



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 14, 2021 – 07:03 pm GMT

PDB ID : 7Q2J
Title : Quaternary Complex of human WDR5 and pVHL:ElonginC:ElonginB bound to PROTAC Homer
Authors : Kraemer, A.; Doelle, A.; Schwalm, M.P.; Adhikari, B.; Wolf, E.; Knapp, S.; Structural Genomics Consortium (SGC)
Deposited on : 2021-10-25
Resolution : 2.50 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.4 (270009), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.23.2
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0267
CCP4 : 7.1.010 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

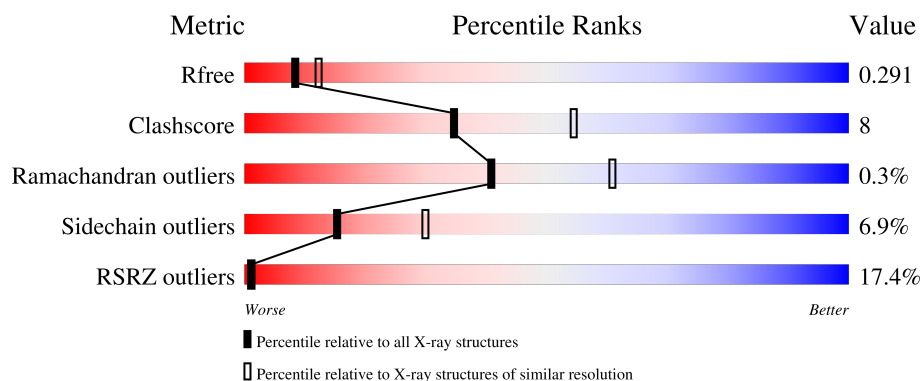
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	104	<div> <div>12%</div> <div>82%</div> <div>15%</div> <div>..</div> </div>
2	B	97	<div> <div>11%</div> <div>71%</div> <div>19%</div> <div>9%</div> </div>
3	C	197	<div> <div>14%</div> <div>47%</div> <div>26%</div> <div>25%</div> </div>
4	D	312	<div> <div>19%</div> <div>79%</div> <div>18%</div> <div>..</div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5028 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 Elongin-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	103	Total	C	N	O	S	0	0	0
			787	497	131	155	4			

- Molecule 2 is a protein called Elongin-C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	88	Total	C	N	O	S	0	0	0
			698	451	112	128	7			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	16	MET	-	initiating methionine	UNP Q15369

- Molecule 3 is a protein called von Hippel-Lindau disease tumor suppressor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	147	Total	C	N	O	S	0	0	0
			1167	742	212	211	2			

There are 37 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	17	MET	-	initiating methionine	UNP P40337
C	18	ASN	-	expression tag	UNP P40337
C	19	THR	-	expression tag	UNP P40337
C	20	ILE	-	expression tag	UNP P40337
C	21	HIS	-	expression tag	UNP P40337
C	22	HIS	-	expression tag	UNP P40337
C	23	HIS	-	expression tag	UNP P40337
C	24	HIS	-	expression tag	UNP P40337
C	25	HIS	-	expression tag	UNP P40337

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Chain	Residue	Modelled	Actual	Comment	Reference
C	26	HIS	-	expression tag	UNP P40337
C	27	ASN	-	expression tag	UNP P40337
C	28	THR	-	expression tag	UNP P40337
C	29	SER	-	expression tag	UNP P40337
C	30	GLY	-	expression tag	UNP P40337
C	31	SER	-	expression tag	UNP P40337
C	32	GLY	-	expression tag	UNP P40337
C	33	GLY	-	expression tag	UNP P40337
C	34	GLY	-	expression tag	UNP P40337
C	35	GLY	-	expression tag	UNP P40337
C	36	GLY	-	expression tag	UNP P40337
C	37	ARG	-	expression tag	UNP P40337
C	38	LEU	-	expression tag	UNP P40337
C	39	VAL	-	expression tag	UNP P40337
C	40	PRO	-	expression tag	UNP P40337
C	41	ARG	-	expression tag	UNP P40337
C	42	GLY	-	expression tag	UNP P40337
C	43	SER	-	expression tag	UNP P40337
C	44	MET	-	expression tag	UNP P40337
C	45	SER	-	expression tag	UNP P40337
C	46	GLU	-	expression tag	UNP P40337
C	47	ASN	-	expression tag	UNP P40337
C	48	LEU	-	expression tag	UNP P40337
C	49	TYR	-	expression tag	UNP P40337
C	50	PHE	-	expression tag	UNP P40337
C	51	GLN	-	expression tag	UNP P40337
C	52	GLY	-	expression tag	UNP P40337
C	53	SER	-	expression tag	UNP P40337

- Molecule 4 is a protein called WD repeat-containing protein 5.

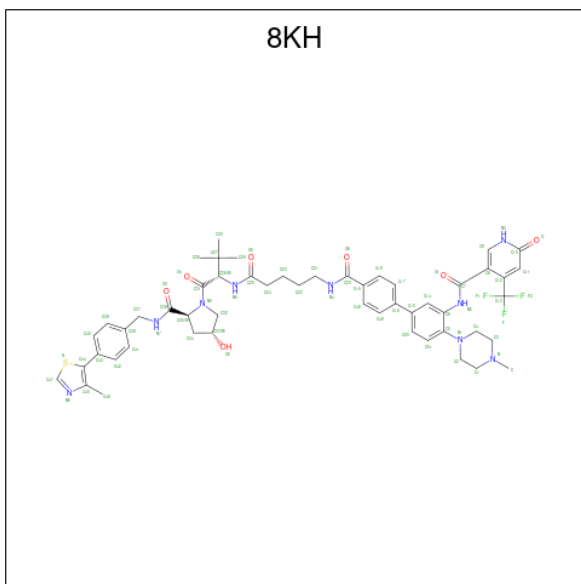
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	304	Total	C	N	O	S	0	0	0
			2280	1454	375	442	9			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	23	GLY	-	expression tag	UNP P61964

- Molecule 5 is N-[5-[4-[[5-[[[(2S)-3,3-dimethyl-1-[(2S,4R)-2-[[4-(4-methyl-1,3-thiazol-5-yl)phenyl]methylcarbamoyl]-4-oxidanyl-pyrrolidin-1-yl]-1-oxidanylidene-butan-2-yl]amino]-

5-oxidanylidene-pentyl]carbamoyl]phenyl]-2-(4-methylpiperazin-1-yl)phenyl]-6-oxidanylidene-4-(trifluoromethyl)-1H-pyridine-3-carboxamide (three-letter code: 8KH) (formula: $C_{52}H_{60}F_3N_9O_7S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	D	1	Total	C	F	N	O	0	0
			72	52	3	9	7		

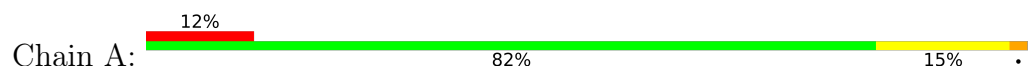
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	6	Total	O	0	0
			6	6		
6	B	1	Total	O	0	0
			1	1		
6	C	3	Total	O	0	0
			3	3		
6	D	14	Total	O	0	0
			14	14		

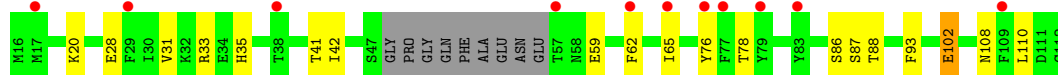
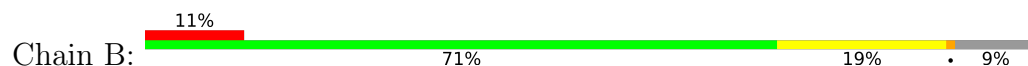
3 Residue-property plots [i](#)

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.

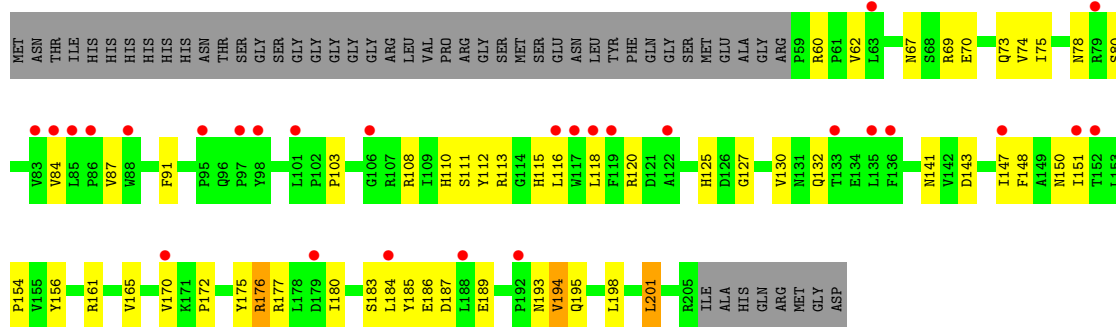
• Molecule 1: Elongin-B



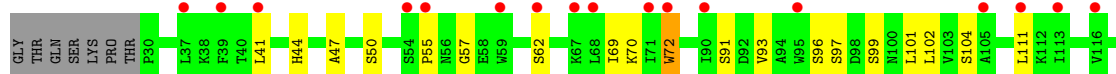
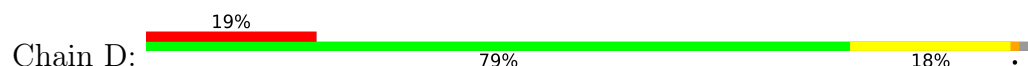
• Molecule 2: Elongin-C

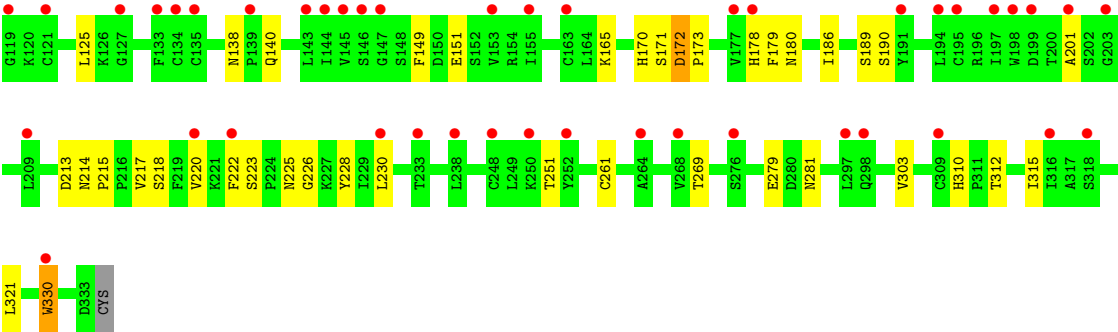


• Molecule 3: von Hippel-Lindau disease tumor suppressor



• Molecule 4: WD repeat-containing protein 5





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	47.70Å 190.81Å 48.70Å 90.00° 115.25° 90.00°	Depositor
Resolution (Å)	47.75 – 2.50 47.70 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.3 (47.75-2.50) 99.3 (47.70-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.80 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.243 , 0.293 0.247 , 0.291	Depositor DCC
R_{free} test set	1368 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	46.1	Xtriage
Anisotropy	1.087	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.014 for l,-k,h	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5028	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.13% 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: 8KH

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	0/803	0.81	0/1090
2	B	0.69	0/712	0.80	0/960
3	C	0.68	0/1199	0.83	0/1642
4	D	0.70	0/2337	0.81	0/3192
All	All	0.69	0/5051	0.81	0/6884

There are no bond length outliers.

There are no bond angle outliers.

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	787	0	756	11	0
2	B	698	0	693	11	0
3	C	1167	0	1133	27	0
4	D	2280	0	2157	36	0
5	D	72	0	0	2	0
6	A	6	0	0	0	0
6	B	1	0	0	0	0
6	C	3	0	0	0	0
6	D	14	0	0	0	0
All	All	5028	0	4739	81	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 8.

All (81) 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:B:87:SER:HA	3:C:132:GLN:OE1	1.78	0.83
3:C:172:PRO:HA	3:C:175:TYR:CE1	2.17	0.79
3:C:161:ARG:O	3:C:165:VAL:HG23	1.85	0.77
4:D:218:SER:HB2	4:D:261:CYS:HA	1.70	0.73
3:C:172:PRO:HA	3:C:175:TYR:CD1	2.24	0.72
4:D:279:GLU:HA	4:D:303:VAL:HG13	1.76	0.67
3:C:73:GLN:OE1	3:C:110:HIS:ND1	2.28	0.67
3:C:176:ARG:HA	3:C:185:TYR:CE1	2.30	0.66
4:D:178:HIS:HD2	4:D:222:PHE:H	1.42	0.65
4:D:225:ASN:OD1	4:D:226:GLY:N	2.31	0.64
4:D:189:SER:HB2	4:D:217:VAL:HG12	1.80	0.63
2:B:62:PHE:CD1	2:B:65:ILE:HD12	2.34	0.62
2:B:108:ASN:ND2	3:C:184:LEU:HD21	2.16	0.61
4:D:220:VAL:HA	4:D:230:LEU:O	2.04	0.58
2:B:87:SER:CA	3:C:132:GLN:OE1	2.51	0.58
4:D:165:LYS:NZ	4:D:201:ALA:O	2.29	0.58
3:C:120:ARG:HD2	3:C:127:GLY:HA2	1.86	0.58
1:A:81:ALA:O	1:A:84:THR:HG22	2.04	0.56
3:C:67:ASN:HB2	3:C:91:PHE:CE1	2.41	0.56
4:D:41:LEU:HD12	4:D:41:LEU:N	2.20	0.56
3:C:73:GLN:HG2	3:C:108:ARG:NH2	2.21	0.55
4:D:93:VAL:HG22	4:D:102:LEU:HD11	1.89	0.55
3:C:176:ARG:NH2	3:C:189:GLU:OE1	2.40	0.55
2:B:20:LYS:HB3	2:B:59:GLU:HG2	1.89	0.55
1:A:97:PRO:HD2	2:B:102:GLU:OE1	2.06	0.55
4:D:57:GLY:O	4:D:310:HIS:CE1	2.60	0.54
4:D:149:PHE:HA	4:D:173:PRO:HB3	1.88	0.54
3:C:74:VAL:HG12	3:C:147:ILE:HB	1.90	0.54
4:D:55:PRO:HD2	4:D:99:SER:OG	2.10	0.52
4:D:178:HIS:CD2	4:D:222:PHE:H	2.26	0.51
4:D:330:TRP:CD1	4:D:330:TRP:N	2.78	0.51
1:A:56:THR:OG1	1:A:59:GLU:HB2	2.12	0.50
3:C:177:ARG:HH11	3:C:177:ARG:HG3	1.76	0.50
3:C:120:ARG:NH1	3:C:125:HIS:O	2.44	0.50
4:D:93:VAL:CG2	4:D:102:LEU:HD11	2.42	0.49
3:C:78:ASN:ND2	3:C:103:PRO:HA	2.28	0.48
2:B:76:TYR:HA	2:B:93:PHE:CE2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:198:LEU:HA	3:C:201:LEU:HD12	1.96	0.48
4:D:180:ASN:HB3	4:D:222:PHE:CE2	2.49	0.47
2:B:41:THR:HB	2:B:110:LEU:HA	1.96	0.47
3:C:154:PRO:HG2	3:C:156:TYR:CE1	2.49	0.47
3:C:194:VAL:O	3:C:198:LEU:HG	2.14	0.47
4:D:214:ASN:N	4:D:215:PRO:HD3	2.30	0.47
1:A:6:MET:HE3	1:A:8:ARG:HD2	1.97	0.47
4:D:172:ASP:HB3	4:D:173:PRO:CD	2.44	0.47
4:D:213:ASP:C	4:D:215:PRO:HD3	2.35	0.47
4:D:47:ALA:HB1	4:D:321:LEU:HA	1.97	0.46
3:C:84:VAL:HG11	3:C:151:ILE:HD13	1.98	0.46
4:D:310:HIS:HD2	4:D:312:THR:H	1.63	0.46
1:A:24:VAL:HG23	1:A:53:ASP:HA	1.98	0.46
4:D:69:ILE:HD11	4:D:104:SER:HB3	1.97	0.46
2:B:42:ILE:HG13	2:B:110:LEU:HD22	1.97	0.46
2:B:35:HIS:ND1	2:B:78:THR:HA	2.32	0.45
3:C:184:LEU:HA	3:C:187:ASP:HB2	1.99	0.45
1:A:24:VAL:CG2	1:A:53:ASP:HA	2.47	0.44
4:D:151:GLU:HB3	4:D:170:HIS:O	2.17	0.44
3:C:177:ARG:HG3	3:C:177:ARG:NH1	2.33	0.44
1:A:37:ARG:HH11	1:A:37:ARG:HG3	1.83	0.43
4:D:269:THR:HB	4:D:312:THR:O	2.18	0.43
4:D:57:GLY:O	4:D:310:HIS:HE1	2.00	0.43
4:D:62:SER:O	4:D:69:ILE:HA	2.19	0.43
3:C:87:VAL:HB	3:C:118:LEU:HD12	1.99	0.43
3:C:75:ILE:HD13	3:C:108:ARG:HA	2.01	0.42
4:D:44:HIS:CE1	4:D:70:LYS:HG3	2.53	0.42
2:B:86:SER:OG	2:B:88:THR:HG22	2.19	0.42
1:A:40:ASP:N	1:A:40:ASP:OD1	2.52	0.42
4:D:179:PHE:CZ	4:D:186:ILE:HD11	2.55	0.42
4:D:179:PHE:CE1	4:D:186:ILE:HD11	2.55	0.42
3:C:130:VAL:HA	3:C:150:ASN:O	2.20	0.41
4:D:138:ASN:HA	4:D:179:PHE:CD2	2.55	0.41
3:C:111:SER:OG	3:C:112:TYR:N	2.53	0.41
1:A:4:PHE:CD1	1:A:17:ASP:HB3	2.56	0.41
4:D:310:HIS:HB2	4:D:315:ILE:HB	2.02	0.41
4:D:41:LEU:HD23	4:D:72:TRP:CD2	2.56	0.41
4:D:96:SER:HB3	4:D:101:LEU:HB2	2.03	0.41
4:D:91:SER:OG	5:D:401:8KH:N2	2.54	0.41
4:D:170:HIS:CG	4:D:190:SER:CB	3.04	0.41
4:D:111:LEU:HB2	4:D:125:LEU:HB2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4:PHE:CE2	1:A:69:PRO:HG3	2.57	0.40
1:A:8:ARG:HB2	1:A:90:ILE:HD12	2.04	0.40
3:C:115:HIS:ND1	5:D:401:8KH:O2	2.54	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	101/104 (97%)	94 (93%)	5 (5%)	2 (2%)	7	12
2	B	84/97 (87%)	78 (93%)	6 (7%)	0	100	100
3	C	145/197 (74%)	128 (88%)	17 (12%)	0	100	100
4	D	302/312 (97%)	266 (88%)	36 (12%)	0	100	100
All	All	632/710 (89%)	566 (90%)	64 (10%)	2 (0%)	41	61

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	47	ASP
1	A	94	SER

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	84/92 (91%)	81 (96%)	3 (4%)	35	61
2	B	77/86 (90%)	73 (95%)	4 (5%)	23	44
3	C	129/176 (73%)	110 (85%)	19 (15%)	3	5
4	D	245/273 (90%)	234 (96%)	11 (4%)	27	51
All	All	535/627 (85%)	498 (93%)	37 (7%)	15	30

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	VAL
1	A	6	MET
1	A	59	GLU
2	B	28	GLU
2	B	31	VAL
2	B	33	ARG
2	B	102	GLU
3	C	60	ARG
3	C	62	VAL
3	C	69	ARG
3	C	70	GLU
3	C	80	SER
3	C	113	ARG
3	C	116	LEU
3	C	141	ASN
3	C	143	ASP
3	C	148	PHE
3	C	170	VAL
3	C	176	ARG
3	C	180	ILE
3	C	183	SER
3	C	186	GLU
3	C	193	ASN
3	C	194	VAL
3	C	195	GLN
3	C	201	LEU
4	D	50	SER
4	D	72	TRP
4	D	97	SER
4	D	140	GLN
4	D	171	SER
4	D	172	ASP
4	D	223	SER

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Mol	Chain	Res	Type
4	D	228	TYR
4	D	251	THR
4	D	281	ASN
4	D	330	TRP

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

Mol	Chain	Res	Type
2	B	27	HIS
3	C	174	ASN
3	C	193	ASN
4	D	170	HIS
4	D	178	HIS
4	D	265	ASN
4	D	289	GLN
4	D	310	HIS
4	D	323	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 ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

1 ligand is modelled in this entry.

There are no bond length outliers.

There are no bond angle outliers.

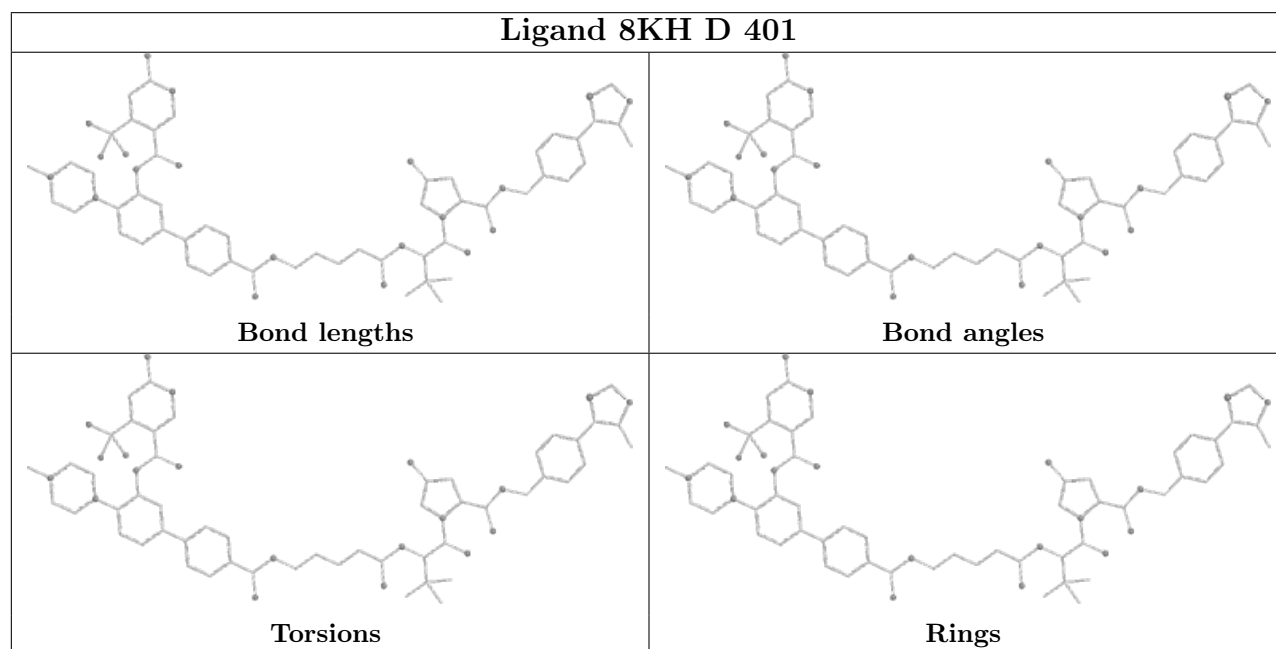
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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	103/104 (99%)	1.09	13 (12%) 3 3	56, 81, 100, 115	0
2	B	88/97 (90%)	1.16	11 (12%) 3 3	51, 69, 90, 113	0
3	C	147/197 (74%)	1.24	28 (19%) 1 1	47, 72, 98, 120	0
4	D	304/312 (97%)	1.26	60 (19%) 1 1	52, 71, 94, 115	0
All	All	642/710 (90%)	1.21	112 (17%) 1 1	47, 72, 96, 120	0

All (112) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	198	TRP	5.2
4	D	248	CYS	5.1
1	A	102	VAL	4.8
4	D	194	LEU	4.5
3	C	98	TYR	4.0
3	C	122	ALA	3.9
4	D	252	TYR	3.8
1	A	76	GLY	3.8
4	D	146	SER	3.7
1	A	34	ILE	3.7
4	D	209	LEU	3.6
4	D	72	TRP	3.5
3	C	152	THR	3.4
4	D	54	SER	3.4
4	D	55	PRO	3.3
2	B	57	THR	3.3
4	D	135	CYS	3.2
3	C	151	ILE	3.1
4	D	268	VAL	3.1
1	A	79	PHE	3.1
1	A	5	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
4	D	330	TRP	3.0
2	B	17	MET	3.0
3	C	135	LEU	3.0
3	C	188	LEU	3.0
4	D	191	TYR	2.9
4	D	222	PHE	2.9
4	D	59	TRP	2.9
4	D	37	LEU	2.9
4	D	233	THR	2.9
4	D	90	ILE	2.9
4	D	238	LEU	2.9
1	A	77	LEU	2.8
1	A	75	VAL	2.8
2	B	62	PHE	2.8
4	D	113	ILE	2.8
3	C	170	VAL	2.8
2	B	77	PHE	2.8
3	C	136	PHE	2.8
4	D	133	PHE	2.8
4	D	119	GLY	2.8
3	C	118	LEU	2.7
3	C	117	TRP	2.7
4	D	71	ILE	2.7
4	D	250	LYS	2.7
2	B	83	TYR	2.7
4	D	62	SER	2.6
4	D	68	LEU	2.6
3	C	97	PRO	2.6
4	D	41	LEU	2.6
4	D	39	PHE	2.6
4	D	144	ILE	2.6
3	C	63	LEU	2.6
3	C	85	LEU	2.5
1	A	74	THR	2.5
4	D	298	GLN	2.5
2	B	79	TYR	2.5
4	D	178	HIS	2.5
2	B	38	THR	2.5
3	C	95	PRO	2.5
1	A	80	ARG	2.4
2	B	76	TYR	2.4
2	B	65	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
4	D	316	ILE	2.4
1	A	84	THR	2.4
3	C	86	PRO	2.4
1	A	24	VAL	2.4
4	D	230	LEU	2.4
4	D	147	GLY	2.4
4	D	199	ASP	2.4
4	D	163	CYS	2.4
1	A	51	LEU	2.3
3	C	116	LEU	2.3
4	D	143	LEU	2.3
3	C	83	VAL	2.3
3	C	119	PHE	2.3
4	D	264	ALA	2.3
4	D	145	VAL	2.3
1	A	64	SER	2.3
4	D	203	GLY	2.3
3	C	184	LEU	2.3
3	C	84	VAL	2.2
4	D	318	SER	2.2
4	D	95	TRP	2.2
4	D	297	LEU	2.2
3	C	88	TRP	2.2
4	D	116	VAL	2.2
3	C	179	ASP	2.1
4	D	153	VAL	2.1
4	D	220	VAL	2.1
4	D	276	SER	2.1
4	D	105	ALA	2.1
4	D	177	VAL	2.1
2	B	29	PHE	2.1
4	D	195	CYS	2.1
3	C	192	PRO	2.1
4	D	134	CYS	2.1
4	D	155	ILE	2.1
2	B	109	PHE	2.1
4	D	201	ALA	2.1
3	C	106	GLY	2.1
4	D	139	PRO	2.1
4	D	309	CYS	2.1
4	D	67	LYS	2.1
3	C	147	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
4	D	127	GLY	2.0
3	C	133	THR	2.0
3	C	101	LEU	2.0
4	D	121	CYS	2.0
3	C	79	ARG	2.0
4	D	111	LEU	2.0
4	D	197	ILE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

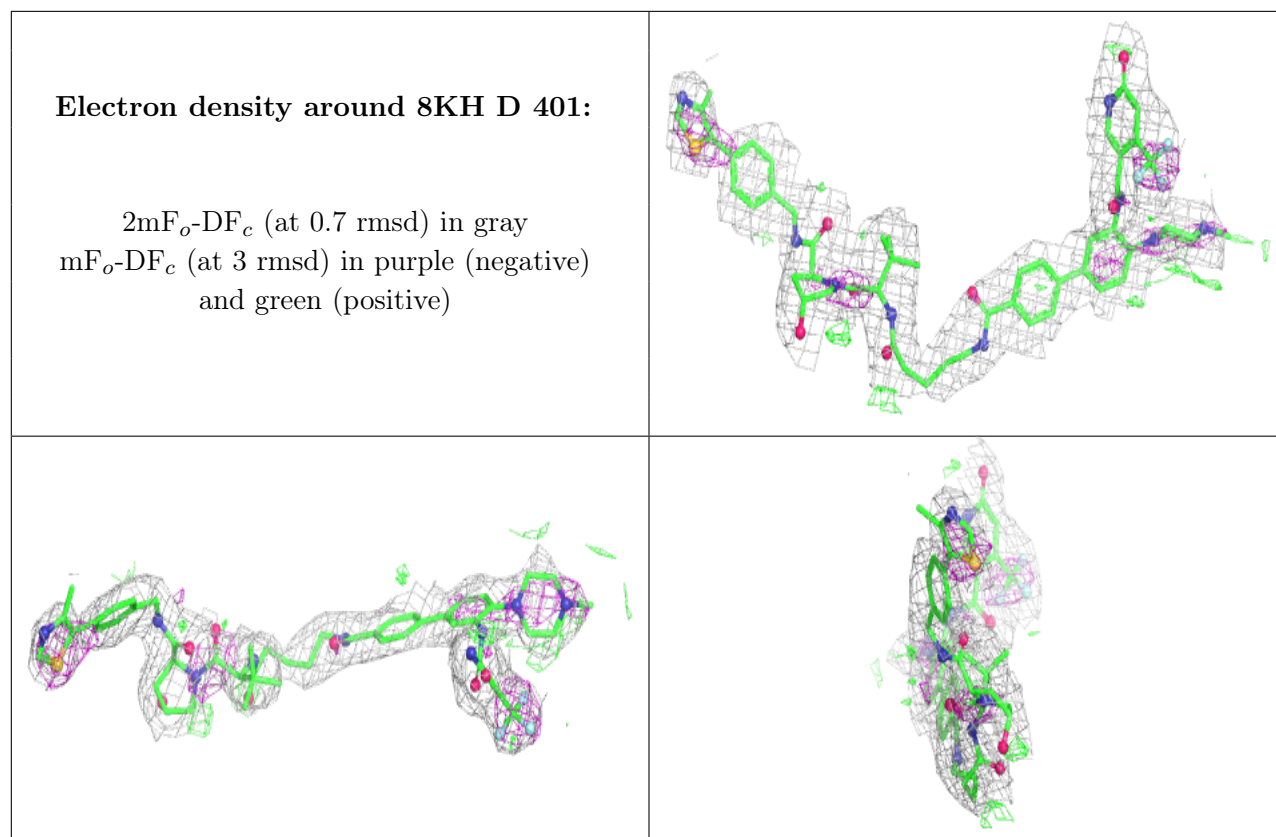
There are no monosaccharides in this entry.

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(\AA^2)	Q<0.9
5	8KH	D	401	72/72	0.81	0.25	54,66,77,87	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.