:A:276:TYR:CE2	1:A:403:GLN:HB3	2.46	0.51
1:A:237:LYS:NZ	1:B:498:ASN:O	2.43	0.51
1:B:506:HIS:ND1	1:B:507:LEU:N	2.59	0.51
1:A:282:THR:HG22	1:A:352:ASN:ND2	2.25	0.51
1:B:297:ARG:HH11	1:B:298:PRO:HD3	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:24:PHE:HD2	1:A:25:ILE:HD13	1.76	0.50
1:A:368:TRP:CG	1:A:368:TRP:O	2.63	0.50
1:B:101:SER:O	1:B:124:GLY:HA3	2.11	0.50
1:A:70:LEU:O	1:A:116:SER:HA	2.10	0.50
1:B:459:THR:OG1	1:B:466:HIS:HB2	2.11	0.50
1:B:468:ILE:HD11	3:B:1562:EUG:H93	1.94	0.50
1:B:398:ARG:O	1:B:402:MET:HG3	2.11	0.50
1:A:192:ASP:OD1	1:A:195:MET:HB2	2.11	0.49
1:A:457:THR:HG22	1:A:458:PHE:O	2.11	0.49
1:A:108:TYR:CE1	1:A:504:ARG:HG2	2.47	0.49
1:A:211:ARG:HD2	1:A:235:TRP:CH2	2.47	0.49
1:A:28:ILE:HA	1:A:31:ILE:HD12	1.94	0.49
1:A:289:LEU:HD22	1:A:351:TRP:CZ2	2.47	0.49
1:A:146:VAL:O	1:A:176:VAL:HG23	2.11	0.49
1:B:123:MET:O	1:B:127:MET:HB2	2.12	0.49
1:A:296:ILE:CD1	1:A:353:PHE:CE1	2.95	0.49
1:B:205:ALA:HB3	1:B:535:VAL:O	2.13	0.49
1:A:183:ARG:NH2	1:B:247:GLY:O	2.35	0.49
1:B:282:THR:HG22	1:B:352:ASN:ND2	2.28	0.49
1:B:443:THR:HA	1:B:491:LEU:CD2	2.42	0.49
1:B:416:TRP:O	1:B:417:LEU:HD23	2.13	0.48
1:A:14:PRO:HG3	1:A:558:TRP:CZ2	2.48	0.48
1:A:197:HIS:HA	1:A:266:GLY:O	2.13	0.48
1:B:522:SER:O	1:B:526:ARG:HG2	2.14	0.48
1:A:487:LEU:HD12	1:A:491:LEU:HD12	1.96	0.48
1:A:330:ARG:HH12	1:A:335:SER:HB3	1.77	0.48
1:B:161:ARG:O	1:B:161:ARG:HG2	2.13	0.48
1:B:425:PHE:HZ	1:B:495:CYS:HG	1.60	0.48
1:A:102:ILE:HG12	1:A:175:SER:HB2	1.94	0.48
1:A:310:THR:HG22	1:A:459:THR:HG22	1.94	0.48
1:A:217:LEU:CD2	1:B:516:THR:HG23	2.44	0.48
1:B:231:GLU:HG3	1:B:231:GLU:H	1.30	0.48
1:B:214:MET:HE2	1:B:245:GLY:HA2	1.95	0.48
1:B:79:ASN:ND2	1:B:82:ASP:H	2.11	0.48
1:B:63:VAL:HG11	1:B:423:LEU:HD22	1.96	0.47
1:A:445:LYS:O	1:A:448:GLN:HB3	2.14	0.47
1:A:257:SER:CB	1:B:248:PRO:HG3	2.44	0.47
1:A:210:LEU:HD23	1:A:211:ARG:N	2.30	0.47
1:A:498:ASN:N	1:A:498:ASN:HD22	2.13	0.47
1:A:79:ASN:HD21	1:A:82:ASP:N	2.10	0.47
1:B:229:LYS:HD2	1:B:231:GLU:OE2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:177:LEU:HB2	1:A:265:ILE:CG2	2.45	0.47
1:B:261:ILE:HD11	1:B:541:ILE:HD12	1.96	0.47
1:A:57:THR:HG22	1:A:74:ILE:HD11	1.96	0.47
1:A:198:SER:HB3	1:A:240:HIS:HA	1.96	0.47
1:A:355:GLY:O	1:A:402:MET:HE3	2.14	0.46
1:A:297:ARG:HG3	1:A:431:VAL:O	2.16	0.46
1:A:525:LEU:O	1:A:529:GLU:HG3	2.14	0.46
1:A:416:TRP:HB3	1:A:472:VAL:HG21	1.96	0.46
1:A:517:TYR:CE1	1:B:246:PHE:HB3	2.51	0.46
1:B:297:ARG:NH1	1:B:298:PRO:HD3	2.29	0.46
1:B:258:ASN:OD1	1:B:532:LYS:HD3	2.15	0.46
1:A:58:HIS:C	1:A:112:ALA:HB2	2.36	0.46
1:B:421:ALA:O	1:B:472:VAL:HA	2.16	0.46
1:A:293:VAL:HA	1:A:296:ILE:HG13	1.98	0.45
1:A:131:LEU:HD12	1:A:141:VAL:HG12	1.98	0.45
1:B:452:LEU:HD11	1:B:471:ILE:HG23	1.98	0.45
1:A:295:ILE:O	1:A:298:PRO:HD2	2.16	0.45
1:B:532:LYS:HE3	1:B:536:ASP:HB3	1.99	0.45
1:A:506:HIS:ND1	1:A:507:LEU:N	2.64	0.45
1:A:278:SER:HA	1:A:356:ALA:HA	1.98	0.45
1:B:177:LEU:HD12	1:B:177:LEU:C	2.36	0.45
1:A:211:ARG:HG3	1:B:519:TRP:CE3	2.51	0.45
1:A:412:LYS:HD3	1:A:412:LYS:HA	1.47	0.45
1:A:7:PHE:N	1:A:7:PHE:CD1	2.85	0.45
1:A:280:LEU:HD11	1:A:282:THR:HG22	1.99	0.44
1:A:79:ASN:ND2	1:A:79:ASN:C	2.71	0.44
1:B:443:THR:HG21	1:B:469:VAL:HG21	1.99	0.44
1:B:278:SER:OG	1:B:399:ASP:OD1	2.20	0.44
1:B:452:LEU:CD1	1:B:471:ILE:HG23	2.47	0.44
1:B:309:PRO:HD2	1:B:460:VAL:HB	1.99	0.44
1:B:125:LYS:HG2	1:B:126:ASN:OD1	2.18	0.44
1:B:504:ARG:HG3	1:B:505:SER:N	2.33	0.44
1:A:425:PHE:CD1	1:A:488:MET:CE	2.99	0.44
1:A:59:ASP:N	1:A:112:ALA:HB2	2.33	0.44
1:A:487:LEU:CD1	1:A:491:LEU:CD1	2.95	0.44
1:B:108:TYR:CZ	1:B:504:ARG:HG2	2.53	0.44
1:B:266:GLY:O	1:B:267:ILE:HD13	2.18	0.44
1:B:464:GLU:OE1	1:B:466:HIS:CE1	2.71	0.44
1:A:386:PRO:HA	1:A:395:LEU:HD23	2.00	0.43
1:A:425:PHE:HZ	1:A:495:CYS:HG	1.66	0.43
1:A:518:ASN:O	1:A:519:TRP:C	2.56	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:210:LEU:HD23	1:A:211:ARG:C	2.38	0.43
1:B:61:HIS:ND1	1:B:421:ALA:HA	2.33	0.43
1:A:276:TYR:CE1	1:A:356:ALA:HB1	2.52	0.43
1:B:423:LEU:CD1	1:B:506:HIS:CD2	3.01	0.43
1:A:112:ALA:HA	1:A:113:PRO:HD3	1.94	0.43
1:B:297:ARG:HB3	1:B:298:PRO:CD	2.48	0.43
1:A:146:VAL:O	1:A:146:VAL:HG12	2.18	0.43
1:A:276:TYR:HE1	1:A:356:ALA:HB1	1.83	0.43
1:B:393:SER:OG	1:B:396:ARG:HB2	2.18	0.43
1:A:123:MET:O	1:A:127:MET:HB2	2.19	0.43
1:A:177:LEU:C	1:A:177:LEU:HD12	2.39	0.43
1:B:309:PRO:HB2	1:B:353:PHE:CE1	2.54	0.43
1:B:341:LYS:O	1:B:345:GLN:HB2	2.19	0.43
1:B:238:ILE:HA	1:B:241:LEU:HD12	2.00	0.42
1:B:61:HIS:CE1	1:B:422:HIS:CE1	3.07	0.42
1:B:518:ASN:O	1:B:519:TRP:C	2.57	0.42
1:A:487:LEU:HD11	1:A:491:LEU:CD1	2.49	0.42
1:B:385:PHE:HB3	1:B:386:PRO:HD2	2.02	0.42
1:B:454:PHE:C	1:B:455:ILE:HG13	2.40	0.42
1:B:103:GLY:CA	2:B:1561:FAD:O1A	2.67	0.42
1:A:175:SER:HB3	1:A:178:GLY:HA3	2.01	0.42
1:B:314:ILE:HG13	1:B:314:ILE:O	2.20	0.42
1:B:201:GLU:CB	1:B:264:LYS:HB2	2.48	0.42
1:B:408:TYR:O	1:B:411:LEU:HB2	2.20	0.42
1:A:290:LYS:HB2	1:A:437:MET:HG3	2.01	0.42
1:A:242:PHE:HA	1:A:243:PRO:HD2	1.89	0.42
1:A:355:GLY:O	1:A:402:MET:HE1	2.19	0.41
1:A:148:TYR:OH	1:A:193:HIS:CE1	2.73	0.41
1:A:211:ARG:HB2	1:A:215:GLY:O	2.19	0.41
1:A:398:ARG:NH1	1:A:410:GLU:OE2	2.52	0.41
1:B:425:PHE:CZ	1:B:491:LEU:HB3	2.56	0.41
1:A:25:ILE:HD12	1:A:25:ILE:HA	1.80	0.41
1:B:171:LEU:HD21	2:B:1561:FAD:HM73	2.02	0.41
1:A:12:LEU:HA	1:A:13:PRO:HD2	1.81	0.41
1:B:514:MET:C	1:B:516:THR:H	2.24	0.41
1:A:330:ARG:CZ	1:A:333:PRO:O	2.68	0.41
1:A:170:ASP:OD2	3:A:1562:EUG:H7	2.20	0.41
1:A:504:ARG:HG3	1:A:505:SER:N	2.34	0.41
1:A:97:LEU:HD13	1:A:121:LEU:HD22	2.03	0.41
1:B:304:ALA:HA	1:B:367:LEU:HD22	2.02	0.41
1:A:211:ARG:CG	1:B:519:TRP:CH2	3.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:194:TRP:O	1:B:197:HIS:HD2	2.04	0.41
1:A:188:THR:HB	1:A:189:PRO:HD2	2.03	0.41
1:A:248:PRO:HA	1:B:255:SER:O	2.20	0.41
1:A:106:SER:HB3	1:A:422:HIS:CE1	2.54	0.41
1:B:283:LEU:HA	1:B:284:PRO:HD3	1.94	0.40
1:B:242:PHE:HA	1:B:243:PRO:HD3	1.86	0.40
1:B:62:HIS:O	1:B:481:LYS:HE3	2.21	0.40
1:B:76:ALA:HA	1:B:77:PRO:HD2	1.97	0.40
1:A:188:THR:C	1:A:190:TYR:N	2.75	0.40
1:A:411:LEU:HD23	1:A:411:LEU:HA	1.78	0.40
1:B:428:ILE:HD11	1:B:503:TYR:HB3	2.04	0.40
1:B:425:PHE:HB3	1:B:469:VAL:HB	2.04	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	546/560 (98%)	494 (90%)	44 (8%)	8 (2%)	12	30
1	B	546/560 (98%)	518 (95%)	23 (4%)	5 (1%)	20	46
All	All	1092/1120 (98%)	1012 (93%)	67 (6%)	13 (1%)	15	37

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	297	ARG
1	B	418	PRO
1	A	199	GLY
1	A	231	GLU
1	B	169	PRO
1	A	274	ARG

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Mol	Chain	Res	Type
1	A	13	PRO
1	A	418	PRO
1	B	157	ALA
1	A	296	ILE
1	B	431	VAL
1	B	390	PRO
1	A	230	PRO

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	470/482 (98%)	415 (88%)	55 (12%)	6	14
1	B	470/482 (98%)	420 (89%)	50 (11%)	8	18
All	All	940/964 (98%)	835 (89%)	105 (11%)	7	16

All (105) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	PHE
1	A	11	THR
1	A	16	LEU
1	A	18	LEU
1	A	25	ILE
1	A	28	ILE
1	A	41	SER
1	A	79	ASN
1	A	84	GLN
1	A	94	SER
1	A	95	PHE
1	A	99	PRO
1	A	106	SER
1	A	118	SER
1	A	132	GLU
1	A	149	HIS

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Mol	Chain	Res	Type
1	A	161	ARG
1	A	177	LEU
1	A	200	MET
1	A	211	ARG
1	A	217	LEU
1	A	222	ARG
1	A	231	GLU
1	A	264	LYS
1	A	283	LEU
1	A	296	ILE
1	A	297	ARG
1	A	301	LEU
1	A	303	MET
1	A	310	THR
1	A	329	SER
1	A	331	THR
1	A	336	ASP
1	A	344	LYS
1	A	346	LEU
1	A	363	ILE
1	A	381	VAL
1	A	396	ARG
1	A	399	ASP
1	A	407	THR
1	A	411	LEU
1	A	412	LYS
1	A	422	HIS
1	A	432	SER
1	A	467	HIS
1	A	475	LYS
1	A	478	LEU
1	A	498	ASN
1	A	502	GLU
1	A	503	TYR
1	A	504	ARG
1	A	516	THR
1	A	523	SER
1	A	551	SER
1	A	552	GLN
1	B	8	ARG
1	B	18	LEU
1	B	25	ILE

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Mol	Chain	Res	Type
1	B	26	GLN
1	B	29	ILE
1	B	41	SER
1	B	52	MET
1	B	53	LYS
1	B	63	VAL
1	B	74	ILE
1	B	79	ASN
1	B	95	PHE
1	B	128	ASN
1	B	142	VAL
1	B	158	ASN
1	B	161	ARG
1	B	163	LYS
1	B	177	LEU
1	B	188	THR
1	B	195	MET
1	B	197	HIS
1	B	211	ARG
1	B	217	LEU
1	B	231	GLU
1	B	237	LYS
1	B	297	ARG
1	B	301	LEU
1	B	310	THR
1	B	336	ASP
1	B	338	GLU
1	B	341	LYS
1	B	344	LYS
1	B	363	ILE
1	B	372	LYS
1	B	373	ASP
1	B	396	ARG
1	B	407	THR
1	B	412	LYS
1	B	422	HIS
1	B	426	SER
1	B	430	LYS
1	B	432	SER
1	B	448	GLN
1	B	457	THR
1	B	467	HIS

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Mol	Chain	Res	Type
1	B	472	VAL
1	B	503	TYR
1	B	513	ILE
1	B	516	THR
1	B	540	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	79	ASN
1	A	197	HIS
1	A	240	HIS
1	A	352	ASN
1	A	467	HIS
1	A	498	ASN
1	A	520	ASN
1	A	552	GLN
1	A	555	HIS
1	B	79	ASN
1	B	197	HIS
1	B	240	HIS
1	B	352	ASN
1	B	467	HIS
1	B	520	ASN
1	B	552	GLN

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

4 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	FAD	A	1561	1	51,58,58	1.35	6 (11%)	54,89,89	1.98	6 (11%)
3	EUG	A	1562	-	11,11,12	1.75	1 (9%)	14,14,15	1.36	2 (14%)
2	FAD	B	1561	1	51,58,58	1.32	6 (11%)	54,89,89	2.03	7 (12%)
3	EUG	B	1562	-	11,11,12	1.73	1 (9%)	14,14,15	1.42	2 (14%)

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	FAD	A	1561	1	-	0/28/50/50	0/6/6/6
3	EUG	A	1562	-	-	0/4/4/5	0/1/1/1
2	FAD	B	1561	1	-	0/28/50/50	0/6/6/6
3	EUG	B	1562	-	-	0/4/4/5	0/1/1/1

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1561	FAD	C2A-N1A	2.07	1.37	1.33
2	B	1561	FAD	C2A-N1A	2.37	1.38	1.33
2	B	1561	FAD	C1'-N10	2.64	1.51	1.48
2	A	1561	FAD	C4X-N5	3.00	1.37	1.33
2	A	1561	FAD	C4-N3	3.01	1.38	1.33
2	B	1561	FAD	C4-N3	3.19	1.38	1.33
2	B	1561	FAD	C4X-N5	3.24	1.38	1.33
2	A	1561	FAD	C1'-N10	3.39	1.51	1.48
2	B	1561	FAD	C10-N1	3.69	1.38	1.33
2	A	1561	FAD	C2A-N3A	3.71	1.38	1.32
2	B	1561	FAD	C2A-N3A	4.04	1.38	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1561	FAD	C10-N1	4.33	1.39	1.33
3	A	1562	EUG	C4-C3	5.13	1.48	1.40
3	B	1562	EUG	C4-C3	5.26	1.48	1.40

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1561	FAD	N3A-C2A-N1A	-10.07	120.09	128.86
2	A	1561	FAD	N3A-C2A-N1A	-9.82	120.31	128.86
2	B	1561	FAD	C4X-C4-N3	-2.88	119.38	123.48
2	A	1561	FAD	C4X-C4-N3	-2.34	120.15	123.48
3	A	1562	EUG	C9-O3-C3	2.19	120.68	117.54
3	B	1562	EUG	C9-O3-C3	2.32	120.88	117.54
2	B	1561	FAD	C4X-N5-C5X	2.72	119.63	116.76
2	A	1561	FAD	C4X-N5-C5X	3.01	119.94	116.76
2	B	1561	FAD	C4B-O4B-C1B	3.14	113.11	109.77
2	B	1561	FAD	C5X-C9A-N10	3.26	120.08	117.66
3	A	1562	EUG	O3-C3-C4	3.68	119.03	114.55
3	B	1562	EUG	O3-C3-C4	3.79	119.17	114.55
2	A	1561	FAD	C5X-C9A-N10	4.41	120.93	117.66
2	A	1561	FAD	C1'-N10-C9A	4.64	122.60	118.35
2	B	1561	FAD	C1'-N10-C9A	4.76	122.71	118.35
2	B	1561	FAD	C4-N3-C2	5.78	120.21	115.16
2	A	1561	FAD	C4-N3-C2	5.81	120.24	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1562	EUG	1	0
2	B	1561	FAD	2	0
3	B	1562	EUG	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	550/560 (98%)	-0.29	2 (0%) 92 93	41, 52, 68, 79	0
1	B	550/560 (98%)	0.14	11 (2%) 65 66	53, 73, 104, 115	0
All	All	1100/1120 (98%)	-0.07	13 (1%) 79 80	41, 61, 97, 115	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	157	ALA	3.8
1	B	347	ASN	3.4
1	B	7	PHE	3.0
1	A	159	ASN	2.6
1	B	24	PHE	2.4
1	B	93	PHE	2.3
1	B	448	GLN	2.3
1	B	180	ALA	2.2
1	A	157	ALA	2.2
1	B	365	ARG	2.1
1	B	184	GLY	2.1
1	B	194	TRP	2.1
1	B	158	ASN	2.1

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
3	EUG	B	1562	11/12	0.95	0.29	2.27	84,85,88,88	0
3	EUG	A	1562	11/12	0.90	0.26	1.87	69,69,71,73	0
2	FAD	A	1561	53/53	0.96	0.16	0.38	53,61,64,65	0
2	FAD	B	1561	53/53	0.96	0.20	0.03	68,76,80,81	0

6.5 Other polymers [i](#)

There are no such residues in this entry.